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Title:
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd
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2: pir2:*
3: pir3:*
4: pir4:*
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Listing first 45 summaries
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S31686
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R:Quishier A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.;
R:Quishier A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.;
R:Quishier A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.;
Submitted to the EMBL Data Library, June 1992

A; Description: Mechanisms that generate human immunoglobulin
A; Description: S31686
A; Accession: S31686
A; Accession: S31686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain V region - human (fragment) (Species: Homo sapiens (man) (C;Species: 22-Nov-1993 #sequence_revision 10-N (C;AccessTon: $31585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molegule type: mRNA
A; Molegule type: mRNA
A; Molegule type: mRNA
A; Residues: 1-140 <CUI>
A; Residues: 1-140 <CUI>
A; Cross references: EMBL: 214205; NID: g30969; PIDN: CAA78574.1; PID: g30970
C; Superfamily: inmunoglobulin V region: immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin C: Keywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-NOV-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31588
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
C;Accession: S1588
A;Reciperence number: S31588
A;Reference number: S31588
A;Recession: S31588
A;Accession: S31588
A;Rolecule type: manual
A;Residues: 1-140 <CUID
A;Cross -references: EMBL:Z14200; NID:330957; PIDN:CAA78569.1; PID:330958
A;Cross -references: EMBL:Z14200; NID:330957; PIDN:CAA78569.1; PID:330958
C;Superfamily: immunoglobulin v region; immunoglobulin homology
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S46390
S31105
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S26889
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S460943
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pred. No. 6.7e-43;
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                              #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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S31598
immunoglobulin diversity operate from
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g heavy chain V r
                          Tonnelle, C.
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C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

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C;Superfamily: in
C;Keywords: hete
F;15-98/Domain:
                                                                                                                                                                                                                                       Ig heavy chain . C: Species: Homo C: Date: 02-Dec-C: Accession: S3
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Kupwords: heterotetramer; immunoglobulin
C;Kupwords: heterotetramer; immunoglobulin
                                                                 A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Moslecule type: mRNA A:Residues: 1-123 <RAA>
                                                                                                                                          R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; pMID:1730252
                                                                                                                                                                                                                      C; Accession: S31114
R; Raaphorst, F.M.; T
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                                                                                                                                                                                                                  Species: Homo sapiens (man)
Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A/Gross-references: EMBL:X62955
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31107
R;Raphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Accession: S31107
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Accession: S31107
A;Accession: S31107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1~119 < RAA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary; nucleic acid sequence not shown; translation not
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                                                                                                                                                                                                                                                                                                                                                                                                      EVOLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
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                                                                                                                                                                                                                                                                                      - human
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' Score 551.5; DB 2; 1
s; Pred. No. 1.6e-42;
" "*smatches 2;
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Pred. No. 1.5e-42;
6; Mismatches 3
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A;Cross-references; EMBL:X62956
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterofetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 02-Dac-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31108
E;Raaphorst, F.M., Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
A;Accession: S31108
                                                                                                                        A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Residues: 1-119 <RAA>
                                                                                                                                                                                                                                                                                                                      Ig heavy chain - human
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Schroeder Jr., H.W; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable , A;Accession: C36005, MUID:90349571; PMID:2117273
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
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Best Local Similarity 87.8
Thes 108; Conservative
                                   loca!
          al Similarity 89.0
                                                                                                                                                                                                                                                                                                                                                                 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLLESGGGIVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY 60
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                    89.7%;
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89.9%;
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Score 545.5;
Pred. No. 5.5e
4; Mismatches
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Pred. No. 2.4e-42;
5; Mismatches 4; Indels 3
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Pred. No. 1.6e-42;
4; Mismatches 4
             DB 2;
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                      Length 119;
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Indels

Gaps

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RESULT 7

$31666

Ig heavy chain V region - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Accession: $31666
R; Culsinier, A. M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A; Description: Mechanisms that generate human immunoglobulin diversity operate from A; Reference number: $31585
A; Accession: $31666
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-138 <CUI>A; Cross-references: EMBL: 214202; NID: 930963; PIDN: CAA78571.1; PID: 930964
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterortetramer; immunoglobulin
C; Keywords: heterortetramer; immunoglobulin
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                                                                                                                                                                        A;Cross-references: EMBL:Z46382; NID:g562324; PIDN:CAA86521.1; PID:g1340167 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-120 <MAH>
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Conservative
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Pred. No. 6.4e-42;
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                                                                                                                    Score 545; DB 2;
Pred. No. 6.le-42;
4; Mismatches 5
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-124 <MOR>
A;Residues: 1-124 <MOR>
A;Cross-references: EMBL:Z11946; NID:g33897; PIDN:CAA78003.1; PID:g33898
A;Cross-references: EMBL:Z11946; NID:g33897; PIDN:CAA78003.1; PID:g33898
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;15-98/Domain: immunoglobulin homology <IMM>
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D36005
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R;Schroeder Jr., H.W.; Wang, J.Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A;Title: Preferential utilization of conserved immunoglobulin A;Reference number: A36005; MUID:90349571; PMID:2117273

A;Accession: D36005
                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V region (M43) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990
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A;Cross-references: GDB:118731; OMIM:146910
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross_references: GB:M34024
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                  61 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKP---FPYFDYWGQGTLVTVSS 116
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Pred. No. 7.8e-42;
                                                                                                                   Score 538.5; DB 2;
Pred. No. 2.3e-41;
"""matches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, submittled to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a A;Reference number: S38488
A;Accession: S38489
                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-127 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995.#text_change 23-Jul-1999
C:Accession: S38489
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C; Superfamily: immunoglobulin V region;
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C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C:Accession: I55673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-121 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: I55673
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                                                                                                                                                                                                                                                      Similarity
      QGTLVTV 127
                                        QGTLVTV 114
                                                                    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKEGPFPASDYYDSSGYYSFDYWG
                                                                                         ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK--PFP-------YFDYWG
                                                                                                                                               QVQLVQSGGGVVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
                                                                                                                                                                     EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY 60
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Pred. No. 4.6e-41;
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Pred. No. 4.4e-41;
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                                                                                                                                                                                                                                                                 Length 127;
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C;Superfamily: immunoglobulin V region; im
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-144 < KIS2>
                                                                                                                                                                                                                                                                                                                                                                                                    R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains A;Reference number: S04601; MUID:89296497; PMID:2500644
                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S04602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-160 <KIS1>
A;Cross-references: EMBL:X14584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change C;Accession: S05271; S04602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:Z14201; NID:g30961; PIDN:CAA78570.1; PID:g30962 C;Superfamily: immunoglobulin v region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin c;Keywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Reference number: S31585 A;Accession: S31699 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, March 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13

S31699
C: Species: Homo sapiens (man)
C: Species: Homo sapiens (man)
C: Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C: Accession: S31699
C: Accession: S31699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: S05270 
A;Accession: S05271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Kishimoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain precursor - human (fragment)
C; Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
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                                                                                                                                                                                    Query Match
Best Local :
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                    61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK------PFPYF--DYWGQGTL 111
                                                                                    20
                                                                                                 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
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02; Conservative
ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAVVRGVISYYYYGMDVWGQGTT
                                                                            EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGGSTYY
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                                                                                                                                                                                                                                  ignal sequence #status predicted <SIG>
: Ig heavy chain (fragment) #status pr
immunoglobulin homology <IMM>
                                                                                                                                                             Conservative
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                                                                                                                                                       Score 526.5; DB 2;
Pred. No. 3.7e-40;
7; Mismatches 5;
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Pred. No. 3.1e-40;
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16-Aug-1996

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Gaps

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submitted to the EMBL Data Library, October 1992
A; Reference number: S30520
A; Recession: S30531
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-125 <MARD
A; Cross-references: EMBL: Z18317
C; Kuperfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
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Search completed: August 20, 2003, 12:42:13 Job time: 82.0602 secs
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140 VTVSS 144
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Scoring table:

Sequence: Title: Perfect score:

US-09-512-082-19 608

Minimum DB Maximum DB

seq length:
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Sequence Sequence Sequence

2, Appli 2, Appli 51, Appl 12, Appl 12, Appl 24, Appli 4, Appli 4, Appli 4, Appli

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20, Appl
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Database

Total number

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protein

Sequence Sequence Sequence

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

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4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
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Gapop 10.0 , Gapext 0.
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US-08-983-607-28
US-09-025-7698-38
US-09-025-7698-69
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US-08-974-899-6
US-08-98-1055-1
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US-08-98-925-11
US-08-362-780-11
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US-08-48-373C-21
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US-08-19-491-8
US-08-19-19-22
US-08-476-349A-99
US-08-476-349A-99
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US-08-983-607-28
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Patent NO. GINUATION:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
APPLICATION UMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MATY M. Krinsky
REGISTRATION NUMBER: 32423
REGISTRATION NUMBER: 32423
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: WORD PROCESSING
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983
FILING DATE: APPLI 27, 1998
CLASSIFICATION: 435
                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEPHORE: 203-773-1183
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" 1.44 Mb diskette
        ORIGINAL SOURCE:
ORGANISM: Homo sapi
ORGANISM: nized wit
INDIVIDUAL ISOLATE:
                                                                                          TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 266 Whit
CITY: New Haven
STATE: Connection
                                                                                                                        LENGTH: 131 residues
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
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          Homo sapiens (melanoma patient immu-
nized with autologous tumor cells)
ISOLATE: peripheral blood lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Molecular Biophysics and Biochemistry, Yale University
                                                                            polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/983,607
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US-08-983-607-46
US-08-428-197-26
US-08-428-197-28
US-08-428-197-28
PCT-US93-10555-24
PCT-US93-10555-28
US-08-428-197-2
PCT-US93-10555-28
US-08-983-607-51
PCT-US93-10555-2
US-08-983-607-51
US-08-983-607-51
US-08-08-437-6428-4
US-08-447-6428-4
US-08-146-206C-4
PCT-US93-00435-14
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                        Query Match
Best Local 9
          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 104;
                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                              NAME: James F. Haley, Jr., 1
REGISTION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MOI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0:
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                      FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF
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LIBRARY: DM414
LIBRARY: fUSE5
                     Local
                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS'
SOFTWARE: Patentin Pains-
                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE:
         105;
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                     Similarity
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                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09025769B
                                                                                                                                        120 amino acids
      Conservative
                                                                                                                                                                                (212)596-9090
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Plueckthun, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DM414 scFv antibodies obtained fUSE5 fusion phage construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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oney, Simon
                   88.7%;
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   Score 539; DB 4; Length 120, Pred. No. 5.7e-47; Findels 5; Indels
                                                                                                                                                                                                                                                      Esq.
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Pred. No. 2e-47;
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Gaps
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EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY

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Knappik, Achim

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'US-09-025-769B-178
Sequence 178, Application US/09025769B
Patent No. 630064
GENERAL INFORMATION:
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US-09-025-769B-63
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Best Local Similarity 87.5
Conservative
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APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: (18-AUG-1995)

ATTORNBY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Piteckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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SOFTWARE: Patentl
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CITY: New York
STATE: New Yor
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                                                                                                                             61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDFAVYYCAK----PFPYFDYWGGGTLYTVSS 116
                                                                                                                                                                             1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
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amino acid
GY: linear
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6300064
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87.5%;
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Pred. No. 5.7e-47;
6; Mismatches 5
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Pack, Peter Ilag, Vic

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; TOPOLOGY: 11; MOLECULE TYPE: US-09-025-769B-178
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acid
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Protein/(Poly)peptide libraries NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: EP 9: FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212)596-9000
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APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                      APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CDlia Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
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                                                                                                  STREET: 1 DNA way
CITY: South San Francisco
STATE: California
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Pred. No. 1.5e-46;
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GENERAL INFORMATION:
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Best Local Similarity
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                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/
EILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2
REFERENCE/DOCKET NUMBER: FD-2
TELECOMMUNICATION INFORMATION:
INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SILVERMAN TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
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LENGTH: 113 amino acids
TYPE: Amino Acid
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REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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ADDRESSEE: Spensley
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STATE: California
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                                                                                                                                                                                                CLASSIFICATION:
                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARG---FDYWGQGTLVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGDGGSTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08428197
                                                                                                                                                                                                                                                                                                                                                                                                                            E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
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650/952-9881
                                                                                                                                                                                                                                                                                                                                                                             USA
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                (619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SILVERMAN, GREGG J.
                                     (619) 455-5100
                  455-5110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THEREOF
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                                                                                                                                                              PCT/US93/10555
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Pred. No. 7.5e-47;
                                                                         FD-2630
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Gaps

SEQUENCE CHARACTERISTICS:

ENGTH:

125 amino acids

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RESULT 7
PCT-US93-10555-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                        TELEFAX: (619) 455-51 (NFORMATION FOR SEQ ID NO:
                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: HOWells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                  TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 10 //
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                STRANDEDNESS:
                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 29-001
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Los Angeles
California
                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                   90067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                                                                                     : (619) 455-5100
(619) 455-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                 linear
                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SILVERMAN, GREGG J.
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                                                                                   amino acids
              peptide
                                                                                                                                                                                                                                                                                  29-OCT-1993
                                                single,
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                                                                                                                                                                                                                                                                                               PCT/US93/10555
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Pred. No. 8.4e-47;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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US-08-983-607-36
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 203-773-1183
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 203-773-9544
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                       MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/9
FILING DATE: April 27, 1998
                                      IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Alan Garen
APPLICANT: Xiaohong C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                    ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: ZUS , TELEPH
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OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/IB
FILING DATE: June 28, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 266 Whit
                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hes 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Department of Molecular Biophysics ADDRESSEE: and Biochemistry, Yale University
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 VTVSS 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mary M. Krinsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Connecticut
                                                                                                                                                                                                                                                                                                                                                                 116 residues
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DM414 scFv antibodies obtained from
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1..125
                                                                                                                                                                                                       polypeptide
                                                                                                                                                                                                                                                                                                      single
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Pred. No. 8.4e-47;
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: LIBRARY: fUSE5 fusion phage construct

: CLONE: V474

: FEATURE: NAME/KEY: heavy chain

US-08-983-607-36
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US-07-988-925-11
                                                                                            ; MOLECULE TYPE: peptide US-07-988-925-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 102; Conservative
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                                              Query Match
Best Local Similarity
                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                         TELEFAX: 7038164100
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                       FILING DATE: 21-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29009
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206422.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB92/01933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Waldmann, Herman
TITLE OF INVENTION: antibody preparation
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS
LENGTH: 119 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                           TYPE: amino acid
STRANDEDNESS: Sir
                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                           ELEPHONE:
                                106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADSVKGRFTISRDNSKNTRYLOMNSLRAEDTAVYYCAKGVAPFDYWGEGTPVTVSS 116
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/07988925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Nixon and Vanderhye pc
lith Floor, 1100 No. 5585097th Glebe Road
                                                                                                                                                                        119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clark, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Routledge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gorman, Scott D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bolt, Sarah L
                                                                                                                               linear
                                                                                                                                                                                                                                              7038164000
                                                                                                                                           single
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87.9%;
                                              87.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/07/988,925
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                                Score 534.5; 1
Pred. No. 1.6e
2; Mismatches
                                <u>ب</u>
                           ; Dr
1.6e-46;
8;
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                                                                Length
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; STRANDEDNESS:
; TOPOLOGY: lin
; MOLECULE TYPE: |
US-08-362-780-11
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US-08-362-780-11
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            RESULT 11
US-09-069-821-3
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Sequence 3,
                                                                                                                                                                                        Matches 106;
                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/862,543

FILING DATE: 23-JUNE-1992

APPLICATION NUMBER: GB 9021679:7

FILING DATE: 05-OCT-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB91/01726

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29009
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Antibody Preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: bun
CTTY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                         Local Similarity 89.1
les 106; Conservative
                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKFRQYSGGFDYWGQGTLVTVSS 119
                                                                     ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKPEPY----FDYWGGGTLVTVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
Application US/0906982:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8th Floor, 1100
                                                                                                                                                                                                                                                                                                                        119 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gorman,
                                                                                                                                                                                                                                                                             SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                       7038164100
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h Floor, 1100 No. 5968509th Glebe Road
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89.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/362,780
                                                                                                                                                                                           2
                                                                                                                                                                                                         Score 534.5; DB 2
Pred. No. 1.6e-46;
                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                       DB 2;
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                                                                                                                                                                                                                       Length 119;
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RESULT 12
US-09-420-592A-6
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                                                                                                                                                                                                                                                            Query Match
-- Tocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LEE, LIHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/063,074 FILING DATE: 27-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 30-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: STERNE, KESSLER, STREET: 1100 NEW YORK AVE.,
                                                                                                                         190 YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGRXGXSLSGXYYYYHYFDYW 249
                                                                                                                                                                                       130 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGKTDGGST
                                                                250
                                                                                              107
                                                                                                                                           59 YYADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKP------FPYFDYW 106
                                                                                                                                                                                                       1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSS--GTT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                 GQGTLVTVSS 116
                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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KIM, JUDITH U.
00
                                                               GQGTLVTVSS 259
                                                                                                                                                                                                                                                                                                                                                                                                   263 amino acids
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                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WANG, MAOLIANG SHORR, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHITLOW, MARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILPULA,
                                                                                                                                                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                      87.3%;
80.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0977.2280003
                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GOLDSTEIN & FOX P.L.L.C
NW, SUITE 600
                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                     No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.30
                                                                                                                                                                                                                                                                          8
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                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 53, Application US/10039785 Patent No. 6538938
                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin V
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                         PRIOR APPLICATION NUMBER: 60/331,310 PRIOR FILING DATE: 2001-11-14 PRIOR APPLICATION NUMBER: 60/331,044
                                                                                                                                                                                                             CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
                                                                                                                                                                                                                                                       FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
                                                                                                                                                                                                                                                                                                                  APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
                                                                                   PRIOR
                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICAMI: ********** Maoliang
APPLICAMI: Wang, Maoliang
APPLICAMI: Whitlow, Marc D.
TITLE OF INVENTION: NO. 6333396el Method for Targeted Delivery of Nucleic Acids
TITLE OF INVENTION: NO. 6333396el Method for Targeted Delivery of Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09420592A Patent No. 6333396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 1999-1
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-10-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: UNSURE
LOCATION: (232)
OTHER INFORMATION: May be any amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 283
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: UNSURE LOCATION: (239)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: UNSURE LOCATION: (234)
OTHER INFORMATION: May be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                         APPLICATION NUMBER: 60/327,364 FILING DATE: 2001-10-09
                                                                                 APPLICATION NUMBER: 60/331,044 FILING DATE: 2001-11-07
                 APPLICATION NUMBER: 60/323,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 YYADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARGRXGXSLSGXYYYYHYFDYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGKTDGGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 YYADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSS--GTT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQGTLVTVSS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQGTLVTVSS 259
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DATE:
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MBER: 60/104,949
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Pred. No. 9.7e-46;
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FILING DATE:

2001-08-02

60/294,981

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 249
TYPE: PRT
ORGANISM: Artificial sequence
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ent No. 5821337
                                                                                                                                                                  CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
ETITING NEEL: 13-THN-1891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                 FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/934,373C FILING DATE: 21-Aug-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: South San Francisco
                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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FILING DATE: 2001-06-04
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                                   650/952-9881
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83.3%;
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                                                                                                   40,378
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Pred. No. 1.2e-45;
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US-08-437-642B-21
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
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                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                           SEQUENCE CHARACTERISTICS
                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-1994
                                                                                                                                                                                FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Paul J. Ca:
APPLICANT: Leonard G.
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winpatin (Genentech)
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                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 21-AU
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0: FILING DATE: 09-May-1995
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/1: FILING DATE: 17-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: South San
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                            TELEFAX:
                                                                                                                                       REFERENCE/DOCKET NUMBER: 40,
                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                 TOPOLOGY:
                                              LENGTH:
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5. 6054297
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                                 Amino Acid
                                                                                                                                                                      Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
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                                                                                             650/952-9881
                 Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genentech, Inc
                                                                                                                                                                                                                                             NUMBER: PCT/US92/05126
15-JUN-1992
                                                                                                                                                                                                     14-JUN-1991
                                                                                                                                                                                                                                                                                                                                           21-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5 inch, 1.44 Mb floppy disk
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Query Match

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Score 528;

DB w --

Length 122;

Search completed: August 20, 2003, 12:44:16 Job time : 81.3614 secs	Db 121 SS 122	Qy 115 SS 116	Db 61 ADSVKGRE	Qy 61 ADSVKGRE	Db 1 EVQLVESG	QY 1 EVQLLESG	Metches 103; Conse
st 20, 2003, 12:44:16` s			61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARGRVGYSLSGLYDYWGQGTLVTV 120	61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTV 114	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGDGGSTYV 60	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY 60	Hest Local Similarity 84.4%; Pred. No. 7.3e-46; Matches 103; Conservative 6; Mismatches 7; Indels - 6; Gaps 1;

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
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Gapop 10.0 , Gapext 0.5
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6 US-10-336-041A-13
6 US-10-336-041A-13
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6 US-10-336-041A-13
6 US-10-255-838B-21
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6 US-10-250-820-843B-20
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6 US-10-292-798-11694
6 US-10-408-765A-1283
6 US-60-490-890-2713
6 US-10-603-113-27128
6 US-00-820-843B-180
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          SUMMARIES
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  Sequence 1, Appli
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Sequence 20, Appl
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RESULT 2
US-10-291-265-332
Sequence 332, Application US/10291265
GENERAL INFORMATION:

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                                                        Sequence 804, Applic GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      SEQ ID NO 334
LENGTH: 312
TYPE: PRT
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                           Query Match
Best Local
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APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
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Best Local Similarity
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PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
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CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
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PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
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APPLICANT: Tang et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-0017 (785)
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0
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TYPE: PRT
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ITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
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| 136 GDGSSGGSGGASTG 149
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                                                                           Application
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Pred. No. 0.041;
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Pred. No. 0.041;
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US-10-291-265-805
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CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
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LENGTH: 384
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Best Local
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APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al
APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
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LENGTH: 384
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PRIOR TILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
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PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
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CURRENT APPLICATION NUMBER: US/
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ilarity 100.0%;
Conservative (
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Pred. No. 0.05;
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Pred. No. 0.05;
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US-10-291-265-806
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-291-265-807
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US-10-336-041A-10
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PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
Sequence 10, Application US/10336041A
GENERAL INFORMATION:
APPLICANT: Schering AG
APPLICANT: Schering AG
FILE REFERENCE: 27041P_MOAS
CURRENT APPLICATION NUMBER: US/10/336,041A
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: EP02 000 315.8
PRIOR APPLICATION NUMBER: US/07358702
PRIOR FILING DATE: 2002-01-03
PRIOR FILING DATE: 2002-02-25
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SOFTWARE: FRATSEQ for Windows Version 3.0

SEQ ID NO 807

LENGTH: 384
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Best Local S
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PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 3.0 iEQ ID NO 806 LENGTH: 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tang et al TITLE OF INVENTION: NOVEL Nucleic Acids and Polypeptides FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
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PRIOR FILING DATE: 2000-01-25
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equence 807, A
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Pred. No. 0.05;
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Pred. No. 0.
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; OTHER INFORMATION: Description of Artificial Sequence: recombinant; OTHER INFORMATION: antibody fragment US-10-336-041A-10
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US-10-336-041A-11
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PRIOR FILING DATE: 2002-02-25
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 240
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                                                                       SOFTWARE: PatentIn Ver. SEQ ID NO 11
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CURRENT APPLICATION NUMBER: US/10/336,041A
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: EPO2 000 315.8
PRIOR FILING DATE: 2002-01-03
PRIOR FILING DATE: 2002-01-03
                                                                                                                                                                                        APPLICANT: Schering AG TITLE OF INVENTION: New methods for diagnosis and treatment of tumours FILE REFERENCE: 27041P_WOAS CURRENT APPLICATION NUMBER: US/10/336,041A CURRENT FILING DATE: 2003-01-03 PRIOR APPLICATION NUMBER: EPO2 000 315.8
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TITLE OF INVENTION: New methods for diagnosis and treatment of tumours
                                                                                                          PRIOR FILING DATE: 2002-01-03
PRIOR APPLICATION NUMBER: US60/358702
PRIOR FILING DATE: 2002-02-25
NUMBER OF SEQ ID NOS: 13
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TYPE: PRT
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                ORGANISM: Artificial Sequence
FEATURE:
                                                     ENGTH: 241
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es 12; Conservat
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100.0%; Pred. No. 0.
tive 0; Mismatches
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US-10-336-041A-9
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US-10-336-041A-9
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; OTHER INFORMATION: antibody fragment
US-10-336-041A-13
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US-10-336-041A-13
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                       Query Match
Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Schering AG
TITLE OF INVENTION: New methods for diagnosis and treatment of tumours
                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
         Matches
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Matches
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                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/336,041A CURRENT FILING DATE: 2003-01-03 PRIOR APPLICATION NUMBER: EP02 000 315.8 PRIOR FILING DATE: 2002-01-03 PRIOR APPLICATION NUMBER: US60/358702 PRIOR APPLICATION NUMBER: US60/358702 PRIOR FILING DATE: 2002-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Schering AG
TITLE OF INVENTION: New methods for diagnosis and treatment of tumours
FILE REFERENCE: 27041P_WOAS
CURRENT APPLICATION NUMBER: US/10/336,041A
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: ED02 000 315.8
PRIOR APPLICATION NUMBER: US/01-03
PRIOR APPLICATION NUMBER: US60/358702
PRIOR APPLICATION NUMBER: US60/358702
PRIOR FILING DATE: 2002-02-25
PRIOR FILING DATE: 2002-02-25
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                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 27041P_WOAS
                                                                                      OTHER INFORMATION: Description of Artificial Sequence: recombinant OTHER INFORMATION: antibody fragment
                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                       LENGTH: 247
TYPE: PRT
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                 84.9%; Score 62;
100.0%; Pred. No.
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100.0%; Pred. No.
tive 0; Mismatc
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                                      DB 6;
                   0.62;
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0.61;
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0.61;
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                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 16: US-10-273-973-16
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US-10-273-973-16
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                                                                         Matches
                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                            TELEFAX: 619-554-6312 INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/133,011
FILING DATE: 08-JUN-1994
APPLICATION NUMBER: US 07/683,602
FILING DATE: 10-APR-1991
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: PCT/US 92/03091
FILING DATE: 10-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                 FRAGMENT TYPE:
                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 22-Jan-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barbas, Carlos
Lerner, Richard A.
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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23 GGGSGGGSEG 36
                                                                         10;
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                                  1 GDGSSGGSGGASTG 14
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                                                                                                                                                                                                                                     TOPOLOGY: unknown
                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: The Scripps Research Institute, Office of Patent Counsel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/273,973
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                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA
                                                                                                                                                                                 internal
                                                                                        71.28;
71.48;
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                                                                       0,
                                                                                        Score 52; DB 6; Pred. No. 7.7;
                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     SCRF 238.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.25
                                                                                                       Length 211;
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                                                                     Indels
                                                                     0;
                                                                 Gaps
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RESULT 14
US-60-485-404-55
; Sequence 55, Application US/60485404
; GENERAL INFORMATION:

0;

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SEQ ID NO 55
SEQ ID NO 55
LENGTH: 433
TYPE: PRT
ORANUEM: BITLIFICIAL
FEATURE: INFORMATION: M13 pIII coat protein for insertion into pUC18 vectors
US-60-485-404-55
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                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21
LENGTH: 498
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-10-225-838B-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-10-225-838B-21
Search completed: August 20, 2003, 12:45:11 Job time: 4.04819 secs
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                                                                                                                                   Query Match
Best Local Similarity 64.3
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Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/10225838B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 10/231,494
PRIOR FILING DATE: 2002-08-30
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2008-08-30
PRIOR APPLICATION NUMBER: US 10/384,060
PRIOR FILING DATE: 2003-03-10
PRIOR FILING DATE: 2003-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTIÓN: Transferrin Fusion Protein Libraries
FILE REFERENCE: 054710-5007-PR
CURRENT APPLICATION NUMBER: US/60/485,404
CURRENT FILING DATE: 2003-07-09
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NeuronZ, Ltd.
APPLICANT: NeuronZ Blosciences, Inc.
APPLICANT: Sieg, Frank
APPLICANT: Sieg, Frank
APPLICANT: Hughes, Paul
TITLE OF INVENTION: Neural Regeneration Peptides and Methods for Their Use In
TITLE OF INVENTION: Treatment of Brain Damage
FILE REFERENCE: NRNZ-1023US1
CURRENT APPLICATION NUMBER: US/10/225,838B
CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: 60/314,952
PRIOR FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/460,829
PRIOR FILING DATE: 2003-04-08
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Prior, Christopher P.
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                                                                                434 GDGGDGGAGGNGTG 447
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Pred. No. 17;
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Title:
Perfect score:
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Maximum DB seq
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                                                                                                                                                                                                                                                      Result
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                                                                                                                                                                                                                                                                                                                                          pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein search, using sw model
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length: 2000000000
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Gapop 10.0 , Gapext 0.5
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73
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A_Geneseq_19Jun03:*
A_Geneseq_19Jun03:*
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Listing first 45 su
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: *
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                                                AAY53773
AAE08818
AAY53775
AAU14225
AAU14227
AAM24101
AAU14461
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	Human novel protei Herbicidally activ Mycobacterium tube Raly protein seque Phage-derived flex GlySer-rich spacer Highly flexible (G peptide linker use Chemically modifie Human interleukin-Linker sequence us Chemically modifie Human interleukin-Linker sequence us Chemically modifie Human interleukin-Linker sequence us Chemically modifie Human interleukin-

ALIGNMENTS

RESULT 1 AAY53773

AAY53773 standard; Peptide; 14

A A

Linker of an antibody with improved specificity for fibronectin

22-FEB-2000 (first entry)

AAY53773;

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scFv; antibody; ED-B domain epitope; fibronectin; marker;
angiogenesis; vascular proliferation; diabetic retinopathy;
age-related macular degeneration; tumour; immunoscintigraphic detection;
blood coagulation; blood vessel occlusion; ocular angiogenesis;
                                                                                                                                                 Synthetic.
WPI; 2000-039074/03
                                                         11-MAY-1998;
28-APR-1999;
                                                                                        11-MAY-1999;
                                                                                                                                                                    angiogenesis-related pathology.
                                    (EIDG-) EIDGENOESSISCHE TECH HOCHSCHULE ZUERICH
                                                                                                          18-NOV-1999.
                                                                                                                              W09958570-A2
                   Tarli L,
                                                          98US-0075338.
99US-0300425.
                                                                                         99WO-EP03210
                   Viti F,
                    Birchler M;
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RESULT 2
AAE08818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a linker component of a modified human C serv antibody which has specific affinity for a characteristic epitope C of the ED-B domain of fibronectin. The affinity of the antibody for C this epitope was improved by introducing a number of mutations in the C complementarity determining region (CDR) residues located at the C complementarity determining region (CDR) residues located at the C periphery of the binding site. The improved antibody is used for rapid C targeting markers of angiogenesis, for detecting diseases characterized C by vascular proliferation, such as diabetic retinopathy, age-related C macular degeneration or tumours. The antibody localizes the respective tissue within 3 to 4 hours after injection. It is used in C immunoscintigraphic detection of angiogenesis and for diagnosis and C therapy of tumours and diseases characterized by vascular proliferation. The antibody can be conjugated to a molecule which induces blood C coagulation and blood vessel occlusion. These conjugates are used in C andiogenesis-related pathologies, especially or the treatment of the preparation of injectable compositions for the treatment of the preparation and pathologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
     The invention relates to
                                    Claim 10; Page 36; 73pp;
                                                                              An antibody, with specific affinity for a characteristic epitope of the ED-B domain of fibronectin for the treatment of diseases characterized
                                                                                                                                         WPI;
                                                                                                                                                                      Neri D,
                                                                                                                                                                                                                                                                                                                                                                                                   SGFv; single-chain variable antibody fragment; coagulant; ED-B domain; fibronectin; tunuor; c vascular proliferation; rheumatoid arthritis; angiogenesis; blood coagulation.
                                                                                                                                                                                                                                    24-FEB-2000; 2000US-0512082
                                                                                                                                                                                                                                                                                                      30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic peptide linker for constructing ScFv L19 antibody
                                                                                                                                                                                                      (EIDG-)
                                                                                                                                                                                                                                                                  23-FEB-2001; 2001WO-EP02062
                                                                                                                                                                                                                                                                                                                                     WO200162800-A1
                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE08818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE08818 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; Page 38;
                                                                    vascular proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iogenesis-related pathologies,
                                                                                                                                     2001-541701/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocular angiogenesis.
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                                                                                                                                                                    Tarli L,
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an antibody with specific affinity for
                                    English.
                                                                                                                                                                  Birchler M;
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Pred. No. 0.0049;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                fragment; cancer; cytotoxic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ocular
                                                                                                                                                                                                                                                                                                                                                                                                            blood vessel occlusion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                         disorder; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 3
AAY53775
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                  Claim 10; Page -;
                                                                                                                                                            antibodies
                                                                                                                                                             Fibronectin ED-B domain epitope specific antibodies and conjugate antibodies - \(\cdot\)
                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                        Neri D,
                                                                                                                                                                                                                                                                        11-MAY-1998;
28-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                          angiogenesis; vascular proliferation; diametric age-related macular degeneration; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful in the detection and/or coagulation of blood vessels. An antibody with improved affinity to the ED-B domain is useful for diagnosis and therapy of tumours and diseases characterised by vascular proliferation, cancer, rheumatoid arthritis, neo-vasculature associated coular disorders and psoriasis. Treatment of angiogenesis related pathologies comprises the injection of conjugates comprising antibody and a molecule capable of inducing blood coagulation and blood vessel occlusion. The present sequence is a peptide linker used for constructing single-chain variable antibody fragment (scFV) L19 antibody related to the invention.
                                                                                                                                                                                                                                            (EIDG-) EIDGENOESSISCHE TECH HOCHSCHULE
                                                                                                                                                                                                                                                                                                            11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                     18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                            W09958570-A2
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                       angiogenesis-related pathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                    blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scFv; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY53775 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY53775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conjugates comprising antibodies with a suitable photoactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              characteristic epitope of the ED-B domain of fibronectin, where antibody has improved affinity to ED-B. The invention also relat
                                                                                                                                                                                               2000-039074/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \mathbf{L}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GDGSSGGSGGASTG 14
                                                                                                                                                                                                                      Tarli L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          vascular proliferation; diabetic
                                                                                                                                                                                                                                                                                   98US-0075338
                                                                                                                                                                                                                                                                      99US-0300425
                                                                                                                                                                                                                                                                                                           99WO-EP03210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ED-B domain epitope; fibronectin; marker;
                                                                                                                               59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              improved specificity for fibronectin.
                                                                                                                                                                                                                        Viti F,
                                                                                                                                                                                                                                                                                                                                                                                                                                 blood vessel occlusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
                                                                                                                                                                                                                      Birchler M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 73; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                              ZUERICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
0.0049;
                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoscintigraphic detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          retinopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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The present sequence represents a modified human scFv antibody which has specific affinity for a characteristic epitope of the ED-B domain of fibronectin. The affinity of the antibody for this epitope was improved by introducing a number of mutations in the complementarity determining region (CDR) residues located at the periphery of the binding site. The improved antibody is used for rapid targeting marker of angiogenesis, for detecting diseases characterized by vascular proliferation, such as diabetic retinopathy, age-related macular proliferation or tumours. The antibody localizes the respective tissue

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within 3 to 4 hours after

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Best Local S
Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antialtergic; dermatological; haemostatic; antialtergic; dermatological; haemostatic; immunogen; antibody; gene therapy; neurological disorder; parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis
The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human novel protein #96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU14225 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-2000; 2000US-0491404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C,
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Pred. No.
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0.084;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, aneamia, Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host diseases, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.
                                                         immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulgant; antiarthritic; cerebroprotective; antifungal; antivital; antibacterial; antiallergic; dermatological; haemostatic; antisathmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis
                                                                                                                                                                                                                                                                                        AAU14227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
Homo sapiens.
                                                                                                                                                                                                         Human novel protein
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                                                                                                                                                                protein; Antianaemic; osteopathic; antiinflammatory.
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Pred. No.
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rne invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of antibodies raised and prevention of disorders caused by the aberrar protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used.
                                                                                                                                                                                              Tang
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                                                                                                                                                                                                                                                                                                            WO200155437-A2
                                                                                                                                                                                                                                           25-JAN-2000;
                                                                                                                                                                                                                                                                  25-JAN-2001; 2001WO-US02623.
                                                                                                        Example
                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                           nervous system disorders,
                                                                                                                                                                                               ΥT,
                                                                                                                                                                          2001-451939/48
                                                                                                       4.
                                                                                                                                                               AAS22532
                                                                                                                                                                                              Liu C,
                                                                                                       Page 576-577;
                                                                                                                                                                                                                                           2000US-0491404
                                                                                                                                                                                                Drmanac
                                                                                                                                        useful
                                                                                                      894pp;
                                                                                                                              and
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                                                                                                                               for treating anti-inflammatory diseases, d for regenerating bone and cartilage -
                                                                                                        English.
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aberrant

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful, in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.
The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
                                                                                                                                                WPI;
                                                                                                                                                                                      Tang
                                                             Claim
                                                                                                                                N-PSDB;
                                                                                       Isolated polypeptide for treatment antibodies and research use -
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15-SEP-2000;
                                                                                                                                                                                                                                                                     25-JAN-2000;
17-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                     Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; tomato; monkey; dog; sea urchin; expressed sequence tag; ES; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                             25-JAN-2001; 2001WO-US02687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM24101 standard; Protein; 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, 1
                                                                                                                               2001-476164/51.
DB; AAH98760.
                                                                                                                                                                                                                                                                                                                                                                                              sapiens
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                                                                                                                                                                      Drmanac
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                                                         Page 1102-1103; 1275pp;
                                                                                                                                                                                     Liu C,
                                                                                                                                                                                                                                          ; 2000US-0491404.
; 2000US-0617746.
; 2000US-0631451.
; 2000US-0663870.
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Zhang
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Pred. No.
                                                                                                                                                                      Werhman
                                                                                                                                                                                     XB,
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                                                                                                 diagnostics, raising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 312;
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                                                         The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to
            raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands Polypeptides of the invention may also be useful in treating platelet
                                                                                                                                                                                                                                                                                                 Example 4; Page 824-825;
                                                                                                                                                                                                                                                                                                                               Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS22766
                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatclogical; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                urchin and tomato. These were derived from expressed sequence to from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JAN-2001; 2001WO-US02623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200155437-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regeneration;
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                                                                                                                                                                                                                                                                                               894pp;
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Pred. No.
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                                isolate receptors or ligands
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The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerbroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
                                                                                                                                                                                                                                                         Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                      Tang
                                                                                                                                                                                                                                     Example
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                                                                                                                                                                                                                                                                                                                                      2001-451939/48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regeneration; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GDGSSGGSGGASTG 14
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                                                                                                                                                                                                                            Page 825-826; 894pp; English.
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Pred. No.
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treatment of a mammal and prevention of disorders caused by the aberran protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and
                                                                  proteins or their active domains. The polypeptides, polypucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberran
                                                                                                              The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antialiergic; dermatological; haemostatic; antiastimatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
                                                                                                                                                                                                 Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                     Example 4; Page 826-827;
                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-2000; 2000US-0491404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoparthritis, anaemia, Alzhelmer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands Polypeptides" of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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DB; AAS22768.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regeneration;
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                                                                                                                                                                 894pp; English.
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Best Local S
Matches 14
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The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant
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                                                                                                                                                                                                                                                      Isolated polypeptides useful for the nervous system disorders, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-)
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)B; AAS22769.
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                                                                                                                                                                                      4; Page 827; 894pp; English
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tory; cytostatic; neuroprotective; vulnerary; nootropic;
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RESULT 15
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                                                                                                                                                                                                                                 Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2002
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56 GDGSSGGSGGASTG
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                                                                                                                                                       NO 1619; 261pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID NO 1619
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                                                                                                                                                                                                                                                                           sequences
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(ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant nucleic acid or amino acid sequences from non-plant organisms suitable search parameters, where plant sequences having an E-value

E-value

plant

using

The invention relates (ABB90790-ABB94016) fo

for '

identifying

target proteins

Claim 5;

SEQ ID

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CC of interest invention describes a method for isolating a polynucleotide CC of interest that is present or is expressed in a genome of a first CC mycobacterium strain and that is absent or altered in a genome of a CC using a bacterial artificial chromosome (BAC) vector. Recombinant BAC CC vectors, which are preferably immobilised, can be used to detect CC mycobacterial nucleic acids (genomic DNA, cDNA or mRNA) in biological CC mycobacterial nucleic acids (dentified are useful as probes or primers CC samples. The polynucleotides identified are useful as probes or primers CC polynucleotides contained in the recombinant BAC vectors it is possible to compare a polynucleoterium of interest. By aligning the CC to physically map a polynucleoterium of interest. By aligning the CC to physically map a polynucleoterium of interest and vectors it is possible to compare genomes between different strains or species and their non-pathogenic strains or species counterparts. ABG62422 to ABB81227 to ABB81230 represent sequences used in the present invention of exemplification of the present invention.
         Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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Best Local S
Matches 11
                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                Isolation of polynucleotides from mycobacterial genomes, useful for detection of Mycobacteria and for combating tuberculosis -
                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 6; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-013262/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09954487-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB81229 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GDGSSGGSGGASTG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buchrieser-Brosch R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                  318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDGSSPGTGGASGG 461
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lum tuberculosis; Mycobacterium bovis; Mycobacterium;
BAC vector; bacterial artificial chromosome; tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                928 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                  ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tuberculosis strain H37Rv PE-PGRS protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0060756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-IB00740
                  74.08;
76.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 318 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.3%;
    Score 54; DB Pred. No. 27; 1; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gordon S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Billault A;
                                21;
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    Ņ
                               Length 318
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    Indels
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Gaps
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0;

Query Match
Best Local Similarity
Matches 10; Conserv

Conservative

72.6%;

; Score 53; DB; Pred. No. 33; 1; Mismatches

20; ω --

Length 296;

0

Gaps

0

Sequence

296

A

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This sequence is the Raly (RNP associated with lethal yellow) protein, CC DNA encoding it can be used in a specific engineered fragment (SEF). CC The invention relates to gene targeting vectors that comprise 2 yeast selectable markers, a mammalian cell selectable marker and gene-specific CC prepared by a method, comprising: (a) preparing a shuttle vector CC comprising a first yeast selectable marker, a bacterial selectable CC comprising a first yeast selectable marker, a bacterial selectable CC comprising a second yeast selectable marker cassette, the CC marker cassette comprising a second yeast selectable marker capable of CC expression in mammalian embryonic stem cells and the marker cassette of being flanked on each side by mammalian gene-specific flanking sequences (CC allowing the shuttle vector and the SEF to recombination; (d) selecting the transformed yeast (c) transforming CC allowing the shuttle vector and the SEF to recombination; (d) selecting the transformed yeast cells for expression (CC targeting vector produced by recombination between the shuttle vector and the SEF to recombine by homologous (CC targeting vector produced by recombination between the shuttle vector and the SEF to recombine by homologous (CC targeting vector produced by recombination between the shuttle vector and the SEF to recombine by homologous (CC targeting vector produced by recombination between the shuttle vector and the SEF to recombine by homologous (CC and sequence information are not regulatory sequences into preselected of genes and their roles in diseases Using the method, detailed mapping constructs or restriction sites which results in a significant saving of time and effort in preparing targeting constructs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
AAY14121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Fig 8; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New gene targeting vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-313353/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX58236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garfinkel D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene function identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR primer; specific engineered fragment; gene targeting vector; yeast selectable marker; mammalian cell selectable marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raly protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY14121 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY14121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Woychik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INC.
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GDGSSGGSGGASTG 14

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RESULT 14
AAW17096
ID AAW17096
ID AAW17096
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                                                                                                                                                                                                                                                                                        The invention relates to a novel haematopoletic protein (HP) comprising CC R2-R1; where R1 and R2 are independently selected from: (I) a modified CC R2-R1; where R1 and R2 are independently selected from: (I) a modified CC (II) a modified human granulocyte-colony stimulating factor (hG-CSF) AA sequence; CC (II) a modified human interleukin-3 (hIL-3) AA sequence; (III) a modified CC (II) a modified human interleukin-3 (hIL-3) AA sequence; (III) a modified CC linker capable of linking R1 to R2. This sequence represents an example CC vectors comprising the nucleic acid molecules are useful for the CC vectors comprising the nucleic acid molecules are useful in CC recombinant production of HP. The nucleic acid molecules are useful in CC gene therapy. The HPs's are useful for stimulating the production of CC haematopoietic cells in patients, selective ex vivo expansion of stem CC can be treated include leukopaenia, neutropeenia, aplastic anaemia and CC thrombocytopaenia. In vitro uses include the ability to stimulate bone can prove the construction and growth before infusion into the
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                                                  δÃ
                                                                                                                         Matches
                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haematopoietic protein; human; granulocyte-colony stimulating factor; G-CSF; interleukin; c-mpl ligand; linker; gene therapy; aplastic anaemia; stem cell expansion; leukopaenia; neutropaenia; vector; bone marrow; thrombocytopaenia; blood cell activation; growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phage-derived flexible linker peptide for chimeric protein construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW17096
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Klein BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9712985-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-OCT-1995;
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                                                                                                                                                                                                                                                                 marrow and l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multi-functional haematopoietic receptor agonists - used to stimulate the production of haematopoietic cells in patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Summers NL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SEAR ) SEARLE & CO G D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 33-34; 616pp; English.
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                                                                                                                         l Similarity
10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDSSSGGGGGSSGG
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Lee SC, McKe
IL, Zurfluh L;
                                                            GDGSSGGSGGASTG 14
      GGGSGGGSEG
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                                                                                                                            Conservative
                                                                                                                                                                                                                                                  AA;
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McKearn JP,
                                                                                                                                                        71.28;
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                                                                                                                                                        Score 52; D
Pred. No. 5.
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McWherter CA, Sta
                                                                                                                                  Mismatches
                                                                                                                                                                                           DB 18;
                                                                                                                                  4.
                                                                                                                                                                                           Length 35
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RESULT 15

Search completed: August 20, 2003, 12:33:40 Job time : 31.7831 secs

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AAR79295
ID AAR7
                                                                                                                                      A new fusion protein is disclosed which has the formula R1-L-R2, CC R2-L-R1, R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or CC variant of human interleukin-3 (hIL-3), R2 is a second colony CC stimulating factor (CSF) including cytokine, lymphokine, interleukin, CC stimulating factor (CSF) including cytokine, lymphokine, interleukin, CC which the present sequence is a specific example). Generic sequences CC are described in AAR03235 - AAR03242, and specifically claimed examples CC are shown in AAR79298-R79335 and AAR79342-R79345. The fusion protein is CC are shown in AAR79298-R79335 and AAR79342-R79345. The fusion protein is CC sequences which encode these proteins are shown in AAQ97167-097204 and CC eall production. It is also useful as an IL-3 antagonist or as a CC cell production. It is also useful as an IL-3 antagonist or as a CC cell production. It is also useful as an IL-3 antagonist or as a CC cell production. It is also useful as an IL-3 antagonist or as a CC cell production. It is also useful as an IL-3 antagonist or as a CC cell production of cappent for production of antibodies useful in CC growth of certain cancer cells and in treatment of asthma. The fusion CC growth of certain cancer cells and in treatment of asthma. The fusion CC construction and growth in vitro before infusion; and to treat diseases activation and growth in vitro before infusion; and to treat diseases activation and activity of both its component proteins, but may have increased synergistic activity and reduced undesired side effects.
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                                                                   Matches
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Easton AM,
Thomas JW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusion proteins comprising a human interleukin-3 variant, a linker and interleukin-3, a variant or a colony stimulating factor useful to increase haematopoietic cell production in a mammal
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lymphokine; mutant; mutein; fusion protein; linker.
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MCKearn JP, Olins PO,
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 Sequence
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111 App1
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RESULT 2 US-09-670-314 Sequence 727 Patent No. (GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: TITLE OF II	Query Match Best Local Matches 1 Qy 1 Db 88	RESULT 1 US-09-060-756-727 US-09-060-756-727 Sequent No. 6183957 GENERAL INFORMATION: APPLICANT: Cole, Ste APPLICANT: Gordon, S APPLICANT: Biliault, APPLICANTION: TITLE OF INVENTION: TITLE OF INVENTION: CURRENT APPLICATION COURSEL 348 TYPE: PRT ORGANISM: MYCODACTE US-09-060-756-727		444444 5443 5443 5443 5443 5443 5443 54
7.727 Application (4) 492506 ECOLE, Sten Buchriese Buchriese Gordon, (4) 40200n E111ault TVENTION: VENTION: VENTION: VENTION: JULICATION 10 LICATION 1	h 7 Similarity 7 10; Conservati 1 GDGSSGGSGGAST 	10-756-727 No. 6183957 LI INFORMATION: COANT: Gole, Stewart CCANT: Gordon, Stephen COANT: Bubhrieser-Brose CCANT: Bilhault, Allain E OF INVENTION: THE GEN E OF INVENTION: LIBRARY REFERENCE: 3495-0169 ENT APPLICATION NUMBER: ENT FILING DATE: 1998-0 ENT FILING DATE: 1998-0 ENT FILING DATE: 1998-0 ON 727 ON 727 ON 727 ON 727 STH. 318 E: PAT ANISM: Mycobacterium sp 10-756-727	,	552 711.2 552 711.2 552 711.2 552 711.2 552 711.2 552 711.2 553 711.2 711.2 711.2 711.2
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PRIOR FILING DATE: 1998-04-16 NUMBER OF SEQ ID NOS: 743

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US-08-470-775-11
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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SEQ ID NO 727
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TYPE: PRT
                                                                                                                                                                                                                       NAME: Bennett, Dennis A. REGISTRATION NUMBER: 34,547 REFERENCE/DOCKET NUMBER: C-TELECOMMUNICATION INFORMATION: TELEPHONE: (708)470-6501
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Bennett, Dennis A.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palan-
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                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co., ADDRESSEE: Corporate Patent Dept. STREET: P. O. Box 5110
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INVENTION: Mutants With Colony Stimulating Factors
F SEQUENCES: 13
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76.9%;
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Pred. No.
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Patent No. 6022535
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                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                             APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3
NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                            APPLICANT:
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COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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COMPUTER READABLE FORM:
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APPLICATION NUMBER: US/08/468,609A FILING DATE: 06-JUN-1995
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                                                                                                                              Illinois
Y: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 amino acids
                                                                                                                                                                                                                                                                        Olins, Peter
Paik, Kumnan
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Braford-Goldberg,
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Klein, Barbara K.
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                                                                                                                                                                       O. Box 5110
                                                                                                                                                                                    Corporate Patent Dept.
                                                                                                                                                                                                   Dennis A. Bennett, G.D. Searle & Co.,
                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                                         Peter 0.
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                                                                                                                                                                                                                                                                                                      John P.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                Sarah
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Best Local Similarity
Tatches 10; Conserve
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INFORMATION FOR SEQ ID NO: 50
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acids
TYPE: amino acid
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            TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
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REFERENCE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-foof
TELEFAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
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                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                        CITY: Chicago
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o. 6057133
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(317) TD NO: 50:
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            (708)470-6501
(708)470-6881
OR SEQ ID NO: 50:
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Thomas, John W.
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Klein, Barbara K.
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; MOLECULE TYPE: peptide US-08-192-325B-50
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                                                       ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-559-267A-11
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Best Local :
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Matches
             Query Match
Best Local Similarity
                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                     REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Olins, Peter O.
APPLICANT: Paik, Kumnan
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Ex-viv
NUMBER OF SEQUENCES: 13
                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                    CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/192,299
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STATE: Illinois
COUNTRY: USA
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CLASSIFICATION:
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Easton, Alan M.
Klein, Barbara K.
Conservative
                                                                                                                                                            (708)470-6881
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                                                                                                                                                                          (708)470-6501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dennis A. Bennett, G.D. Searle & Co.
                                                                                                                                                                                                                                                                               04-FEB-1994
                                                                                                                                                                                                                                                                                                                                         15-NOV-1995
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71.4%;
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             Score 52; I
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APPLICANT:

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                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 10
                                                                                      Patent No. 6361977
GENERAL INFORMATION:
                                                                                                                  Sequence 50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11,
Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                            RECISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEPAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 11:
                                                         APPLICANT: Abrams, APPLICANT: Bauer, S
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CITY: Illinois
TISA
 APPLICANT:
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MEDIUM TYPE: Floppy disk
                APPLICANT:
                               APPLICANT:
                                            APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bennett, Dennis REGISTRATION NUMBER: :
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6361977
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6132991
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                         Braford-Goldberg,
Caparon, Maire H.
                                                         Bauer, S. C.
Klein, Barbara K.
            Easton, Alan M.
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Paik, Kumnan
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Klein, Barbara K.
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N: 530
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                                                                       Mark A.
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71.4%;
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                                                                                                                                                                                                                                                                           Score 52;
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                                         Sarah R.
                                                                                                                                                                                                                                                 Mismatches
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US-08-762-227A-50
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                                                                                                                                                                                                                                                                                                Sequence 50, Application US/08762227A Patent No. 6436387 GENERAL INFORMATION:
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Best Local S
Matches 10
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TELEFAX: (314)737-697
INFORMATION FOR SEQ ID NO:
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APPLICANT: Thomas, J
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS LENGTH: 36 amino acid:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: C-TELECOMMUNICATION INFORMATION: (314)737-6986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,872A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CITY: Chicago
CITY: Illinois
TISA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bennett, Dennis A. REGISTRATION NUMBER: 34,547
                                                              Thomas, John W.
TITLE OF INVENTION: multivariant IL-3 Hematopoiesis
Fusion Protein
NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                APPLICANT:
                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Similarity
10; Conserv
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ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co., Corporate Patent Dept.
STREET: P. O. Box 5110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                      McKearn, John P. Olins, Peter O. Paik, Kumnan
                                                                                                                                                                                          Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
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Pred. No.
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ZIF: COULTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

STATE: Illinois

COUNTRY: USA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 50, Application PC/TUS9501185 GENERAL INFORMATION:
Query Match
Best Local Similarity
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                                                                                                                                         FILING DATE: 14-FEB-1994
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                     TOPOLOGY:
                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
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                                                                                                      amino acid
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R APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/762,227A FILING DATE: 09-Dec-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bennett, Dennis A. REGISTRATION NUMBER: 34,547 REFERENCE/DOCKET NUMBER: C-2790/5
                                                                                                                        36 amino acids
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71.2%;
71.4%;
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71.48;
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Score 52;
Pred. No.
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RESULT 13
US-08-468-609A-194
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natent No. 6030812
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US-08-469-318-194
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NUMBER OF SEQUENCES: 19
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy d:
                                   STREET: F.
CHICAGO
CITY: Chicago
STATE: Illinois
STATE: USA
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LENGTH: 49 amino acids
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SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM: 'MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide
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                                                                                                                                                    NUMBER OF SEQUENCES:
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ITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (I
IUMBER OF SEQUENCES: 197
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Local Similarity 71.48;
es 10; Conservation
                               COUNTRY: UZIP: 60680
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Caparon, Maire H.
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SYSTEM: PC-DOS/MS-DOS
                                                                                                        Corporate Patent Dept.
                                                                                                                     Dennis A. Bennett, G.D.
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                                                                                         Box 5110
                                                                                                                                                                                                                                 John P.
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                                                                                                                        Searle & Co.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 194,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (314)737-697 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                    STREET: F.
STREET: F.
CITY: Chicago
CITY: Illinois
TTATE: IISA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
TERMATION FOR SEO ID NO. 10.
                        PRIOR APPLICATION DATA:
                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: APPLICANT:
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MOLECULE TYPE:
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APPLICATION NUMBER: US 0
FILING DATE: 14-FEB-1994
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                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICATION NUMBER: US 08/192,325 FILING DATE: 14-FEB-1994
                                                            APPLICATION NUMBER: US/08/446,872A FILING DATE: 06-JUN-1995
                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS
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Paik, Kumnan
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Klein, Barbara K.
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Bauer, S. C
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                                                                                                                                                                                                                                                                                  Dennis A. Bennett, G.D. Searle & Co.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                   Corporate Patent Dept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US/08/468,609A
06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-762-227A-194
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Best Local Similarity
Matches 10; Conserv
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INFORMATION FOR SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Bennett, Dennis A.
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                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/762,227A FILING DATE: 09-Dec-1996 CLASSIFICATION: <Unknown>
                                                                                  NAME: Bennett, Dennis A. REGISTRATION NUMBER: 34,547
                                                                                                                                         APPLICATION NUMBER: US 0 FILING DATE: 06-JUN-1995
                                                                                                                                                                            APPLICATION NUMBER: US 08/192,325 FILING DATE: 14-FEB-1994
                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                  TELEPHONE: (708)470-6501
                                                                   REFERENCE/DOCKET NUMBER: C-2790/5
                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60680
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Corporate Patent Dept.
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Paik, Kumnan
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Klein, Barbara K.
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                (708)470-6881
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71.4%;
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Pred. No.
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SEQUENCE CHARACTERISTICS:
LENGTH: 49 and no acids
TYDE: anino acids
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-08-762-227A-194

Query Match
Best Local Similarity 71.4%; Pred. No. 2.5;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Matches 10; Gonservative 0; Mismatches 0; Gaps 0;
DSSGGSGGSTG 14
Db 10 GGCSGGSGGSEG 23

Search completed: August 20, 2003, 12:44:17
Job time: 10.5988 secs
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Listing first 45 summaries
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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AAW16651
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AAG65311
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AAY39564
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Anti-cancer specif
Anti-platelet glyc
Anti-IL-18 antibod
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CTLA-4 VLD CDR2 re
Clone selected aft
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	selected selected selected selected selected selected selected selected selected

ALIGNMENTS

RESULT 1
AAY39626
ID AAY3

AAY39626 standard; peptide;

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23-NOV-1999

(first entry)

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New binding agent comprising monomeric one complementarity determining region
                           WPI; 1999-551040/46.
                                            Coia G,
                                                                                                                   10-SEP-1999.
                                                                                                                                     WO9945110-A1.
                                                                                                                                                     Synthetic.
Homo sapiens.
                                                                                                                                                                               CTLA-4; cytotoxic T-lymphocyte associated antigen 4; binding agent; VLD; variable-like domain; human; diagnosis; cancer; blood clot.
                                                                                                                                                                                                          CTLA-4 VLD CDR loop replacement.
                                                             (DIAT-) DIATECH PTY LTD.
                                                                               06-MAR-1998;
                                                                                                 05-MAR-1999;
                                          Galanis M,
                                                                                98AU-0002210
                                                                                                 99WO-AU00136
                                             Hudson
                                             PJ,
                                           Irving
V-like domain in which at least loop is modified, useful for
                                            RΑ,
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Example diagnosis

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of cancer

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RESULT 2
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Best Local
The present sequence is the heavy chain complementarity determining region 2 of an anti-cancer specific antigen human monoclonal antibody (hMAb). The hMAb can be used in medicine, e.g. clinical diagnosis of cancer or immunotherapy, or to purify cancer specific antigen. The industrial scale production of large amounts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                has at least one CDR (complementarity determining region) loop sequence, or part of it, modified or replaced so that, compared to unmodified VLD, its solubility is increased and/or the size is altered and/or a disulphide bond is created within, or between, one or more CDR loops. (I) are used for diagnosis, e.g. in vivo detection/localisation of cancer, blood clots etc., also in vitro when immobilised on solid supports or blosensors and therapeutically, modified VLD may have binding affinity for drugs, steroids, pesticides, antigens, growth factors, tumour markers, cell or viral proteins. Modification of VLD improves solubility and alters binding specificity. Since VLD are derived from human proteins, the need for a humanizing step (to avoid adverse immune responses) is avoided, and modification also improves expression in
                                                                                                        Claim
                                                                                                                                     cDNA encoding human monoclonal antibody - useful in medicine, or purify cancer specific antigen
                                                                                                                                                                                     WPI; 1997-275445/25
N-PSDB; AAT66783.
                                                                                                                                                                                                                                                                                                                                                              JP09098786-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Heavy chain; variable region; cancer specific antigen; human; monoclonal antibody; hMAb; diagnosis; cancer; immunotherapy; purification; complementarity determining region 2; CDR2.
                                                                                                                                                                                                                                                                                     06-OCT-1995;
                                                                                                                                                                                                                                                                                                                    06-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                  15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-cancer specific antigen MAb heavy chain CDR2.
                                                                                                                                                                                                                                    (MOMI ) MORINAGA & CO LTD.
(SHKJ ) SHINGIJUTSU JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW16651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW16651 standard; Peptide; 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is variable-like domain (VLD) of the human cytotoxic T-lymphocyte associated antigen 4 (CTLA-4) CDR loop replacement, used in the binding agent of the invention. The binding agent (I) comprises least one monomeric VLD that is derived from a non-antibody ligand and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
                                                                                                  9; Fig 12; 7pp; Japanese.
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6; Conser
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Pred. No.
   immunotherapy, or to purify cancer scale production of large amounts
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Sequence

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Best Local
                                                                             attractive potential reagents for therapeutic purposes. They provide a new class of antithrombotic agents, useful for the prevention of platelet-dependent thromb in diseased arteries, bypass grafts, dialysis etc., and can also be used as diagnostic reagents. Methods of inhibiting aggregation of platelets, of binding human platelet GPID alpha and of selecting a VH or VL region of an antibody that inhibits platelet aggregation are claimed. Fragments of the ScFV VH or VL chain, including CDR
                                                                                                                                                                                                                                                                                                                                       against platelet glycoprotein Ib (GPIb). The HID series of scFv was isolated from a human synthetic VH and VL scFv library on the basis of their binding to platelet GPIb. Whether displayed as surface proteins on a phagemid or secreted as free scFv by Escherichia coli, the HID scFv clones are capable of inhibiting von Willebrand factor dependent aggregation of platelets. The second of platelets of the scFv companies of platelets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of complementarity determining 2 (CDR2) of the heavy chain variable region (VH) of human single chain antibody (scFv) Hib-3 (see AAY95219), which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Variable heavy chain; single chain antibody; scFv; human; HIb-3; glycoprotein Ib alpha; platelet; aggregation; antiaggregant; antithrombotic; thrombus; therapy; diagnostic; CDR2;
                                                                                                                                                                                                                                                                                                                  are composed of native human protein sequences and are therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Fig 7; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-365744/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL/) MILLER J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AISGSG
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding anti-human platelet useful for producing antibodies which
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                                                                                                                                                                                                    The invention provides isolated antibodies, or antigen-binding portions, CC that are capable of binding to human interleukin-18 (II-18). The CC antibodies may be used to inhibit human II-18 activity in, and treat a CC disorder where II-18 is detrimental in, a human subject suffering from, CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease, CC (e.g., Huntington's chorea, Parkinson's disease, Albeimer's disease, and CC (e.g., Huntington's chorea, Parkinson's disease, Albeimer's disease, and CC (e.g., depression and schizophreia). Treatment with an anti-II-18 CC (e.g., depression and schizophreia). Treatment with an anti-II-18 CC (e.g., depression and schizophreia). Treatment with an anti-II-18 CC second agent selected from an antibody, or fragment, capable of binding CC human II-12, methotrexate, anti-tumor necrosis factor, corticosteroids, CC cyclosporin, rapamycin, FK506, and non-steroidal anti-Inflammatory CC depends. The present sequence represents an anti-II-18 antibody LT28 heavy chain CDR2 fragment.
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Best Local Similarity
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Duncan AR,
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antidepressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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                                                      0
                                                                                  Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 28; DB
Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              æ
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                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuroleptic;
                                                                                  61;
                                                                                                       BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Labkovsky B,
Shorrock CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 17;
                                                                                                       Length 17;
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                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salfeld J;
Thompson JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                      Gaps
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RESULT 6
ABR01548
ID ABR0

ABR01548 standard;

peptide; 17

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RESULT 5
AAG65317
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                                                                                                                                                     The invention provides isolated antibodies, or antigen-binding portions, ct that are capable of binding to human interleukin-18 (IL-18). The cc antibodies may be used to inhibit human IL-18 activity in, and treat a cisorder where IL-18 is detrimental in, a human subject suffering from, inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease, inflammatory bowel disease, and osteoarthritis), neurological disorders (e.g., Huntington's chorea, Parkinson's disease, Alabimer's disease, and ctroke), heart failure, myocardial infarction, autoimmune diseases such as autoimmune hepatitis and autoimmune neutropeania, and mental disorders (e.g., depression and schizophrenia). Treatment with an anti-IL-18 cc (e.g., depression and schizophrenia). Treatment with an anti-IL-18 cc (e.g., depression and schizophrenia) or after administration of a second agent selected from an antibody, or fragment, capable of binding thuman IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids, cyclosporin, rapamycin, FK506, and non-steroidal anti-Inflammatory cc chain variable region fragment.
                                                             Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ghayur T,
Duncan AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interleukin-18 useful for treating, e. neurological disorders, heart failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  II-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
immunosuppressive; antidepressant; neuroleptic; hepatotropic; LT28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG65317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG65317 standard; protein; 17 AA.
                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 36; Page · 78; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel antibodies and compounds capable of binding to human interleukin-18 useful for treating, e.g., inflammatory disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-550020/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-FEB-2001; 2001WO-US04170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-IL-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lennard SN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AISGSG
                                                             Similarity
6; Conserv
                            AISGSG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dixon RW, Roguska
Brocklehurst SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody heavy chain variable region fragment.
                                                                                                                             17
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                             Α,
                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating, e.g., inflammacos, cart failure, myocardial infarction,
                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mankovich
                                                                              Score 28;
Pred. No.
                                                              Mismatches
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                                                                               61,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Labkovsky B,
Shorrock CP,
                                                                                             22;
                                                              0
                                                                                           Length 17;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salfeld J;
Thompson JE;
                                                              0,
                                                                Gaps
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RESULT 7
AAY39564
ID AAY3
XX
AC AAY3
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ZX
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ZX
Z3-1
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                                                                                                                                                                                                                                                                                                              The invention relates to a novel purified preparation of a human CC antibody, which binds to a tissue inhibitor of metalloprotease-[(TIMP-1)] CC and neutralises a matrix metalloprotease (MMP)-inhibiting activity of CC and neutralises a matrix etalloprotease (MMP)-inhibiting activity of CC IMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and CC a variable light chain (VLC)DR3 region. An antibody preparation of the CC invention has hepatotropic, cytostatic, nephrotropic and cardiant CC activity. The human antibody is useful for decreasing an MMP-inhibiting CC extivity of a TIMP-1. It is especially useful for ameliorating the CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic CC pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon CC cancer. The antibody is also useful for detecting a TIMP-1 in a test celevated. The present sequence represents a VHCDR1 region of an antibody of the invention
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                           Matches
 23-NOV-1999
                                 AAY39564;
                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a in which TIMP-1 is elevated, e.g. liver fibrosis, benign pros
                                                               AAY39564 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3; matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis; acute coronary syndrome; alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypertrophy or lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MORP-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-APR-2001; 2001US-285683P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-APR-2002; 2002WO-US12801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human anti-TIMP-1 Fab VHCDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lupus nephritis; glomerulosclerotic renal disease; lung cancer; VHCDR1;
                                                                                                                                                                                                           Local Similarity hes 6; Conserv
                                                                                                                                                                           1 AISGSG
                                                                                                                                                                                                                                                                                                          invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Page 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Knorr AM, Schauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MORPHOSYS
                                                                                                                                               AISGSG
                                                                                                                                                                                                                                                                            17 AA;
                                                                                                                                                                                                             Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ĀG
                                                             peptide;
                                                                                                                                                                                                          100.0%; ; 1
100.0%; I
ntive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228pp; English.
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                                                                                                                                                                                                                          Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hirth-dietrich C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   benign prostate hypertrophy; colon cancer
                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                         DB
61;
                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                        Length 17;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            benign prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kraft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ś
                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krebs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorder
                                                                                                                                                                                                        Gaps
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RRSULT 8
AAV0251
ID AAVC
XX AAVC
XX AAVC
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XX AAVC
XX Clon
XX Clon
XX Scre
XW Scre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              has at least one CDR (complementarity determining region) loop sequence, or part of it, modified or replaced so that, compared to unmodified VLD, its solubility is increased and/or the size is altered and/or a disulphide bond is created within, or between, one or more CDR loops. (I) are used for diagnosis, e.g. in vivo detection/localisation of cancer, blood clots etc., also in vitro when immobilised on solid supports or blosensors and therapeutically. Modified VLD may have binding affinity for drugs, steroids, pesticides, antigens, growth factors, tumour markers, cell or viral proteins. Modification of VLD improves solubility and alters binding specificity. Since VLD are derived from human proteins, the need for a humanizing step (to avoid adverse immune responses) is avoided, and modification also improves expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is a variant of the CDR2 of the variable-like domain (VLD) of the human cytotoxic T-lymphocyte associated antigen 4 (CTLA-4), used in the binding agent of the invention. The binding agent (I) comprises at least one monomeric VLD that is derived from a non-antibody ligand and
                                                         Synthetic
                                                                                                                enrichment;
                                                                                                                                            Screening;
                                                                                                                                                                                             Clone selected after
                                                                                                                                                                                                                                                    15-JUL-1999
                                                                                                                                                                                                                                                                                                          AAY02512
                                                                                                                                                                                                                                                                                                                                                                 AAY02512 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New binding agent comprising mor
one complementarity determining
diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 18; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-551040/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTLA-4; cytotoxic T-lymphocyte associated antigen 4; binding agent; VLD; variable-like domain; human; diagnosis; cancer; blood clot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTLA-4 VLD CDR2 region variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DIAT-) DIATECH PTY LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AISGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AISGSG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galanis
                                                                                                          functional polypeptide;
single chain antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                          panning a NNK library of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hudson
                                                                                                                                                                                                                                                                                                                                                                 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monomeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Irving RA,
                                                                                                             ligand; non-functional;
ScFv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V-like domain in which at least loop is modified, useful for
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WO9920749-A1

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RESULT 9
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Best Local 9
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                                                                                                                                                                       Synthetic
                                                                                                                                                                                                Screening; functional polypeptide; ligand; enrichment; single chain antibody; ScFv.
                                                                                                                                                                                                                                     Clone selected after panning a NNK library of the invention
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                                                                                                                                                                                                                                                                                          AAY02516;
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             (MEDI-) MEDICAL RES COUNCIL
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llarity 100.0%;
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RESULT 10
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13-NOV-1997;
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The specification describes a method for screening for functional polypeptides which bind a ligand. The method comprises contacting repertoire of polypeptides with a generic ligand, and then screen
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enrichment; single chain antibody;
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                                                                                                                                                  Fig 4; 67pp; English.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening for functional polypeptides which bind a ligand
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ses 6; Conserv
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  expressed. The polypeptides obtained can be used in prophylactic and therapeutic procedures. AAV02473-Y02525 as selected after panning primary and somatic NNK antigens (bovine ubiquitin, rat BIP, bovine histone)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         functional polypeptide; ligand; non-functional;
  single chain antibódy; ScFv.
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97GB-0022131.
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Pred.
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1 AISGSG 6 |||||| 6 AISGSG 1

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RESULT 1:
AAY02520
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Best Local Similarity
6; Conserve
                                                                               The specification describes a method for screening for functional polypeptides which bind a ligand. The method comprises contacting a crepertoire of polypeptides with a generic ligand, and then screening selected functional polypeptides with a target ligand. The method comprises contacting a crepertoire of polypeptides, those contacts the removal from a chosen repertoire of polypeptides, those which are non-functional, e.g. as a result of the introduction of frame-shift mutations, stop codons, folding mutants or expression mutants which would be or are incapable of binding to any target ligand. The method also permits the enrichment of a chosen repertoire of polypeptides for those polypeptides which are functional, well folded and highly expressed. The polypeptides which are functional can be used in diagnostic, prophylactic and therapeutic procedures. AAY02473-Y02525 clibraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
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           Query Match
Best Local
 Matches
                                                  Sequence
                                                                                                                                                                                                                                                                                                                                 WPI; 1999-288302/24
                                                                                                                                                                                                                                                                              Example 3; Fig 4; 67pp; English.
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20-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                          13-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enrichment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening; functional polypeptide; ligand; non-functional
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Similarity 6; Conserv
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                                                  56 AA;
 Conservative
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                                                                        hen egg
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ilarity 100.0%;
Conservative 0
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97GB-0022131
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                                                                          Lysozyme).
           100.0%;
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           Score 28;
Pred. No.
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Pred. No.
 Mismatches
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             2e+02;
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Gaps
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RESULT 14
AAY02524
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XX
AC AAY02
XX
DT 15-JU
XX
DE Clone
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AAY02522
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                                                                                                                                             Query Match
Best Local Similarity
""" 6; Conserve
                                                                                                                                                                                                 The specification describes a method for screening for functional CC polypeptides which bind a ligand. The method comprises contacting a CC repertoire of polypeptides with a generic ligand, and then screening CC selected functional polypeptides with a target ligand. The method comprises contacting a CC permits the removal from a chosen repertoire of polypeptides, those CC which are non-functional, e.g. as a result of the introduction of CC frame-shift mutations, stop codons, folding mutants or expression CC migand. The method also permits the enrichment of a chosen repertoire CC ligand. The method also permits the enrichment of a chosen repertoire CC of polypeptides for those polypeptides which are functional, well folded and highly expressed. The polypeptides which are functional, well folded CC and highly expressed. The polypeptides obtained can be used in CC diagnostic, prophylactic and therapeutic procedures. AAY02473-Y02525 CC represent clones selected after panning primary and somatic NNK CC libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone, CC NIP-BSA and hen egg lysozyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-NOV-1997;
20-OCT-1997;
13-NOV-1997;
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Clone selected after panning a NNK library of the invention.
                     15-JUL-1999
                                        AAY02524;
                                                           AAY02524 standard; Protein;
                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                       Screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Tomlinson I,
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                                                                                                               AISGSG 11
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                    (first entry)
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97GB-0022131.
97US-0065428.
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Pred. No. 2e+02;
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AAY02525
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Best Local :
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20-OCT-1997;
13-NOV-1997;
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                                                             Synthetic.
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 20-OCT-1998;
                      29-APR-1999
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6; Conserv
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                                                                                                                                                                                                                                                                                                                56
                                                                                                                                  (first entry)
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97GB-0022131.
97US-0065428.
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                                                                                                                                                                            Protein;
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CC The specification describes a method for screening for functional CC polypeptides which bind a ligand. The method comprises contacting a CC repertoire of polypeptides with a generic ligand, and then screening CC selected functional polypeptides with a target ligand. The method CC permits the removal from a chosen repertoire of polypeptides, those CC which are non-functional, e.g. as a result of the introduction of CC frame-shift mutations, stop codons, folding mutants or expression CC mutants which would be or are incapable of binding to any target CC ligand. The method also permits the enrichment of a chosen repertoire CC of polypeptides for those polypeptides which are functional, well folded CC and highly expressed. The polypeptides obtained can be used in CC diagnostic, prophylactic and therapeutic procedures. AAYO473-Y02525 represent clones selected after panning primary and somatic NNK CC Ilbrarles with 5 antigens (bovine ubiquitin, rat BIP, bovine histone, CC NIP-BSA and hen egg lysozyme).
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Screening; functional polypeptide; enrichment; single chain antibody;
                                                                                                       Clone selected after panning a NNK library of the invention
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ilarity 100.0%;
Conservative
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Pred. No. 2e+
D; Mismatches
ligand; non-functional; ScFv.
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                                                                    Query Match 100.0%; Score 28; DB 20; Length 56; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 6; Conservative 0; Mismatches 0; Indels
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20-OCT-1997;
13-NOV-1997;
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                                                                                                                                                           Sequence
                                                                                                                                                                                              NIP-BSA and hen egg lysozyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-288302/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Fig 4; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tomlinson I, Winter G;
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                    1 AISGSG 6
6 AISGSG 11
                                                                                                                                                         56 AA;
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97GB-0022131.
97US-0065428.
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Search completed: August 20, 2003, 12:33:41 Job time: 14.1928 secs

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Total number
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Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB DB
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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1 AISGSG 6
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
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2 US-08-983-607-22
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2 US-08-983-607-38
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PCT-US93-10555-48
US-08-428-197-2
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US-08-428-197-48
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GENERAL INFORMATION:
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                              Matches
                                          Query Match
Best Local
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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ALIGNMENTS

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TELEPHONE: (619) 455-51
TELEFAX: (619) 455-511
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                             REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1800 -
STREET: LOS Angeles
CITY: California
                                                                                TOPOLOGY: 11
MOLECULE TYPE:
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 Similarity
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GY: linear
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1880 Century Park East - Suite 500
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                  Score 28; DB 2;
Pred. No. 1.6e+02;
   Mismatches
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; MOLECULE TYPE: protein
PCT-US93-10555-48
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PCT-US93-10555-48
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TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 48
                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
COMPUTER READABLE FORM
                                                                                                                             CORRESPONDENCE ADDRESS:
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LENGTH: 98 amino acids
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
                                                                                                                                              UMBER OF SEQUENCES:
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                                                                          CITY:
                                                                                        STREET:
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REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD
                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/
FILING DATE: 29-OCT-1993
CLASSIFICATION:
                                                                                                             ADDRESSEE:
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1880 Century Park East - Suite 500
                                   USA
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ZENTION: METHOD FOR STIMULATING PRODUCTION OF

ZENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH

ZENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Patent No. 614vz...
Patent No. 614vz...
PANERAL INFORMATION:
Alan C
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FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB
FILING DATE: June 28, 1996
CLASSIFICATION: 435
                                                                                                            OPERATING SYSTEM: MS DOS SOFTWARE: Word Processing CURRENT APPLICATION DATA:
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Huma
TITLE OF INVENTION: bod:
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                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                           APPLICATION NUMBER: US/08/9 FILING DATE: April 27, 1998 CLASSIFICATION: 435
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                                                                                                                                                                                                         COUNTRY: United ZIP: 06520-8114
                                                                                                                                                            COMPUTER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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United States of America
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                                                                                                                                                                                                                                                                                     Department of Molecular Biophysics and Biochemistry, Yale University
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                               PCT/IB96/01032
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Pred. No.
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US-08-983-607-36
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GENERAL INFORMATION:
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Best Local :
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amin
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                                                                             APPLICATION NUMBER: PCT/US93/1
FILING DATE: 29-OCT-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (6.9) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 116 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SILVERMAN TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
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ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
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REGISTRATION NUMBER:
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Similarity 100.0%;
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           116 amino acids
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1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                          USA
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VENTION: METHOD FOR STIMULATING PRODUCTION OF VENTION: VARIABLE RECION GENE FAMILY RESTRICTED ANTIBODIES THROUGH VENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
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Pred. No. 1
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Best Local Similarity
"hes 6; Conserva
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US-08-545-809A-109
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Best Local S
Matches 6
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SEQUENCE CHARACTERISTICS
LENGTH: 117 amino acid
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MEDIUM TYPE: Diskette
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/545,809A FILING DATE: 27-MAR-1996
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM:
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                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                            NAME: Freeman, John W
REGISTRATION NUMBER:
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69 AISGSG
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SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
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Pred. No.
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Pred. No.
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RESULT 7 US-08-983-607-46

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RESULT 8
US-08-652-816A-12
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Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: Osbourn
APPLICANT: Allen, 1
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US-08-983-607-46
                                                 Sequence 12, Application US/08652816A Patent No. 5872215
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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3.5" 1.44 Mb diskette
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APPLICANT: Xiaohong Cai
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nes 6; Conserv
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FILING DATE: April 27, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DESCRIPTION:
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REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 0
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STRANDEDNESS: single
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 Allen, DJ
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              Osbourn, JK
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cytes
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                                                                      Patent No. 6140470 GENERAL INFORMATION:
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Best Local (
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APPLICANT: Alan Garen APPLICANT: Xiaohong CaTITLE OF INVENTION: HUTITLE OF INVENTION: bc
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER:
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les 6; Conserv
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FILING DATE: 02-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                     118 amino acids
                                                                                                                                                                                                                                          Conservative
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/BNTION: Specific binding members, materials
                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                     312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: GB 9206318.9
24-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-1991
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23-SEP-1992
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             Human Anti-Tumor Monoclonal Anti-
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Pred. No.
                                                                                                                                                                                                                                          Mismatches
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ches 0;
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NUMBER OF SEQUENCES:

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; NAME/KEY: heavy chain US-08-983-607-22
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                                                                                                                                                                        ENERAL INFORMATION:
                                                                                                                                                                                       tent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" 1.44 Mb diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
DESCRIPTION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                  APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                    APPLICANT:
                                                                                                                      APPLICANT:
                                                                                                                                      APPLICANT:
                                                                                                      APPLICANT:
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....EE: amino acid
STANDEDNESS: "'
"OPOLOGY: "
"CULF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/IB96/01032 FILING DATE: June 28, 1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States of America ZIP: 06520-8114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Department of Molecular Biophysics ADDRESSEE: and Biochemistry, Yale University STREET: 266 Whitney Avenue CITY: New Haven
                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 6; Conserv
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6300064
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Ilag, Vic
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ilarity 100.0%;
Conservative (
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April 27, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide
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F. Haley, Jr., Esq. c/o Fish & Neave
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                               Mismatches
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RESULT 11
US-09-025-769B-63
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INFORMATION FOR SEQ ID NO:
                                                                                                tent No.
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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION UNMER: EP 95
APPLICATION UNMER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: EP 9
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Leg York
                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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TOPOLOGY: linear
                                                                                        COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                            TLE OF INVENTION:
                                                                                                                                                                                                  CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: James F. Haley, Jr., NAME: James F. Haley, Jr., 194
                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocal Similarity
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5. 6300064
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Pred. No.
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NAME: James F. Haley, REGISTRATION NUMBER: 2

Jr.,

Esq.

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RESULT 13
US-08-428-197-38
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                                                                                                                                        Query Match
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Best Local :
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                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,897
FILING DATE: 21-0CT-1996
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212)596-9090 INFORMATION FOR SEQ ID NO: 63: SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
APPLICANT:
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TOPOLOGY: 1:-
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CLONE: 2G
                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Johnson, Kevin
TITLE OF INVENTION: Specif
TITLE OF INVENTION: materi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 600
STREET: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: MO
TELECOMMUNICATION INFORMATION:
                                                                                                              Local Similarity
les 6; Conserv
                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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5977319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pritchard,
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anthony R
                                                                                                                          100.0%;
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                                                                                                                          Score 28;
Pred. No.
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Pred. No.
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2e+02;
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                                                                                                                                     Length 122;
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RESULT 14
PCT-US93-10555-38
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Best Local Similarity
Matches 6; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: W
TITLE OF INVENTION: V
TITLE OF INVENTION: T
TITLE OF INVENTION: T
NUMBER OF SEQUENCES:
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                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                        STREET: 1000
CITY: Los Angeles
STATE: California
                                                                                                                                                                             TITLE OF INVENTION: VA
TITLE OF INVENTION: TH
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-CCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Howells, Stacy L. REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1880 Centu
CITY: Los Angeles
STATE: California
                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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                                                                         90067
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                                                                                                                                                                                                                                                                                                                           Application PC/TUS9310555
                                                                                                                                            E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 amino acids
                                                                                                                                                                                                                                                                                        SILVERMAN, GREGG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SILVERMAN, GREGG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                  55
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                   METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
                                                                                                                                                                                                                    THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED VACCINATION WITH A B-CELL SUPERANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34,842
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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AND CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-10555-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-983-607-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative 0
                                                                                                            APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEPHONE: 203-773-9544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human An
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                          TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (619) 455-5110 NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quence 51, Application US/08983607 tent No. 6140470
                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS DOS
SOFTWARE: WORD PROCESSING
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: FD TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" 1.44 Mb diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Department of Molecular Biophysics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TY: New Haven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 AISGSG 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RY: United States of America 06520-8114
                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 Whitney Avenue
                                      124 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xlachong Cai
VENTION: Human Anti-Tumor Monoclonal Anti-
                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC
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single
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; NAME/KEY: heavy chain US-08-983-607-51
Search completed: August 20, 2003, 12:44:18 Job time: 5.15663 secs
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                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                         LIBRARY: VH antibodies obtained from fUSE5
LIBRARY: fusion phage construct
CLONE: E-13
                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens (melanoma patient ORGANISM: immunized with autologous tumor cells) INDIVIDUAL ISOLATE: peripheral blood lympho-INDIVIDUAL ISOLATE: cytes
                                                                    50 AISGSG 55
                                                                                                  1 AISGSG 6
                                                                                                                                  100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide
                                                                                                                                    Score 28; DB
Pred. No. 2e+
0; Mismatches
                                                                                                                                                                        DB 3; Length 124;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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28
1 AISGSG 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_AA: *
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) /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
) /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
1. /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
2. /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
3. /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
4. /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
5. /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
6. /cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
6. /cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
7. /cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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       177
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 US-09-968-561A-14
US-09-968-561A-38
US-09-968-561A-74
US-09-968-561A-86
US-09-968-561A-86
US-09-968-561A-128
US-09-968-561A-128
US-09-968-561A-128
US-09-968-561A-134
US-09-968-561A-146
US-09-968-561A-146
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Sequence 27, Appl
Sequence 10, Appl
Sequence 14, Appl
Sequence 38, Appl
Sequence 68, Appl
Sequence 74, Appl
Sequence 80, Appl
Sequence 12, Appl
Sequence 122, Appl
Sequence 124, Appl
Sequence 124, Appl
Sequence 146, Appl
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45	44	43	42	41	40	39	38	37	36	3 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16 .
28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28
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17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17
12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	11	10	10	10	10	10	10	10	10	10	10	10
-09-968-7442	9-968-7442	-09-968-7442	-09-968-7442	-09-968-7442	-7442	9-968-	-744F	-7442	-968-7442	-968-744P	-968-744F	-09-968-744P	-09-968-744P	-09-968-7442	-09-968-744P	-09-968-744A	-968-744A	S-09-972-656-	-09-968-561A	-968-561A-	-968-561A	9-968-561A	-09-968-561A-	-561A-	ե	-09-968-561A-	-09-968-561A-	-09-968-561A-	US-09-968-561A-194
260,	e 236,	e 218,	212,	•	e 188,	146,	e 140,	e 134,	128,	122,	e 92, /	86,	, 08	74,	68,	38,	14,	45,	314	e 308	e 296,	e 284,	e 272,	•	•	e 236,	•	e 212,	-
App	App	App	App	App	App	App	App	App	Αpp	App	1dö	Appl	1do	op1	Appl	pp1	1dd	ppl	, App	dd∖	dd	dd	ddy	ďď€	App	ģ	dd	dd	qq

ALIGNMENTS

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; OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B; OTHER INFORMATION: antibody clone US-09-300-425B-27
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                                                                                                                                                                                                                                                                        SOFTWARE: F
SEQ ID NO 27
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27, Application US/09300425B Publication No. US20030045681A1
                                                                            Matches
                                                                                                                                                                                                                                                                                                                              APPLICANT: NERI, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: VIII, Francesca
APPLICANT: VIII, Francesca
APPLICANT: BIRCHLER, MADÍTE
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
TITLE OF INVENTION: ANGIOGENESIS
FILE REFERENCE: SCH-1733P1
CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1998-05-11
NUMBER: OF SEQ ID NOS: 34
NUMBER: OF SEQ ID NOS: 34
NUMBER: OF SEQ ID NOS: 34
                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                     1 AISGSG 6
1 AISGSG
                                                                          Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                PatentIn Ver. 2.1
                                                                            Conservative
                                                                                             100.0%;
                                                                              0
                                                                          Score 28; DB 11;
Pred. No. 4.5e+05;
); Mismatches 0;
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                                                                                                                 Length 6;
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RESULT 2

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                                                                                          RESULT 4
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US-09-968-561A-14
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                     GENERAL
                                    Sequence 38, Application US/09968561A Patent No. US20020164642A1
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: P
SEQ ID NO 14
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local Similarity' 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 10
LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
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CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver. 2.0
APPLICANT:
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TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
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APPLICANT: Tomlinson, Ian
TITLE OF INVENTION: Methods
FILE REFERENCE: 3789/72916
                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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Tomlinson, Ian M
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Matches 6
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SEQ ID NO 68
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LENGTH: 17
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PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
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PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
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TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
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                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 350
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CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
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TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
FILE REFERENCE: 8039/1073B
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RESULT 6 US-09-968-561A-74 ; Sequence 74, Application US/09968561A

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-80
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CURRENT APPLICATION NUMBER: US/09/968,561A

CURRENT FILING DATE: 2001-10-01

PRIOR APPLICATION UMBER: GS 9722131.1

PRIOR FILING DATE: 1997-10-20

PRIOR FILING DATE: 1997-11-21

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: US 60/065,729

PRIOR APPLICATION NUMBER: US 60/066,729

PRIOR FILING DATE: 1997-11-21

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: US 60/061,729

PRIOR APPLICATION NUMBER: US 60/061,729

PRIOR APPLICATION NUMBER: US 60/061,729

PRIOR APPLICATION NUMBER: US 60/0511,939

PRIOR FILING DATE: 1998-10-20

PRIOR FILING DATE: 1908-20-24
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US-09-968-561A-74
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ITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
ILE REFERENCE: 8039/1073B
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ITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
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FILING DATE: 1997-11-21
APPLICATION NUMBER: PCT/GB98/03135
FILING DATE: 1998-10-20
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US-09-968-561A-86
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                                                                                  ; ORGANISM: Homo sapiens US-09-968-561A-92
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PRIOR FILING DATE: 1997-10-20

PRIOR PPLICATION NUMBER: US 60/065,248

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: US 60/066,729

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: PCT/GB98/03135

PRIOR FILING DATE: 1998-10-20

PRIOR FILING DATE: 1998-10-20
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PRIOR FILLING DATE: 1997-10-20

PRIOR PELICATION NUMBER: US 66/065,248

PRIOR FILLING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: US 66/066,729

PRIOR FILLING DATE: 1997-11-21

PRIOR FILLING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: PCT/GB98/03135

PRIOR FILLING DATE: 1998-10-20
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  Matches
                     Query Match
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TITLE OF INVENTION: Wethod to Screen Phage Display Libraries
FILE REFERENCE: 8039/1073B
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APPLICANT: Winter, Gregory
TITLE OF INVENTION: Wethod to Screen Phage Display Libraries with Different Ligand
FILE REFERENCE: 8039/1073B
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TYPE: PRT
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US-09-968-561A-128
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                                                                                                                                                                        SEQ ID NO 128
      Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR APPLICATION 11997-11-21
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR APPLICATION NUMBER: US 60/066,729
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PRIOR FILING DATE: 1998-10-20
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TIFLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
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PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
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APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
                                                                                                                               LENGTH: 17
TYPE: PRT
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                     Local Similarity
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Score 28; DB Pred. No. 28; 0; Mismatches
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US-09-968-561A-134
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JS-09-968-561A-140
                                                                                 SEQ ID NO 140
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Patent No. US20020164642A1
                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: GB 9722131.1 PRIOR FILING DATE: 1997-10-20 PRIOR APPLICATION NUMBER: US 60/065,248 PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
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                                                                                                         SOFTWARE:
                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 8039/1073B
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TITHE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
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PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
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                   ORGANISM: Homo sapiens
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OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
                                                                                                                                                                    APPLICATION NUMBER: US 09/511,939
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US-09-968-561A-188
; Sequence 188, Application US/09968561A
; Patent No. US20020164642A1
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                                                                                CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
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CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR APPLICATION NUMBER: PCT/GB98/03135
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PRIOR FILING DATE: 1998-10-20
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SOFTWARE: Paten
SEQ ID NO 146
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APPLICANT: Tomlinson, Ian M
APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
SEQ ID NO 188
LENGTH: 17
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TYPE: PRT
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TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
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; ORGANISM: Homo sapiens US-09-968-561A-188
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Query Match 100.0%; Score 28; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 AISGSG 6
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Db 1 AISGSG 6

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Title: Perfect score: Sequence: Result No. Minimum Maximum Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s Total number of hits satisfying chosen parameters: Scoring table: OM protein - protein search, using sw model Database Searched: 9 Pred. score and is B B Score No. 1s the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
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1: p1r1:*
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4: p1r4:* BLOSUM62 Gapop 10.0 , 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 100.00 August 20, 2003, 12:25:56; Search time 4.19277 Seconds (without alignments)
137.621 Million cell updates/sec 283308 seqs, 96168682 residues Copyright Length GenCore version (c) 1993 - 2003 DВ Gapext PH1649 S24250 S24250 S24250 S69911 PH16477 S24247 S24247 S24247 S2550 B34964 \$24259 \$24259 \$24258 \$24258 \$24257 \$24260 \$24255 \$24255 Į summaries 0 SUMMARIES 5.1.6 Compugen Ltd. 283308 Description heavy chain v r heavy chain pre heavy chain pre heavy chain pre heavy chain v r heavy chain - h heavy chain - h

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R;Stewart, A.K.; Huang, C.;
submitted to the EMBL Data L
A;Description: A single VH g
A;Reference number: S24247
A;Accession: S24257
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S24260
                                                                                    Ig heavy chain V region (VH26-DA1-JH4) - human C;Species: Homo sapiens (man) C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_C;Accession: S24260 R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S. submitted to the EMBL Data Library, June 1992
                                 A; Description: A single VH
A; Reference number: S24247
A; Accession: S24260
   A; Molecule
                    A;Status:
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C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24258
C:Accession: S4.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
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A;Molecule type: DNA
A;Residues: 1-100 <STE>
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A;Accession: S24258
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Pred. No. 35;
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S24249
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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C;Accession: S24249
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C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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A; Cross-references: EMBL:X67068
A; Cross-references: EMBL:X67068
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 5-87/Domain: immunoglobulin homology <IMM>
                                                                                                                                F;10-92/Domain: immunoglobulin homology
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A; Residues: 1-105 <STE>
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A; Accession: S24255
A; Status: preliminary
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C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
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A; Residues: 1-104 <STE>
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44 AISGSG
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C;Accession: PH1648
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1642; MUID:93301610; PMID:8315388
A;Molecule type: mRNA
A;Residues: 1-108 <HIL>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-106 <STE>
A;Cross-references: EMBL:X67064; NID:g38385; PIDN:CAA47449.1; PID:g38386
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;4-86/Domain: immunoglobulin homology <IMM>
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A; Molecule type: DNA
A; Residues: 1-106 <STE
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submitted to the EMBL Data Library, June 19
A;Description: A single VH gene predominate
A;Reference number: $24247
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                                                         A; Molecule type: mRNA
A; Residues: 1-109 <HIL>
A; Residues: 1-109 <HIL>
A; Experimental source: B cell
C; Superfamily: immunoglobulin V region; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
E; 7-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                              R:Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1649
                                                                                                                                                                                                                                                                                 Ig heavy chain V region (clone 2E7) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1649
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A; Decewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S. submitted to the EMBL Data Library, June 1992
A; Description: A single VH gene predominates in the rearr A; Reference number: S24247
A; Accession: S24253
A; Accession: S24253
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A;Residues: 1-109 <STE>
A;Residues: 1-109 <STE>
A;Cross-references: EMBL:X67062
A;Cross-refamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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C;Keywords: heterotetramer; immunoglobulin
F;12-94/Domain: immunoglobulin homology <I</pre>
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A; Reference number: S24247
A; Accession: S24254
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submitted to the EMBL Data Library, June 1992
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R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Sci
submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates:
A;Reference number: S24247
                                                               Ig heavy chain V region (VH26-DN1-JH4) - C;Species: Homo sapiens (man) C;Date: 19-Feb-1994 #sequence_revision 10 C;Accession: $24250
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A; Residues: 1-109 <STE>
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predominates in the

rearranged

and

expressed

human

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Ig heavy chain V region (clone 2D10) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1647
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyld A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Molecule type: mRNA
A;Residues: 1-112 <HIL>
A;Residues: 
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-111 <SAH>
A;Cross-references: EMBL: 233401
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMN>
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Leukemia 8, 1285-1289, 1994
A;Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of mult.
A;Reference number: S69909; MUID:94335315; PMID:8057663
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A;Cross-references: EMBL:X67071
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-110 <STE>
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A; Status: preliminary
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"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

1- FUNCTION: Together with moaA, is involved in the conversion of a
Archaeoglobus fulgidus.
Archaea; Euryarchaeota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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RESULT 4
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        Smith D.R., Doucette-Stamm I.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shmer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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Nature 390:364-370(1997).
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                                                                                                                                                                                                                                                                          Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Ko Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; Rubota K., Sako Y., Kikuchi H.; Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Ki.";
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SEQUENCE 1
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                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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Desulfurococcaceae; Aeropyrum.
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                                                                    Hypothetical protein;
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15-SEP-2003 (Rel. 42, Last sequence update)
Serine--pyruvate aminotransferase, mitochondrial precursor
(EC 2.6.1.51) (SPT) (Alanine--glyoxylate aminotransferase)
(EC 2.6.1.44) (AGT).
AGXT OR AGT1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILUMD M.J., Purdue P.E., Danpure C.J.;

"Molecular evolution of alanine/glyoxylate aminotransferase 1

"ntracellular targeting. Analysis of the feline gene.";

Eur. J. Blochem. 221:53-62(1994).

-I- FUNCTION: DUAL METABOLIC ROLES OF GLUCONEOGENESIS (IN THE
MITOCHONDRIA) AND GLYOXYLATE DETOXIFICATION (IN THE PEROXISOMES)

-I- CATALYTIC ACTIVITY: L-serine + pyruvate = 3-hydroxypyruvate + L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: L-alanine + glyoxylate
-!- COFACTOR: Pyridoxal phosphate.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX
-!- ALTERNATIVE PRODUCTS:
Event-Alternative initiation;
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Mammalia; Eutheria; Carnivora;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   are produced by alternative : IMILARITY: Belongs to class-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Comment-2 isoforms, Mitochondrial (shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000192; Aminotransfv.
                                                                                                                     414
                 100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                        231
                                                                                                                                                                                                                                                                                         Aminotransferase; Pyridoxal phosphate; Peroxisome;
n; Transit peptide; Alternative initiation.
23 AMITOCHONDRION (BY SIMILARITY).
24 414 SERINE--PYRUVATE AMINOTRANSFERASE,
1SOFORM MITOCHONDRIAL.
                                                                                                                                                                                                                                                                     23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116
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                                                                                                                                                                                                                                                                     414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  us (Cat).
Chordata; Craniata; Vertebrata;
Carnivora; Fissipedia; Felidae;
                                                                                                                                                                      23
231
414
                                                                                                                        45507
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                       0
                                                                                                                   SIMILARITY).
, OD1B01E0E9A199B3 CRC64;
                    Score 28; DE Pred. No. 92; ); Mismatches
                                                                                                                                                                         MICROBODY TARGETING
                                                                                                                                                                                          FOR ISOFORM PEROXISOMAL.
PYRIDOXAL PHOSPHATE (BY
                                                                                                                                                                                                                                                                     SERINE -- PYRUVATE AMINOTRANSFERASE,
                                                                                                                                                                                                                                              ISOFORM PEROXISOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                     Length 414;
                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostom1;
                                                                                                                                                                         SIMILARITY)
NAL (BY
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99

AISGSG

104

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RESULTA

AC P5

AC AG

AC P5

AC AG

AC P5

AC AG

  RN OCC OCC DT DT AC
                                                                                                                                                                                                                                                                                        RESULT
DHE4_AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                   P54387;
01-OCT-1996
01-OCT-1996
16-OCT-2001
Agaricales; Agar
NCBI_TaxID=5341;
[1]
                                             Eukaryota; Fungi; Basidio
Agaricales; Agaricaceae;
                                                                                                                        GDHA.
                                                                                                                                    01-OCT-1996 (Rel. 34, C)
01-OCT-1996 (Rel. 34, La
01-OCT-2001 (Rel. 40, La
NADP-specific glutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF02812; GLFV_dehydrog_N; 1.
PRINTS; PR00082; GLFDHDRGNASE.
PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P54388;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation updat
NADP-specific glutamate dehydrogenase (EC 1
                                                                                            Agaricus bisporus
                                                                                                                                                                                                                                                               DHE4_AGABI
                                                                                                                                                                                                                                                                                           AGABI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006095; GLFV_dehydrog.
InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
InterPro; IPR000205; NAD_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lorillou S.S., Martin F.F.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ
-!- CATALYTIC ACTIVITY: L-glutamate + H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; NADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laccaria bicolor.
Eukaryota; Fungi; Basidiomycota;
Agaricales; Tricholomataceae; Lac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBUNIT: Homohexamer (By similarity).
-1- SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-S238N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=29883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DHE4_LACBI
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                                                                                                                                                                                                                                                                                                                                                                                        223 AISGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U31369; AAA82936.1; P24295; 1AUP.
                                                                                                                                                                                                                                                                                                                                                                                                                   1 AISGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               450 AA; 48474 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                . 34, Createu,
. 34, Last sequence upda
1. 40, Last annotation ur
1. 40, dest annotation ur
                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                     228
                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                             Basidiomycota; Hymenomycetes; caceae; Agaricus.
                                                                                          (Common mushroom)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ta; Hymenomycetes; Laccaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B803A30FBAF22090 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.
                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                               457
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(EC 1.4.1.4)
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(EC 1.4
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                                                                                                                                                                                                                                                               AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.4.1.4) (NADP-GDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J databases.
+ NADP(+) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                   Homobasidiomycetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homobasidiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                         (NADP-GDH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2-oxoglutarate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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HSSP; P24295; 1AUP.
InterPro; IPR006095; GLFV_dehydrog_C.
InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF02812; GLFV_dehydrog; 1.
PF10312; PF02812; GLFV_DEHYDROGENASE; 1.
PRINTS; PR00082; GLFV_DEHYDROGENASE; 1.
PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
Oxidoreductase; NADP
ACT_SITE 11 11
BY SIMILARITY
SEQUENCE 457 AA; 49557 MW; 1BF0E97F670;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-89384423; PubMed-2550758;

MEDLINE-89384423; PubMed-2550758;

Hawkins A.R., Gurr S.J., Montague P., Kinghorn J.R.;

"Nucleotide sequence and regulation of expression of nidulans gdhA gene encoding NADP dependent glutamate nidulans gdhA gene encoding NADP dependent glutamate

"Com Genet. 218:105-111(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P18819;
01-NOV-1990
01-NOV-1990
01-OCT-1996
                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no protections of the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
NADP-specific glutamate dehydrogenase (EC 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96180651; PubMed-8602149; Schaap P.J., Mueller Y., Baars J.J.P., Op den Camp H.J.M., Sonnenberg A.S.M., van Griensven L.J.L.D., Visser J.; "Nucleotide sequence and expression of the gene encoding NADP+dependent glutamate dehydrogenase (gdhA) from Agaricus bisporus."; Mol. Gen. Genet. 250:339-347(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eurotiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DHE4_EMENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOÎ. Gen. Genet. 250:33y-34/(בידים).
-!- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NADP(+) = 2-oxoglutarate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBUNIT: Homohexamer (By similarity).
-1- SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-Horst H39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G
                                                                                                                                                                                                                    CATALYTIC ACTIVITY: L-glutamate + H(2)0 + + NH(3) + NADPH.
SUBUNIT: Homohexamer.
                                                                                                                                                                                    SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 AISGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X83393; CAA58312.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AISGSG 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trichocomaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a; Pezizomycotina;
Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28;
Pred. No.
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1BF0E97F67078AC4 CRC64;
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Best Local S
Matches
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMI1_MYCTU
005835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X16121; CAA34252.1; ...
HSSP; P24295; 1AUP.
InterPro; IPR006095; GLFV_dehydrog.
InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
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Pfam; PF02812; GLFV_dehydrog_N; 1.
PRINTS; PR00082; GLFDHDRGNASE.
PROSITE; PS00074; GLFV_DEHYDROGENASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative amidase amiA2 (EC 3.5.1.4).
AMIA2 OR RY2363 OR MT2432 OR MTCY27.17C.
                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Peterson J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Stolonay J.F., Nelson W.C., Umayam L.A., Khouri H., Gill J., Mikula,

Peterson A., Utterback T., Weldman J., Khouri H., Gill J., Mikula,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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ACT_SITE 114 11
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European Bioinformatics Institute. The by non-profit institutions as long
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REMBL; AE007082; AAK46726.1; -.

REMBL; AF007082; AAK46726.1; -.

RIGR; M72432; -.

Tuberculist; Rv2363; -.

RIGR; M72432; -.

InterPro; IPR000120; Amidase.

Pfam; PF01425; Amidase; 1.

RPGOSITE; PS00571; AMIDASES; 1.
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bowditch R.D., Baumann P., Yousten A.A.;

"Cloning and sequencing of the gene encoding a 125-kilodalto surface-layer protein from Bacillus sphaericus 2362 and of a cryptic gene.";

J. Bacteriol. 171:4178-4188(1989).

-I- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.

-I- SUBCELLULAR LOCATION: Cell wall.

-I- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1994 (Rel. 30,
01-OCT-1994 (Rel. 30,
01-FEB-1996 (Rel. 33,
Surface-layer 125 kDa
                                                                                                                                                                                                          Signal;
SIGNAL
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MEDLINE=89327128; PubMed=2666389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus sphaericus.
Bacteria; Firmicutes;
NCBI_TaxID=1421;
                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                      EMBL; M28361; AAA50256.1; PIR; A33856; A33856.
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                                                                                                                                                                                                                                                     Pfam; PF00395; SLH; 3. PROSITE; PS01072; SLH_DOMAIN;
                                                                                                                                                                                                                                                                             InterPro; IPR001119; SLH. Pfam; PF00395; SLH; 3.
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protein precursor.
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                                                                                         POTENTIAL.
SURFACE-LAYER 1
SLH 1.
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Pred. No. 2.7
0; Mismatches
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                                    EMBL; M33557; AAA25975.1; -. EMBL; AE004476; AAG03782.1; -. EMBL; M55524; AAA25958.1; -. PIR; JQ0418; JQ0418. InterPro; IPR000304; P5CR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-APCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrene, Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lag Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E. M., Lory S., Olson M.V.;
                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                           Pfam; PF01089; P5CR; 1.
                                                                                                                                                            modified
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Mattick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Savioz A., Jeenes D.J., Kocher H.P., Haas D.; "Comparison of proC and other housekeeping genes of Pseudo aeruginosa with their counterparts in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                        "Characterisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF STRAIN-ATCC 15692 / PAO1;
STRAIN-90185238; PubMed-2107123;
MEDLINE-90185238; PubMed-2107123;
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01-AUG-1991 (Rel. 19, La
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Pyrroline-5-carboxylate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonadaceae;
NCBI_TaxID=287;
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carboxylate + NAD(P)+
PATHWAY: Proline biosynthesis; third (last) step.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
SIMILARITY: BELONGS TO THE PYRROLINE-5-CARBOXYLAT
                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Encopean Bioinformatics Institute. There are no resti
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                                                                                                                                                                                                                                                                                                                                                                                  "Over-expression of a new photo-active halorhodopsin salinarium.";
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Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                     TRANSMEM
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                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
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MEDLINE=96130249; PubMed=8541296;
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PA6725;
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Pyrroline-5-carboxylate reductase (FPROC OR ML2430 OR B2168_C2_211.
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Barrell B.G.;

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I parhway: Proline biosynthesis; third (last) step.
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Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                          SEQUENCE
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TIGRRAMS; TIGRO1112; PTOC; 1.
PROSITE; PS00521; P5CR; 1.
Oxidoreductase; Proline blosy
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Barrell B.G.;
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01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C., III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.";
Submitted (APR-2001) to the
-!- CATALYTIC ACTIVITY: L-pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umbyam L.A., Ermolaeva M.D., Salzberg

Rolcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FDB-2003 (Rel. 41, Last annotation updat
Pyrroline-5-carboxylate reductase (EC 1.5.)
PROC OR RV0500 OR MT0520 OR MTCY20G9.26.
                                                                                                                                                                                                                                                                 TubercuList; Rv0500;
InterPro; IPR000304;
Pfam; PF01089; P5CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z77162; CAB00926.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98295987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitted (APR-2001) to the EMBL/GenBank/DDBJ databases CATALYTIC ACTIVITY: L-proline + NAD(P)(+) = 1-pyrro carboxylate + NAD(P)H.

PATHWAY: Proline blosynthesis; third (last) step.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE PYRROLINE-5-CARBOXYLATE
                                                                                                                                                                                                                                                                                                                                                                          ; AE006952; AAK, G70745; G70745;
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5; Conser
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                                                                                                                                                             ine biosynthesis; NADP; Complete proteome. 30171 MW; F95C3F407BE5408F CRC64;
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83.3%;
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Search completed: August 20, 2003, 12:34:52
Job time: 4.38822 secs

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Q27589
Q9N8A7
Q9NWZ1
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Q8NQH7
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                  Q9n8a7 trypanosoma
Q8xxv21 ralstonia s
Q8nq77 corynebacte
Q971j2 clostridium
Q93tv0 pseudomonas
Q94129 aspergillus
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0976j2 sulfolobus
08zx34 pyrobaculum
0980x4 sulfolobus
0980x7 cryptospori
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Q8pug7 methanosarc
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ALIGNMENTS

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RESULT 1
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STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; PubMed-11466286;

MEDLINE-21359325; PubMed-11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing

bacterium Clostridium acetobutylicum.";

J. Bacteriol 183:4823-4438(2001).

EMBL, AE007554; AAK78377.1; -.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Pred. No. 3e+
); Mismatches
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EMBL; AP000981; BAB55155.1; -
InterPro; IPR001347; SIS.
Pfam; PP01380; SIS; 1
Hypothetical protein; Complete p
SEQUENCE 195 AA; 21350 MW; A
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Q976J2;
Q1-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                                                           "Genome sequence of the hyperthermophilic crenarchaeon aerophilum.":
                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=IM2 / ATCC 51768 / PubMed=11792869;
                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21, conserved protein with sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;
                                                                            Proc. Natl. Acad. Sci. U.S.A. EMBL; AE009824; AAL63515.1; -InterPro; IPR001347; SIS.
                                                                                                                                                                                                    Thermoproteaceae; NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                   Q8ZX34;
                                                                                                                                                                                                                                                                                                                Q8ZX34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-JCM 10545
PubMed=11572479;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein ST0198.
                                                                                                                                            Fitz-Gibbon S.T., Ladner H.,
                                                                                                                                                                                                                                    Pyrobaculum aerophilum.
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                                                                                                                                   Miller J.H.;
                                                                                                                                                                                                                      Archaea; Crenarchaeota; Thermoprotei;
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                                                                    PF01380; SIS;
                                                                                                                                                                                                                                                                                                                                                                      84
 Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          AISGSG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crenarchaeota;
                                             Complete 202 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                              Pyrobaculum
                                             proteome.
22092 MW;
          100.0%;
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100.0%; F
tive 0;
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Last annotation update)
r isomerase (SIS) domain
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                                                                                                                                            Kim U.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB
Pred. No. 3.2
); Mismatches
         Score 28;
Pred. No.
                                                                                                  99:984-989(2002)
                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteome.
ABAD918947DB8BBF
                                           138068682FE1C45A CRC64;
 Mismatches
                                                                                                                                                                                                                                                                                                                202
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                                                                                                                                                                                                                                                                                                                                                                                                                         DB 17;
. 3.2e+02;
           3.4e+02;
                                                                                                                                            Stetter K.O.,
                       DB 17;
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on update)
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                    Length 202;
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Indels
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                                                                                                                                            Simon M.I.,
                                                                                                                      Pyrobaculum
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Gaps
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RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
        Chung P.A., Johnson J., Khramtsov N.V., Upton S.J.;

"Cloning and molecular characterization of a gene encoding a
Cryptosporidium parrum putative 20s proteasome betal-type subunit.";

DNA seq. 11:309-314(2000).

-I- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX

WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH AR

PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL

SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN-ATCC 35092 / DSM 1617 / P2;

MEDLINE-21332296; PubMed-11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

She Q., Singh R.K., Confalonieri F., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.I., Doolittle W.F., Duguet M., Gaasterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                           MEDLINE=20541292; PubMed=11092745;
                                                                                                                                         STRAIN-KSU-
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                            Eukaryota; Alveolata;
Cryptosporidiidae; Cry
                                                                                                                                                                                                                        Cryptosporidium parvum
                                                                                                                                                                                                                                                                                01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                             Q9NJV7;
                                                                                                                                                                                                                                                                                                                            Q9NJV7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
D-arabino 3-hexulose 6-phosphate formaldehyde lyase
                                                                                                                                                                                                                                                      Proteasome B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2287;
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SE 209 AA; 22980
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MBLrel. 15,
MBLrel. 22,
e subunit.
                                                                                                                                                                                              Cryptosporidium
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                                                                                                                                                                                                             Apicomplexa;
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Last sequence update)
Last annotation updat
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Pred. No.
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           E LEAVING GROUP AT NEUTRAL OR AN ATP-DEPENDENT PROTEOLYTIC
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RX MEDLINE-C1929760; pubMed=11932238;

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

RA Allen N., Naylor J., Stange-Thomann N., DeArellano'K., Johnson R.,

Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Linton L., McEwan P., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

RA Linton L., McEwan P., Kokernan K., Talamas J., Tirrell A., Ye W.,

RA Linton L., McEwan P., Kokernan K., Talamas J., Tirrell A., Ye W.,

RA Linton L., McEwan P., Kokernan K., Talamas J., Tirrell A., Ye W.,

RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

RA Hedderich R., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,

RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Metcalf W.W., Birren B.;

RA Metcal
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Best L
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Best Local (
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PRINTS; PR00141; PROTEASOME.
PROSITE; PS00854; PROTEASOME_B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanococci;
Methanosarcinaceae; Methanosarcina.
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                                                                                                                                                                                                                                                                                                        Pfam; PF01380; SIS;
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                                                                                                                                                     Local
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SIMILARITY: BELONGS TO I
L; AF097521; AAF72737.1;
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SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTIC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE (BY
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105
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AISGSG 110
                                                                                                                                                                                                                                                 Complete 216 AA;
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22962 MW; 1
                                                                                                                                                                                                                                              proteome.
23538 MW;
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Pred. No.
                                                                                                                     Score 28; DB 17;
Pred. No. 3.6e+02;
; Mismatches 0;
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3.5e+02;
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                                                                                                                                                                                Length 216;
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STRAIN-GOE1 / GO1 / ATCC BAA-199 / DSM 3647 /
MEDLINE-22120827; PubMed-12125824; Merkl [
                                                                        MEDLINE-98037514; PubMed-9371463;
Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabbakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                       027589
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SEQUENCE
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01-JAN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanococc
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Ul-MAR-2003 (TrEMBLrel. 23, La
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                                                                                                                         MEDLINE-21681879; PubMed-11823852;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Cholsne N., Claudel Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Mature 415:497-502(2002).
EMBL; AL646071; CAD16391.1; -.
Interpro; IPR000304; P5CR.
Pfam; PF01089; P5CR; 1.
                         TIGREAMS; TIGRO0112; proC; 1. PROSITE; PS00521; P5CR; 1. Oxidoreductase; Complete prot
SEQUENCE
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable oxidoreductase pyrroline-5-carboxylate red
peptide protein (EC 1.5.1.2)
PROC OR RSC2684 OR RS00037.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-GMI1000;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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RESULT
Q8NQH7
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Best Local Similarity
6; Conserve
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Best Local S
Matches 6
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01-OCT-2002
01-OCT-2002
                Tatusov R.L., Sabathe F., Doucette-Stamm I Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis bacterium Clostridium acetobutylicum."; J. Bacteriol. 183:4823-4838(2001).
                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makar Gibson R., Lee H.M., Dubois J., Qiu D., Hitti
                                                                                                                                                                                                    01-OCT-2001 (TrEMBLrel. 01-OCT-2001 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genomic sequence of Submitted (MAY-2002) to the EM EMBL; AP005278; BaB98850.1; -. InterPro; IPR000281; HTH_RpIR. InterPro; IPR001347; SIS.
                                                                                                                                         Clostridium.
NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-ATCC 13032 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcriptional regulators CGL1457.
                                                                                                                                                              Bacteria;
                                                                                                                                                                      Clostridium acetobutylicum
                                                                                                                                                                                           Aspartate semialdehyde dehydrogenase
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NCBI_TaxID=1718;
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                                                                                                                                                                                                                                                                                                                                 6; Conserv
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(Tremburel.)
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                                                                                                                                                              Clostridia; Clostridiales; Clostridiaceae;
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18,
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Last annotation update)
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EMBL/GenBank/DDBJ
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Last sequence update)
Last annotation update)
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Pred. No. 5e+
0; Mismatches
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Pred.
                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / NCIB 10025;
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                                                                   , Makarova K.S.,
Hitti J., Wolf Y
m L., Soucaille F
                                                                                                                                                                                                                                                                                                                                           5e+02;
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                                                solvent-producing
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                                                            Y.I.,
P., Daly M.J.,
                                                                                       Zeng
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.nterPro;

PF01118; Semialdhyde_dh;

IPR000534; Semialdh_dh

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RESULT OF ALCO OF ALCO
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ID Q93TV
AC Q95T
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                       094129;
094129;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-1999 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *Pseudomonas putida glutamate dehydrogenase (gd submitted (MAY-2001) to the EMBL/GenBank/DDBJ d. BMBL; AF321093; AAK49517.2; -. InterPro: Trochia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-PML1;
Syn C.K.C., Magnuson
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O1-DEC-2001 (TrEMBLrel.
O1-DEC-2001 (TrEMBLrel.
O1-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                         GDHA.
Aspergillus awamori.
Aspergillus awamori.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Asperg
NCBI_TaxID-105351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE: PS00074; GLFV_DEHYDROGENASE; NON_TER 1 1 1 038462:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro: IPR006095; GLFV_dehydrog.
InterPro: IPR006096; GLFV_dehydrog_C.
InterPro: IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF02812; GLFV_dehydrog_N; 1.
PRINTS; PR00082; GLFDHDRGNASE.
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                                                                    STRAIN-ATCC 22342;
Cardoza R.E., Mora
Martin J.F.;
   *Characterization and nitrogen source regulation transcriptional level of the gdhA gene of Aspegi
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                094129
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llarity 100.0%;
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                                                                                                      F.J., Gutlerrez S., Casqueiro

    Created)
    Last sequence update)
    Last annotation update)
    GdhA (Fragment).

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Pred. No. (
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          awamori encoding
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InterPro; IPR006096; GLFV_dehydrog_N.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF00812; GLFV_dehydrog,N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an NADP-dependent glutamate dehydrogenase."; submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases EMBL; Y15784; CAA75779.1;
                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIR-TUCSON 15010-1001.10;
STRAIR-TUCSON 15010-1001.10;
MEDIJINE-224746072; PubMed-12537575;
Bergman C.M., Pfeiffer B.D., Rincon-Limas D.E., Hos Gnirke A., Mungall C.J., Wang A.M., Kronmiller B., Stapleton M., Wan K., George R.A., de Jong P.J., Be Celniker S.E.;
                                                                                                                                                                                                                                                                                                 Drosophila littoralis.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=47316;
                                                                                                                                                                                                                                                                                                                                                                                                                         Q8I192;
Q8I192;
                                                                                                                                           "Assessing the impact of comparative genomic sequence functional annotation of the Drosophila genome."; Genome Biol. 3: RESEARCH0086.1-RESEARCH0086.20(2002).
EMBL; AX190955; AAO01080.1; ...
SEQUENCE 379 AA; 42266 MW; 07B6AE9C97AE5EC6 CRC64;
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01-MAR-2003
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                               Q96qp2 homo sapien
Q96qp3 xylella fas
Q3184 caenorhabdi
Q3303 caenorhabdi
Q3306 caenorhabdi
Q1347 caenorhabdi
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Q9Tr48;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Amphoterin (Fragment).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
MCBI_TaxID-9913;
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Q96QP2;
Q96QP2;
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                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-96029671; PubMed-7592757;
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RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA HO P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Marino C.L.,
RA Manchado M.A., Marsins E.A.L., Martins E.M.F., Marino C.L.,
RA Manchado M.A., Marsins E.A.L., Martins E.M.F., Marino C.L.,
RA Manchado M.A., Narscimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Mantin A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
Perison V.E., Jr., de Sa R.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA de Soluza A.P., Tereirai M.F., Silva W.A., Jr.,
RA de Soluza A.P., Tereirai M.F., Silva W.A., Jr.,
RA de Soluza A.P., Tereirai M.F., Silva W.A., Jr., Silva W.A., Jr., Wellon M.A., Matture 406:151-159(2000).
REMEL; AR003870; ARF82976.1; -.
RA Wrootherical Toother of the plant pathogen Xylella fastidiosa.";
RM Wrootherical Toothern of the plant pathogen Xylella fastidiosa.";
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O1-OCT-2000 (TrEMBLrel. 1
O1-OCT-2000 (TrEMBLrel. 1
O1-MAR-2002 (TrEMBLrel. 2
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Mammalia; Eutheria;
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Tissue factor pathway inhibitor-2 (Fragment).
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Catarrhini;
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Best Local
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SEQUENCE
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ZC412.7 prot
                 Submitted (NOV-1996) to the EMBL; 72067; CAB01526.1; - EMBL; 720849; CAB07428.1; - EMBL; 722849; CEI5223. WormPep; H12D21.1; CEI5223. WormPep; ZC412.7; CEI5223.
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                 SEQUENCE FROM N.A.
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Science 282:2012-2018(1998).
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Eukaryota; Metazoa; Nematoda;
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Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
NCBI_TaxID-6239;
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EMBL; Z78067; CAB01529.1; -.
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Shimizu N.S., Shimizu N.G., Takeuchi Y., Ho "Isolation and characterization of human in variants Onfectious to brain-derived cells: mutations in the V3 region of the env gene mutations in the V3 region of the env gene J. Virol. 68:6130-6135(1994).

EMBL: D34603: BAA07002.1; -.
InterPro; IPR000777; GPF20.

Pfam; PF00516; GPF20; 1.
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RESULT 11
Q76282
ID Q7628
AC Q7628
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DT Q1-NO
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GN ENV
OS Human
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Q76282;
01-NOV-1996 (
01-NOV-1996 (
01-OCT-2002 (
                                         SEQUENCE FROM N.A.
STRAIN-HIV-1[GUN-4];
                                                                                                Viruses; Retroid viruses; NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus
                                                                                                                                                                                  Envelope glycoprotein (Fragment).
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MEDLINE-94335139; Pu
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01-NOV-1996 (TYEMBLrel. 01, Last sequence update)
01-CCT-2002 (TYEMBLrel. 22, Last annotation update)
Envelope glycoprotein (Fragment).
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Shimizu N.S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
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01-NOV-1996
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4; Conserv
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(TrEMBLrel. 22,
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ilarity 100.0%;
Conservative (
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Pred. No.
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Pred. No.
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7.9e+02;
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Q8KAT7
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P74973;
P74973;
01-FEB-1997
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01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M., Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H., Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F., Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey I Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune I Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A., Venter J.C., Tettelin H., White O., Fraser C.M.; The complete genome sequence of Chlorobium tepidum TLS, a photosynthetic, anaerobic, green-sulfur bacterium."; Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
                                                                                                                                                                          Hypothetical SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-TLS / ATCC 49652 / DSM 12025;
MEDLINE-22103685; PubMed=12093901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Isolation and characterization of human immunodeficiency virus variants Onfectious to brain-derived cells: detection of common mutations in the V3 region of the env gene of the variants.";
J. Virol. 68:6130-6135(1994).
EMBL; D34601; BAA077000.1;
InterPro; IPB000777
                                                                                                                                                                                                 EMBL; AE012956; AAM73285.1; TIGR; CT2068; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein CT2068.
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                                                                                                                                                                                                                                                                                                                                                                                                  Chlorobium
                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Chlorobi;
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MEDLINE=94335139; Pu
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                                                                                                                                                                        11 protein; Complete proteome.
37 AA; 4349 MW; 545A837202D7F219 CRC64;
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                       PRELIMINARY;
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CT2068
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                       PRT;
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Pred. No. 8.4e+02;
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RESULT 15
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                                                                                                                                                                                                                                             STRAIN-DSM 4527;
Niessen M.L., Vogel R.F.;
"Specific identification of Fusarium graminearum
                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Galactose oxidase (Fragment).
                                                                                                                                                                                                                                                                                                        Gibberella zeae (Fusarium graminearum).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Hypocreales; Nectriaceae; Gibberella.
NCBI_TaxID-5518;
                                                                                                                                            SEQUENCE
                                                                                                                                                                       InterPro; IPR002048; EF-hand.
InterPro; IPR000421; FA58_C.
PROSITE; PS00018; EF_HAND; 1.
                                                                                                                                                                                                                                        targeted primers.";
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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InterPro; IPR005467; His_kinase.
Pfam; PF02518; HATPase_c; 1.
PROSITE; PS50109; HIS_KIN; 1.
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STRAIN-BXPF65;
Chan J.W.Y.F., Maynard S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative histidine kinase (Fragment).
Xanthomonas campestris.
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A two-component signal tranduction system of Xanthomonas pv. phaseoli var. fuscans strain BXPF65."; Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U69111; AAB09063.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xanthomonadaceae; Xanthomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=339;
                                                                                                           Local
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                                                                            1 GLSI 4
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                                                       GLSI 14
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  PRELIMINARY;
                                                                                                  Conservative
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                                                                                                                                       1AA403C08523D564 CRC64;
                                                                                                        Score 18;
Pred. No.
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Pred. No. 9.7e+02;
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 PRT;
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                                                                                            red. No. 1e+03;
Mismatches
46
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Å
                                                                                                                  DB 3; Length 45;
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                                                                                              Indels
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Search completed: August 20, Job time: 11.6774 secs

2003,

12:40:22

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Best Local S
Matches 4
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Genes for sensor and regulator protein (Fragment).
                                                                                                                                                                                                                                                          STRAIN-pathovar: campestris;
MEDLINE-91042416; PubMed-2233675;
Osbourn A.E., Clarke B.R., Stevens B.J.H., Daniels M.J.;
"Use of oligonucleotide probes to identify members of two-component systems in Xanthomonas campestris pathovar campestris.";
MOI. Gen. Genet. 222:145-151(1990).
-i- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
                                                                                                            SEQUENCE
                                                                                                                          Kinase; Phosphorylation; Sensory transduction; Transferase NON_TER
                                                                                                                                                                                                                                   KINASES.
EMBL; X54015; CAA37962.1;
                                                                                                                                                 PROSITE; PS50109; HIS_KIN; 1.
                                                                                                                                                                               Pfam; PF02518; HATPase_c;
                                                                                                                                                                                          InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR004358; Bact_sens_pr_C.
InterPro; IPR003467; His_kinase.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=339;
                          1 GLSI 4
                                                     4.
                                                                  Similarity
GLSI 12
                                                                                                           46 AA; 4824 MW;
                                                     Conservative
                                                                 100.0%;
                                                                                                        1A3C266837B0F6C5 CRC64;
                                                    0;
                                                               Score 18;
Pred. No.
                                                    Mismatches
                                                               1.1e+03;
                                                                              DB 2;
                                                                           Length 46
                                                  Indels
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Title:
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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0: //SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
1: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query		}	•	5 1 1 1 1 1 1 1
80	Score	Match	Length	B	ID	Description
—	18	100.0	œ	23	AAU98275	M. tuberculosis Ag
2	18	100.0	9	15	AAR51217	A generic Bradykin
ω	18	100.0	9	16	AAR82116	Melanoma-specific
4	18	100.0	10	15	AAR51218	A generic Bradykin
U.	18	100.0	10	22	AAG95974	Human complementar
6	18	100.0	. 10	22	AAG86718	Saccharomyces cere
7	18	100.0	10	22	AAG86810	Saccharomyces cere
8	18	100.0	10	22	AAG86812	Saccharomyces cere
9	18	100.0	14	16	AAR67162	Bovine glial cell

45	44	43	42	41	40	39	38	37	36	ယ G	ω 4	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	, 18	18	18	18	18	18	18	18	18	18	18					œ	
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7.2	21	20	19	17	17	16	16	16	16	16	16	16	16	16	16	16	16	16	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	14
24	24	24	23	24	12	24	24	24	24	23	23	23	22	22	17	17	16	16	24	24	23	22	22	22	22	22	22	22	22	21	19	19	18	15	17
ABR390/U	ABR39064	AAE30406	ABU50695	ABP83375	AAR10034	ABU11958	ABU11957	ABU11946	ABU11945	ABP46969	ABP46175	ABP46163	AAG98655	AAE12281	AAR86636	AAR86634	AAR67160	AAR67158	ABU56363	ABU56362	AAU86315	AAJ03068	AAB97737	AAB97736	AAB98127	AAB98126	AAB86753	AAB86752	AAB86751 '	7	AAW75599	59	7	œ	AAR86638
optoo metanoma anc	melanoma	retinoic	Helicobacter pylor	G protein-coupled	Neutralising domai	Human HGPRBMY11v1	Human HGPRBMY11v1	Human HGPRBMYll N-	Human HGPRBMY11 N-					-	GGF I tryptic pept	tryptic	ine gliai c	Bovine glial cell	Mycobacterium tube	Mycobacterium tube	Oestrogen receptor	itis	gp100 derived IFN-	derived	Interferon-gamma s	Interferon-gamma s	Human cytomegalovi	Human cytomegalovi	Human cytomegalovi	Oestrogen receptor	M. tuberculosis 30	tuberculosi	Immunodominant epi	7	GGF I tryptic pept

ALIGNMENTS

RESULT 1 AAU98275

Key Region Ag85; epitope; vaccine; tuberculosis; mycolyltransferase; HLA-A*02001; Mycobacterium tuberculosis; Mycobacterium leprae; Mycobacterium bovis; Mycobacterium ulcerans; Mycobacterium avium; antibacterial; Mycobacterium avium; antibacterial; Mycobacterium avium; antibacterial; Mycobacterium avium; antibacterial; M. tuberculosis Ag85 derived immunodominant T cell epitope #2 AAU98275 standard; peptide; 8 Mycobacterium tuberculosis 15-AUG-2002 (first entry) AAU98275; 30-NOV-2000; 2000EP-0204268 30-NOV-2000; 2000EP-0204268 EP1211260-A1 Region 05-JUN-2002 /note- "Amino acid contributing to the HLA-A*02001 binding motif" $\label{eq:motif}$ Location/Qualifiers /note= "Amino acid contributing to binding motif" A the HLA-A*02001

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RESULT 2
AAR51217
ID AAR5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to peptide (P1) derived from an Ag85 protein of mycobacterium (which is associated with mycolyltransferase activity and is involved in cell wall synthesis), comprising 8-11 amino acids, and capable of inducing proliferation of MHC class I-restricted CBC+ T cells in vivo. Also included are (1) a peptide comprising P1 flanked by amino acids representing antigen processing sites; (2) a polypeptide comprising the above acids representing antigen processing sites; (2) a polypeptide comprising the comprising the claimed peptides or polypeptides; (4) a vector comprising the above nucleic acid or concentration of the claimed peptides or polypeptides; (4) a vector comprising the above nucleic acid; (5) a host cell comprising the above nucleic acid or vector; and (6) detecting and/or enumerating CDB+T cells against mycobacterium, comprising tetrameric complexes of MHC (major histocompatibility group) class I and one of the claimed peptides or polypeptides. The molecules of the invention are used to prepare a vaccine against mycobacterium (e.g. Mycobacterium tuberculosis, Mycobacterium ulcerans, tuberculosis. The present sequence is an M. tuberculosis Ag85 tuberculosis. The present sequence is an M. tuberculosis Ag85 (human leukocyte antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
            08-SEP-1993;
                                                                     WO9406453-A1
                                                                                                                Misc-difference
                                                                                                                                                            Modified-site
                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                   Treatment
                                                                                                                                                                                                                                                  Bradykinin
                                                                                                                                                                                                                                                                         A generic Bradykinin antagonist peptide.
                                                                                                                                                                                                                                                                                                        25-MAR-2003
02-NOV-1994
                                                                                                                                                                                                                                                                                                                                                      AAR51217;
                                                                                                                                                                                                                                                                                                                                                                                 AAR51217 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (human leukocyte antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 6; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mycobacterium cells and are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide of 8-11 amino acids derived from the Ag85 protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ZIEK-) ACAD ZIEKENHUIS LEIDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GLSI 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                n antagonist peptide; of inflammatory react
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ā,
                                                                                                                                                                                                                                                                                                       (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         induce proliferation of MHC class I-restricted CD8+ {\bf T} useful to vaccinate against infection by mycobacterium
          93WO-US08220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Geluk
                                                                                                                /note=
                                                                                                                                                             Location/Qualifiers
                                                                                                 'note-
                                                                                                                                            'label=
                                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                               "D-form residue
                                                                                                                                                                                                                           tide; 5-position; non-aromatic residue reactions; reduce pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rred. No. 9.3e+05;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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RESULT 3
AAR82116
ID AAR8
XX
AC AAR8
AC AAR8
DT 25-M
XX
DE Mela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                          Melanoma-specific immunogen comprises epitope(s) homologous with pMel.17 - are highly potent stimulators of HLA-A2+CTL's useful in adoptive immuno-therapy
                                                                                                                                                                                                                                                                                            Melanoma; cytotoxic
                                                                                                       WPI; 1995-302688/39
                                                                                                                             Cox AL,
                                                                                                                                                                       29-APR-1994;
16-FEB-1994;
                                                                                                                                                                                                       16-FEB-1995;
                                                                                                                                                                                                                                                   W09522561-A2
                                                                                                                                                   (UYVI-)
                                                                                                                                                                                                                             24-AUG-1995
                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                       Melanoma-specific mutant immunogen epitope 9mer peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR51217 is an example of a generic bradykinin antagonist peptide having a non-arcmatic residue in the 5-position. The antagonist peptide inhibits the bradykinin reponse when injected as a bolus admixture of bradykinin plus antagonist by either the ia. or iv. route of administration, or when administered as an infusion. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                 25-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                      AAR82116;
                                                                                                                                                                                                                                                                                                                                                                                           AAR82116 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antagonistic bradykinin analogues with non-aromatic amino acid in the 5-position - are useful for treating inflammatory reactions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gera L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 44; Page 19; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-118152/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypotension, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GERA/) GERA L.
(SRIV/) SRIVASTAVA V.
(STEW/) STEWART J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-1992;
                                                                                                                                                  UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GLSI 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 4; Conserv
                                                                                                                            Engelhard VH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Srivastava V,
                                                                                                                                                                                                                                                                                          immunogen; epitope; homologue; vaccine; immunotherapy;
T cell; lymphocyte; HLA-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nilarity (100.0%)
Conservative 0
                                                                                                                                                  VIRGINIA PATENT FOUND
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                      94US-0234784.
94US-0197399.
                                                                                                                                                                                                       95WO-US01991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-0942317
                                                                                                                                                                                                                                                                                                                                                                                         peptide;
                                                                                                                            Hunt DF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pages; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stewart
                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18;
Pred. No.
                                                                                                                            Shabanowitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 9.3e+05;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 15;
                                                                                                                            ď,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9;
                                                                                                                           Slingluff CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0;

A melanoma-specific immunogen homologous with pMel-17 comprises or more CTL (cytotoxic T lymphocyte) epitopes from the group AAI AAR82194 capable of eliciting a CTL response. The epitopes AAR8.

Example

8; Page 51; 148pp; English.

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RESULT
AAR5121
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR82108 are of particular interest. The immunogen can be used for partial protection in mammals against melanoma peptides which are homologous with pMel-17 are highly potent stimulators of HLA-A2+CTLs in several cell lines and can be used in immunotherapy or incorporated into immunogenic conjugates as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bradykinin antagonist peptide; 5-position; non-aromatic residue Treatment of inflammatory reactions; reduce pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A generic
                     AAR51217 is an example of a generic bradykinin antagonist peptide having a non-aromatic residue in the 5-position. The antagonist peptide inhibits the bradykinin reponse when injected as a bolus admixture of bradykinin plus antagonist by either the ia. or iv. route of administration, or when administered as an infusion. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                       08-SEP-1993;
                                                                                                                                                                                                                                                                                                              31-MAR-1994
                                                                                                                                                                                                                                                                                                                                    W09406453-A1
                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
02-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR51218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR51218 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                              Gera L,
                                                                                                                                     Antagonistic bradykinin analogues with non-aromatic amino acid in the 5-position - are useful for treating inflammatory reactions,
                                                                                                                                                                                                                   (GERA/) GERA L.
(SRIV/) SRIVASTAVA V.
(STEW/) STEWART J M.
                                                                                                                                                                                                                                                                   11-SEP-1992;
                                                                                                    Example 45; Page 19;
                                                                                                                          hypotension,
                                                                                                                                                                         1994-118152/14.
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                                                                                                                                                                                              Srivastava
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bradykinin antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                            etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (updated)
(first entry)
                                                                                                                                                                                                                                                                   92US-0942317
                                                                                                                                                                                                                                                                                       93WO-US08220
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                note-
                                                                                                                                                                                                                                                                                                                                                                                            /label=
                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "D-form residue"
                                                                                                                                                                                              ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                     29
                                                                                                                                                                                                                                                                                                                                                                                            4нур
                                                                                                    Pages; English.
                                                                                                                                                                                              Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB
Pred. No. 9.3
D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
                                                                                                                                                                                               ĭ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16;
. 9.3e+05;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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Sequence

10

Saccharomyces

cerevisiae;

complementary peptide; peptide

identification;

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RESULT 5
AAG95974
ID AAG9
XX
AC AAG9
XX
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RESULT 6
AAG86718
ID AAG8
XX
AC AAG8
XX
DT 11-S
XX
DE Sacc
XX
XX
Sacc
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Best Local S
Matches 4
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                 The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.
                                                                                                                                                                                                                                                                                                                             A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200142277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG95974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG95974 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                          13-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-408419/43
                                                                                                                                                                                                                                                                                                                                                                                                  Roberts GW,
                                                                                AAG86718 standard;
                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                           Example 4; Page 353; 646pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      (PROT-) PROTEOM LTD.
                     Saccharomyces
                                        11-SEP-2001
                                                            AAG86718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complementary peptide; ligand; drug discovery; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GLSI 4
                                                                                                                                  6 GLSI
                                                                                                                                                     1 GLSI 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
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                                                                                                                                                                          Similarity
4; Conserv
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                                                                                                                                                                                                                  10 AA;
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                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   Heal JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-GB04776
                                        (first entry)
                     cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                          99GB-0029464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide;
                                                                                 Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide,
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                                                                                                                                                                                 100.0%;
                      peptide,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
                                                                                                                                                                          Score 18; DB 22;
Pred. No. 1.2e+02;
; Mismatches 0;
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                      SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ö.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 15;
                       NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2e+02;
                       1667.
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RESULT 7
AAG86810
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                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
Identifying complementary peptides by
                       WPI; 2001-367863/38.
                                           Roberts GW,
                                                                                   13-DEC-1999;
                                                                                                        13-DEC-2000;
                                                                                                                            14-JUN-2001
                                                                                                                                                                                             Saccharomyces cerevisiae; complementary peptide; peptide identification;
                                                                                                                                                WO200142276-A1
                                                                                                                                                                   Saccharomyces
                                                                                                                                                                                         drug
                                                                                                                                                                                                                      Saccharomyces
                                                                                                                                                                                                                                           11-SEP-2001
                                                                                                                                                                                                                                                               AAG86810;
                                                                                                                                                                                                                                                                                 AAG86810 standard; Peptide; 10 AA
                                                              (PROT-) PROTEOM LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins encoded in the eukaryote genome The proteins
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                encoded in the eukaryote genome. The peptides may be used as reag
and drugs for drug discovery and as lead ligands for drug design
development. The present sequence is a complementary peptide from
carcharomyces convictor
                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to the identification of complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying complementary peptides by nucleotide sequence databases, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roberts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PROT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug discovery; drug
                                                                                                                                                                                        discovery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-367863/38.
                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                             4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Page 260; 488pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEOM LTD.
                                                                                                                                                                                                                                                                                                                                       GLSI 8
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                                                                                                                                                                                                                                                                                                                                                                                                                       10 AA;
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                      2000WO-GB04773.
                                          Heal JR;
                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heal JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-GB04773
                                                                                                                                                                                                                    cerevisiae peptide, SEQ ID NO: 1759.
                                                                                                                                                                   cerevisiae
                                                                                  99GB-0029471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cerevisiae
                                                                                                                                                                                       drug
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100.0%; I
tive 0;
                                                                                                                                                                                      design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        design.
                                                                                                                                                                                                                                                                                                                                                                                      Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                             Mismatches
 analysis of protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analysis of protein in drug design -
                                                                                                                                                                                                                                                                                                                                                                                    1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                22;
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                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            design and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as reagents
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KESULT 8
AAG86812
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  Query Match
Best Local Similarity
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Best Local Similarity
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                                                                           The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from
                                                                                                                                                                                     Example 3; Page 272; 488pp; English.
                                           Sequence
                                                                    Saccharomyces cerevisiae.
                                                                                                                                                                                                                   nucleotide
                                                                                                                                                                                                                             Identifying complementary peptides by
                                                                                                                                                                                                                                                                                     Roberts GW,
                                                                                                                                                                                                                                                                                                                                        13-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                  13-DEC-2000; 2000WO-GB04773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae; complementary peptide; peptide identification; drug discovery; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complement are present sequence in a complement are present sequence.
                                                                                                                                                                                                                                                                                                              (PROT-) PROTEOM LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                     WO200142276-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG86812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins
                                                                                                                                                                                                                                                                                                                                                                                            14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG86812 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleotide sequence databases, useful in drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GLSI 4
||||
4 GLSI 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                         10
                                                                                                                                                                                                                   sequence databases, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 272; 488pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 AA;
                                                                                                                                                                                                                                                                                   Heal JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a complementary cerevisiae.
                                                                                                                                                                                                                                                                                                                                        99GB-0029471
 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
 Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:
                                                                                                                                                                                                                analysis of protein in drug design -
DB 22;
1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
```

Matches

4

Conservative

0;

Mismatches

Indels

0;

Gaps

0;

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RESULT 9
AAR67162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
RESULT 10
AAR86638
ID AAR86
XX
AC AAR86
XX
DT 03-JU
                                                                                                                 밁
                                                                                                                                     S
                                                                                                                                                                    Matches
                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glial cell growth factor-1; GGF-1; mammalian muscle cell treatment; skeletal; cardiac; smooth; acetylcholine receptor deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                 Treating GGF2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
02-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR67162 standard; peptide; 14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR67162;
                                                                                                                                                                                                                                         AAR67153-R67163 and AAR67174-R67183 are bovine glial cell growth factor-1 (GGF-1) peptide fragments. A 30-36kD polypeptide factor known to have glial cell mitogenic activity, which includes one of the above peptide fragments in its amino acid sequence is claimed. The polypeptide can be used to treat a variety of mammalian skeletal, cardiac and smooth muscle diseases, including acetylcholine receptor deficiency.

(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAY-1993;
08-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09426298-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine glial
                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                          Example 9; Page 90; 241pp; English
                                                                                                                                                                                                                                                                                                                                                                                     receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-006353/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gwynne DI, Marchionni M, Sklar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CAMB-) CAMBRIDGE NEUROSCIENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-NOV-1994.
 03-JUL-1996
                          AAR86638;
                                                    AAR86638 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  w
                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLSI
                                                                                                                1 GLSI 4
| | | | |
6 GLSI 9
                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLSI 6
                                                                                                                                                                                                                                                                                                                                                                                               mammalian muscle diseases and disorders - by admin. of other specified polypeptide(s) which bind the pl85erbB2 \,
                                                                                                                                                                                                                    14 AA;
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell growth factor-1 (GGF-1) peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (updated)
(first entry)
 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0059022.
94US-0209204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US05083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Lys, Arg"
                                                  peptide; 14
                                                                                                                                                                             100.0%;
                                                                                                                                                                    0
                                                                                                                                                                 Score 18; DB 16;
Pred. No. 1.8e+02;
Mismatches 0;
                                                     Š
                                                                                                                                                                                            Length
                                                                                                                                                                       Indels
                                                                                                                                                                                               14;
                                                                                                                                                                     0
                                                                                                                                                                    Gaps
                                                                                                                                                                       0
                                                                                                                                                                                                                                                                          ARASSULT 11
AAR49865
ID AAR49865
XX AAR45
XX AAR45
XX AAR45
XX 125-M2
DT 25-M2
DT 12-SH
XX Seque
DE (GGF
                                                                                                                                                                        밁
                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                           AAR86629-R86657 represent fragments of bovine glial growth factor I
(GGF-I). These fragments were obtained by lysyl endopeptidase and
protease v8 digests. These sequences have Schwann cell mitogenic
activity in the presence of foetal calf plasma. These sequences (and
human GGF2, see AAR86628) are used to stimulate mitogenesis of glial
cells, for prophylaxis or treatment of a pathophysiological condition of
the nervous system in a mammal. Also, for identification of a receptor,
for treatment of conditions of peripheral nerve damage (e.g.
centreatment of conditions of peripheral nerve damage (e.g.
demyelination/damage/loss of Schwann cells), treatment of
neurodegenerative disorders in mammals, for inducing neural
centreated by inhibiting this sequence binding to its receptor.
These peptides are also able to induce synthesis of acetylcholine
                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glial growth factor; GGF; human; hGGF2; Schwann cell; mitogenesis; GGF-I; glial cell; therapy; peripheral nerve damage; demyelination; bovine; glial tumour; fibroblast proliferation; wound repair; multiple sclerosis; neurodegenerative disorder; neural regeneration; acetylcholine receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGF I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen MS, Goodearl AD, Hil Stroobant P, Waterfield M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glial growth factors with Schwann prophylaxis or treatment of nerve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-030329/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CAMB-) CAMBRIDGE NEUROSCIENCE. (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9532724-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Fig 9; 199pp;
                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                   sclerosis
      Sequence of (GGF III).
                                            25-MAR-2003
12-SEP-1994
                                                                                 AAR49865;
                                                                                                         AAR49865 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tryptic peptide GGF-I 10.
                                                                                                                                                                         σ
                                                                                                                                                                                                1 GLSI 4
                                                                                                                                                                                                                           4.
                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                        GLSI 9
                                                                                                                                                                                                                                                                                                   in a patient.
                                                                                                                                                                                                                                                                           14 AA;
                                                                                                                                                                                                                         100.0%;
illarity 100.0%;
Conservative (
                  tryptic digest peptide of bovine glial growth factor III
                                            (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-0249322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-US06846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Lys, Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hiles I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                        Score 18; DB 17;
Pred. No. 1.8e+02;
                                                                                                             B
                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell mitogenic activity - for disorders, e.g. Multiple Sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marchionni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ĭ
                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minghetti
                                                                                                                                                                                                                                                   Length 14;
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0

Gaps

0

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RESULT 12
AAW18171
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                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 4
    06-DEC-1995;
23-MAY-1995;
20-OCT-1995;
31-OCT-1995;
                                                      23-MAY-1996;
                                                                                               WO9637219-A1
                                                                                                                                                                                                                                                                                                                                                                                 A novel polypeptide was purified from bovine pituitaries. It has mitogenic activity stimulating the division of Schwann cells, and exhibits a mol. wt. of 43-35kD when carrying native glycosylation. It was digested with trypsin and lysylendopeptidase to obtain novel peptides AAR49858-R49866 and AAR49867-R49871 respectively. When peptides AAR49860-R49866 were sequenced to completion it was found that none of these sequences is apparently related to GGF-I or GGF-II peptide sequences. A polypeptide contg. any of the sequences in AAR49858-AR49871 is claimed, as is DNA encoding each of the peptides. (Updated on 25-MAR-2003 to correct PN field.)
                                                                          28-NOV-1996
                                                                                                                   Mycobacterium
                                                                                                                                             Vaccine; vaccinating agent; M.tuberculosis;
                                                                                                                                                                      Immunodominant
                                                                                                                                                                                                               AAW18171;
                                                                                                                                                                                                                               AAW18171 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 32; Page 31; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide factor and peptide(s) from bovine pituitary having mitogenic activity in stimulating division of Schwann cells, used for therapy, prophylaxis, diagnosis of neuro-degenerative disease, glial cell tumours, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glial growth factor; GGF III; mitogen; Schwann cell.
                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goodearl ADJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9404560-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1994-083104/10
                                                                                                                                     fungus;
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                     GLSI 10
                                                                                                                                                                                                                                                                                                         GLSI 4
                                                                                                                                                                                                                                                                                                                                                                    15 AA;
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                       (first entry)
            95US-0568357.
95US-0447398.
95US-0545926.
                                                                                                                   tuberculosis
                                                                                                                                                                 epitope from Mycobacterium tuberculosis 30KD protein.
                                                                                                                                       protozoan;
                                                    96WO-US07781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stroobant P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92GB-0017316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93WO-GB01721
                                                                                                                                                                                                                                                                                                                                     100
                                                                                                                                                                                                                                                                                                                                     0.0%;
                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterfield MD,
                                                                                                                                                                                                                                                                                                                                    Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                   1.9e+02;
                                                                                                                                                                                                                                                                                                                                               DB 15;
                                                                                                                                              pathogen; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goodearl AD;
                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                        0;
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(REGC) UNIV CALIFORNIA

21-JAN-1997;

97US-0786533 98WO-US00942

15-JAN-1998;

23-JUL-1998. WO9831388-A1 Mycobacterium Synthetic

tuberculosis

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AAW7
                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                          AAW75598
                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC against Mycobacterium pathogens comprises at least one immunodominant epitope of at least one majorly abundant CC extracellular protein, i.e. the M.tuberculosis 110, 80, 71, 58, 45, CC 32A, 32B, 30, 24, 23.5, 23, 16, 14 or 12 kD proteins, or their CC analogues, homologues and subunits. The present sequence represents an CC immunodominant epitope from the major abundant extracellular product CC 30 KD protein. The vaccinating agents are used to protect against (or CC tuberculosis) while the epitopes can also be used to detect presence CC of an immune response to a Mycobacterium pathogen. The vectors, CC containing the DNA for the extracellular proteins, are used to transform CC cells for production of recombinant DNA molecules. More generally the DNA from other pathogens can be used in vaccines, e.g. against other CC DNA can be used, a wide range of effective compositions can be produced. CT they generate a response against the antigens most often found on CC infected cells during the infection, regardless of the strength or CC specificity of the immune response. The vaccines are easy to produce CC and less toxic than known killed or attenuated vaccines, so can be given to the monocompromised subjects, e.g. those with HIV infection.
                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Mycobacterium tuberculosis; vaccination; extracellular product; immunodominant epitope; interleukin-12; MF59; immune response; opsonising humoral response; intracellular pathogen.
                                                                              M. tuberculosis 30 kD protein
                                                                                                                         23-OCT-1998
                                                                                                                                                                                                AAW75598 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccines derived from M.tuberculosis major abundant extracellular proteins - are easy to prepare and less toxic than conventional killed or attenuated vaccines, useful for protecting against or treating Mycobacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harth G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                   1 GLSI 4
                                                                                                                                                                                                                                                                                                                                                                          4;
                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                 GLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Horwitz MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193pp;
                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                              derived peptide 12 (residues 56-70).
                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 18;
Pred. No. 1.9e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 15;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0;

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Gerived from the native 30kD major secretory protein of M. tuberculosis. CC derived from the native 30kD major secretory protein of M. tuberculosis. CC These peptides are used for splenic lymphocyte profileration assays to contain the immunodomnant T-cell epitope of the 30kD protein. The cc invention provides an agent for vaccinating mammals against Mycobacterium. The agent comprises at least one of the major abundant cc extracellular 110, 80, 71, 88, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14 or 12 kD proteins of M. tuberculosis, or at least 1 of their immunodominant cc epitopes and interleukin-12 (II-12) or MF59 as adjuvants. The agent cc containing the nucleic acid encoding the extracellular products are used to raise a protective or therapeutic immune response against cc an also be used (typically M. tuberculosis. The immunodominant epitopes detect an immune response to vaccination. Preparation of the agent does not require selection of the most immunogenic products, so large scale component are easy, resulting in a consistent, cc strong cell-mediated component) and are safe even in immunocompromised cc subjects. They prevent development of an opsonising humoral response that xx might spread intracellular pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccines against Mycobacterium containing major extracellular proteins - used to, e.g. induce protective and therapeutic immune responses, and for detecting an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harth G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 28; Page 96; 236pp; English.
                                                                                                                                                                                                                                           Mycobacterium tuberculosis; vaccination; extracellular product; immunodominant epitope; interleukin-12; MF59; immune response; opsonising humoral response; intracellular pathogen.
                                                                                                                                                                                                                                                                                                                                                                     AAW75599
              Harth G,
                                                                                                         15-JAN-1998;
                                                                                                                                                                      W09831388-A1
                                                                                                                                                                                                                                                                                                          M. tuberculosis 30 kD protein
                                                                                                                                                                                                                                                                                                                                       23-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                  AAW75599 standard; peptide; 15
                                                                           21-JAN-1997;
                                                                                                                                                                                                   Mycobacterium
                                           (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 GLSI 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GLSI 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Horwitz MA,
                 Horwitz MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ξ
                                                                                                                                                                                                   tuberculosis
                                                                           97US-0786533
                                                                                                          98WO-US00942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB
Pred. No. 1.9
D; Mismatches
                                                                                                                                                                                                                                                                                                          derived peptide 13 (residues 61-75).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19;
1.9e+02;
hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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RESULT 15
AAY65578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences shown in AAW75587 to AAW75641 represent synthetic peptides CC derived from the native 30kD major secretory protein of M. tuberculosis. CC These peptides are used for splenic lymphocyte profileration assays to condentify the immunodominant T-cell epitope of the 30kD protein. The CC invention provides an agent for vaccinating mammals against comproved by the immunodominant T-cell epitope of the 30kD protein. The CC extracellular 110, 80, 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14 or CC extracellular 110, 80, 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14 or CC epitopes and interleukin-12 (IL-12) or AF59 as adjuvants. The agent CC containing the nucleic acid encoding the extracellular products are used to raise a protective or therapeutic immune response against CC extraces a seed (typically in a cutaneous hypersensitivity test) to CC detect an immune response to vaccination. Preparation of the agent does not require selection of the most immunogenic products, so large scale production and purification are easy, resulting in a consistent, CC standardised formulation, having lower toxicity than killed or attenuated consultated component) and are safe even in immunocompromised subjects. The agents development of an opsonising humoral response that CC might spread intracellular pathonens.
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 Query Match
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Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 28; Page 96; 236pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-413815/35
                                                               23-APR-1998;
09-SEP-1998;
08-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                               Oestrogen receptor; estrogen; estradiol; oestrogen response element; ERE; binding; biological activity; fingerprint; molecular braille; cellular braille; modulation; tamoxifen; breast cancer; ovarian cancer; menopause; osteoporosis; selective oestrogen receptor modulator; identification; characterisation; classification.
                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY65578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY65578 standard; Peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                   Oestrogen receptor
                                                                                                                                                                                                 W09954728-A2
                                                                                                                                                                                                                                                     Synthetic.
                               (NOVA-) NOVALON PHARM CORP.
                                                                                                                                  26-MAR-1999;
                                                                                                                                                                   28-OCT-1999
                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spread intracellular pathogens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
Hamilton PT,
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                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                               98US-0082756.
98US-0099656.
99US-0115345.
                                                                                                                                    99WO-US06664
                                                                                                                                                                                                                                                                                                                                                                                       beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                     ERE binding peptide 178-beta.
   Fowlkes
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Pred. No.
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   Ŋ,
     Buehrer B,
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.9e+02;
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   Barnett T;
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The present invention describes a method for predicting the biological activity of new receptor modulating compounds (I) using novel oligomeric CC peptides (blokeys) which have differential abilities to bind to 2 CC different receptor conformations. The method is used to identify new CC that target various receptors, which are involved in certain disease CC conditions. The system may be used as a primary screening tool to CC identify hits, to classify lead compounds from a drug screen to, CC characterise selective oestrogen receptor modulators (SERMs) in terms of CC agonist and antagonist function and to predict possible clinical effects of SERMs such as tissue and receptor specificity. The method can also be CC compounds to the fractionation of mixtures of SERMs to determine which CC applied to the fractionation of mixtures of SERMs to determine which CC may be used with other receptors (e.g. progesterone, androgen, CC epidermal growth factor, to identify, characterise and classify De used to modulators of receptor activity. Peptides comprising a LXXLL motif may be used to modulate the oestrogen receptor in treating e.g. breast and CC ovarian cancer and ameliorating the effects of menopause, including costeoporosis. AAV65439 to AAV65623 represent oestrogen receptor in the exemplification of the present invention. AAZ35740 to AAZ35745 cc invention.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2.2; Page 162; 219pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methods for identifying new receptor modulators, especially estrogen modulators to treat tamoxifen refractory breast cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McDonnell DP, Christensen DJ;
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15 AA;

B δÃ Matches Query Match Best Local Similarity 9 GLSI 12 1 GLSI 4 h 100.0%; Similarity 100.0%; 4; Conservative 0; Score 18; DB 21; Pred. No. 1.9e+02; ; Mismatches 0; Length 15; Indels 0; Gaps 0;

Search completed: August 20, 2003, 12:33:42 Job time: 9.79518 secs

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protein 9

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protein search, using sw model

Minimum DB Maximum DB

seq seq

length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published_Applications_AA:*

Result No.

Score

Match

Length

BB

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SUMMARIES

100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0

Query

110: 110: 112: 113: 114: 115: 116:

Scoring table: Sequence: Title: Perfect score:

BLOSUM62 Gapop 10.0 ,

Gapext 0.5

US-09-512-082-29

GLSI 4

Searched:

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Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                August 20, 2003, 12:40:51; Search time 4.33735 Seconds (without alignments) 121.698 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_HEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/JCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/JCTUS_PUBCOMB.pep:*
US-09-300-4258-29

US-09-572-4048-3168

US-10-190-082-599

US-09-953-510-48

US-09-953-510-49

US-10-147-255-48

US-10-147-255-49

US-09-800-748-2174

US-09-800-748-2174

US-09-800-748-2186

US-09-800-748-2186

US-09-801-225-61

US-09-991-225-62

US-09-991-225-62
                                                                                                                                                                                                                                                                                                       Description
       Sequence 29, Appl
Sequence 599, App
Sequence 599, App
Sequence 49, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 50, Appl
Sequence 2174, Appl
Sequence 2174, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 63, Appl
                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: SCH-1733P1
CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B; OTHER INFORMATION: antibody clone US-09-300-425B-29
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US-09-300-425B-29
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               RESULT
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                                                                                                                                            Matches
                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: NERI, Dario
APPLICANT: TARLI, LOTENZO
APPLICANT: VITI, Francesca
APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfred
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
TITLE OF INVENTION: ANGIOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                              LENGTH: 4
                                                                                                                                                                Local Similarity
                                                                                                           1 GLSI 4
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                                                                      GLSI 4
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100.0%; Pred. No. 4.4
tive 0; Mismatches
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14 US-10-044-703-66
15 US-10-225-567h-2048
16 US-09-814-604-26
17 US-09-922-226-12
17 US-09-922-226-15
18 US-09-922-226-165
19 US-09-64-761-41951
10 US-09-64-761-41951
12 US-09-991-225-12
12 US-09-991-225-12
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US-09-864-761-48199
US-09-864-761-43280
US-09-864-761-43280
US-09-864-761-43280
US-09-864-761-43280
US-09-861-717-34
US-09-764-800-550
US-09-764-800-57
US-09-864-761-48544
US-09-764-853-419
US-09-764-853-1059
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US-09-764-877-1059
US-09-764-877-726
US-09-764-877-726
US-09-764-877-726
US-09-764-877-726
US-09-809-391-575
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                                                                                                                                                                    4.4e+05;
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                                                                                                                                                                                       Length 4
                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 74, Appl Sequence 2048, Appl Sequence 2048, Appl Sequence 12, Appl Sequence 155, Appl Sequence 157, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18997, A Sequence 40950, A Sequence 4129, A Sequence 4129, A Sequence 43120, A Sequence 550, Appl Sequence 550, Appl Sequence 550, Appl Sequence 119, Appl Sequence 119, Appl Sequence 1954, Appl Sequence 1959, 
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US-09-953-510-48
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OTHER INFORMATION: Synthetic
US-10-190-082-599
                                                                             Sequence 48, Application US/09953510
Patent No. US20020131975A1
GENERAL INFORMATION:
APPLICANT: Horwitz, Marcus A.
TITLE OF INVENTION: Abundant Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-10-190-082-599
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                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Publication:
GENERAL INFORMATION:
APPLICANT: Lasky, Lawrence A.
APPLICANT: Sidhu, Sachdev S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-572-404B-2168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 599, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/190,082 CURRENT FILING DATE: 2002-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sidhu, Sachdev S.
APPLICANT: Held, Helke A.
TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2168
                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 12
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/303,634
PRIOR FILING DATE: 2001-07-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Complementary peptide ligands from the human genome FILE REFERENCE: Human patent CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Proteom Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: sequence located in PMEL17 OR D12S53E at 164-173 and may interact OTHER INFORMATION: Sequence 2167 in this patent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo Sapiens FEATURE:
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                                                                                                                                                                                                                                                                                                    Local Similarity 100.0%; es 4; Conservation
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                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Kurt A.
                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                        1 GLSI 4
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 STREET: 2029 Century Park East,
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                      Kurt A. MacLean
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                                                                    Products and
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                                                                                                                                                                                                                                                                                                                    Score 18;
Pred. No.
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Pred. No.
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                                                               Methods for Their Production
Suite 3800
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                                                                                                                                                                                                                                                                                                         RESULT 5
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Query Match
Best Local Similarity
"""+" 4; Conserve
                                                                                                                                                                                                                                                                               Sequence 49, Application US/09953510 Patent No. US20020131975A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 48: SEQUENCE CHARACTERISTICS:
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                       APPLICANT: Horwitz, Marcus A.
TITLE OF INVENTION: Abundant Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                    10 GLSI 13
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FILING DATE: 23-MAY-1995
APPLICATION NUMBER: US 08/289,667
FILING DATE: 12-AUG-1994
APPLICATION NUMBER: US 08/156,358
FILING DATE: 23-NOV-1993
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                               ZIP:
                                                                                             COUNTRY: U.S.A.
                                                                                                             CITY: Los Angeles
STATE: California
                                                                                                                                            STREET: 2029 Century Park East,
                                                                                                                                                                  ADDRESSEE: Kurt A. MacLean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN: Erdman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 15 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MacLean, Kurt A. REGISTRATION NUMBER: 31,118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 14-Sep-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/953,510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 90067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 18; DB 10; ilarity 100.0%; Pred. No. 1.6e+02; Conservative 0; Mismatches 0;
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: (310) 27
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                                                                                                                                                                                                                    Products and Methods for Their Production
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                                                                                                                                                Suite 3800
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STRAIN: Erdman SEQUENCE DESCRIPTION: SEQ ID NO: 49: US-09-953-510-49
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US-10-147-255-48
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48, Application US/10147255 Publication No. US20030152584A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
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TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: MacLean, Kurt A.
REGISTRATION NUMBER: 31,118
REFERENCE/DOCKET NUMBER: 112-272
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PEM PC COMPATION

COMPUTER: Patentin Release #1.0,

Version #1.30
                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/147,255
FILING DATE: 15-Way-2002
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Kurt A. MacLean
                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/226,539A
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Horwitz, Marcus A.

TITLE OF INVENTION: Abundant Extracellular

Products and Methods for Their Production and Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GLSI 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/289,667
FILING DATE: 12-AUG-1994
APPLICATION NUMBER: US 08/156,358
FILING DATE: 23-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/447,398 FILING DATE: 23-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/953,510 FILING DATE: 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                        STREET: 2029 Century Park East, Suite 3800
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Pred. No. 1.6e+02;
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Best Local :
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; STRAIN: Erdman; SEQUENCE DESCRIPTION: SEQ ID NO: 48: US-10-147-255-48
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US-10-147-255-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49, Application US/10147255 Publication No. US20030152584A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (310) 277-1
INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                        ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
                                                                                                                  APPLICATION NUMBER: US/10/147,255
PILING DATE: 15-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                  Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Kurt A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HOTWITZ, Marcus A.
TITLE OF INVENTION: Abundant Extracellular
Products and Methods for Their Production and Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 GLSI 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/156,358 FILING DATE: 23-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/447,398
FILING DATE: 23-MAY-1995
APPLICATION NUMBER: US 08/289,667
FILING DATE: 12-AUG-1994
FILING DATE: 12-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: MacLean, Kurt A
                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
                                   APPLICATION NUMBER: US/09/226,539A FILING DATE: <Unknown> APPLICATION NUMBER: US 08/447,398 FILING DATE: 23-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 2029 Century Park East, Suite 3800
APPLICATION NUMBER: US 08/289,667 FILING DATE: 12-AUG-1994
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APPLICATION NUMBER:

US 08/156,358

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APPLICANT: Katz, Lawrence C.

APPLICANT: Katz, Lawrence C.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING

TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING

TITLE OF INVENTION: CELL DEATH

FILE REFERENCE: 10001-005-999

CURRENT PRICE STATE: 2001-08-03

PRIOR APPLICATION NUMBER: US/09/461,697

PRIOR FILING DATE: 2001-08-03

PRIOR FILING DATE: 1999-12-14

NUMBER OF SEQ ID NOS: 466

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 99

LENGTH: 16

TYPE: PRT

CDCANTEM: Homo Sapiens
                RESULT 9
US-09-813-333-66
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                                                                                                                                                                                                      ; ORGANISM: Homo sapiens US-09-922-261-99
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Sequence
                                                                                                                                             Matches
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: COGENT NEUROSCIENCE, Inc. APPLICANT: Lo, Donald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (310) 788-50
TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity es 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: NO ANTI-SENSE: NO FRACMENT TYPE: internal ORIGINAL SOURCE:
66, Application US/09813333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: MacLean, Kurt A.
REGISTRATION NUMBER: 31,118
REFERENCE/DOCKET NUMBER: 112-272
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99, Appitus
10. US20020111471A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 23-NOV-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                          1 GLSI 4
                                                                                                                                         4;
                                                                                                                                                        Similarity
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                                                                              GLSI 6
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Barney, Shawn
Thomas, Mary Beth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09922261
                                                                                                                                         Conservative
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                                                                                                                                                     100.0%;
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                                                                                                                                                     Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18; DB 12;
Pred. No. 1.6e+02;
; Mismatches 0;
                                                                                                                                    Mismatches
                                                                                                                                                     1.8e+02;
                                                                                                                                                                    DB 10;
                                                                                                                                                               Length 16;
                                                                                                                                    Indels
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RESULT 11
US-09-880-748-2186
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                                                                                                        Sequence 2186, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
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APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CHERENT FILING DATE: 2001-06-15
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                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2174, Application US/09880748 Publication No. US20030059937A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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TYPE: PRT
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NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver. 2.1
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CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,834
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TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
FILE REFERENCE: 17999-004 US
                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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Pred. No.
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Pred. No.
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1.8e+02;
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APPLICATION NUMBER: 60/212,210

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; ORGANISM: Homo sapiens
US-09-880-748-2980
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PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2186
Sequence 61, Application US/09991225
Publication No. US20030153063A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED HI
TITLE OF INVENTION: HEART AND VARIANTS THEREOF
FILE REFERENCE: D0075.NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 2980
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Best Local Similarity
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-08-15
PRIOR ETLING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR ETLING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
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Pred. No. 1.
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RESULT 15
US-09-991-225-73
; Sequence 73, Application US/09991225
; Publication No. US20030153063A1
; Publication No. US20030153063A1
; GENERAL INFORMATION:
    A FELICANT: BITSTOL:
    A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED;
    TITLE OF INVENTION: HEART AND VARIANTS THEREOF
; FILE OF INVENTION: HEART AND VARIANTS THEREOF
; FILE OF INVENTION: HEART US/09/991,225
; CURRENT APPLICATION NUMBER: US/09/991,225
; CURRENT ELLING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/257,611
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Sequence 62, Application US/09991225
Publication No. US20030153063A1
GENERAL INFORMATION:
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Matches 4
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PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/257,611
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/305,818
PRIOR FILING DATE: 2001-07-16
NUMBER OF SEQ ID NOS: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED
TITLE OF INVENTION: HEART AND VARIANTS THEREOF
FILE REFERENCE: D0075. MP
CURRENT PRILOR OF THE STATE COUPLED
CURRENT PRILOR DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/249,613
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/257.611
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/257.811
PRIOR APPLICATION NUMBER: 60/257.818
PRIOR APPLICATION NUMBER: 60/305,818
PRIOR FILING DATE: 2001-07-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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TYPE: PRT
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Perfect score:
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| cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
| cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
| cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
| cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
| cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
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          PCT-USO2-27760-524
PCT-USO2-27760-157
PCT-USO2-27760-196
PCT-USO2-27760-377
PCT-USO2-27760-394
PCT-USO2-27760-394
PCT-USO2-27760-456
US-10-462-850-2168
US-10-631-401-2489
US-10-631-441-2489
US-10-631-441-2489
US-10-612-783-6551
US-10-268-897-2654
US-10-268-898-2654
US-10-10-286-897-2654
US-10-10-286-898-2654
US-10-10-286-898-2654
US-10-10-286-898-2654
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	14336, A	202, App		25585, A	21294, A	141, App	17866, A	79, Appl	68, Appl	2, Appli	22075, A	5684, Ap	5074, Ap	23917, A	21820, A	23903, A	21166, A	26666, A	3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

ALIGNMENTS

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; LENGTH: 6
; TYPE: PRT
; ORGANISM: HOMO S
PCT-US02-27760-730
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APPLICANT: Challita-Eid, Pia M
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Jakobovits, Aya
Sequence 142, Application PC/TUS0227760

GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Chalita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENVITLED 2051B5 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51582004340
CURRENT APPLICATION NUMBER: PCT/US02/27760
CURRENT FILING DATE: 2003-07-21
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Best Local Similarity
Matches 4; Conser
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APPLICANT: Hubert, Rene S.
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEEC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF CANCER
TILE REFERENCE: 51182004440
CURRENT APPLICATION NUMBER: PCT/US02/27760
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 60/316,664
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 736
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 1.1e+05;
tive 0; Mismatches 0;
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RESULT 4
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PCT-US02-27760-350
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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-USO2-27760-142
                                                                   APPLICANT: Raitano, Arthur B.
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582004340
CURRENT APPLICATION NUMBER: PCT/US02/27760
CURRENT FILING DATE: 2003-07-21
CUBRENT FILING DATE: 2003-07-21
SEQ ID NO 406
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PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 736
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 350
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APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eld, Pia M.
APPLICANT: Raitano, Arthur B.
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 142
                                                        PRIOR APPLICATION NUMBER: US 60/316,664
PRIOR FILING DATE: 2001-08-31
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               SOFTWARE: FastSEQ for Windows Version 4.0
                                      NUMBER OF SEQ ID NOS: 736
                                                                                                                                                                                                                                                                          APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Faris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT &
FILE REFERENCE: 511582004340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: PCT/US02/27760 CURRENT FILING DATE: 2003-07-21
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Local Similarity 100.0%;
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Pred. No. 1
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; ORGANISM: Homo sapiens PCT-US02-27760-157
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                                     NUMBER OF SEQ ID NOS: 736
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 157
LENGTH: 10
TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 524
LENGTH: 9
TYPE: PRT
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Best Local
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                                                                                                                                                           APPLICANT: Hubert, Rene S.
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT !
FILE REFERENCE: 511582004340
CURRENT APPLICATION NUMBER: PCT/US02/27760
CURRENT FILLING DATE: 2003-07-21
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Best Local Similarity
                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/316,664 PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                               APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Rattano, Arthur B.
APPLICANT: Faris, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: PCT/US02/27760 CURRENT FILING DATE: 2003-07-21 PRIOR APPLICATION NUMBER: US 60/316,664 PRIOR FILING DATE: 2001-08-31
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APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511522004340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Agensys, Inc
APPLICANT: Challita-Eic
APPLICANT: Raitano, Art
APPLICANT: Faris, Mary
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TYPE: PRT
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CURRENT APPLICATION NUMBER: PCT/US02/27760
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 60/316,664
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEO ID NOS: 736
SOFTWARE: FASTSEQ for Windows Version 4.0
SEO ID NO 275
LENGTH: 10
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GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Jakobovits, Ays
TITLE OF INVENTION: MUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF CANCER
TITLE OF INVENTION NUMBER: PCT/US02/27760
CURRENT APPLICATION NUMBER: PCT/US02/27760
CURRENT APPLICATION NUMBER: US 60/316,664
PRIOR APPLICATION NUMBER: US 60/316,664
PRIOR FILING DATE: 2001-08-31
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PCT-US02-27760-196
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                                                                                                               ; ORGANISM: Homo sapiens
PCT-US02-27760-275
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SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 196
LENGTH: 10
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 275, Application PC/TUS0227760
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Challite-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
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                                       Matches
                                                                        Query Match
                                                                                                                                                                                                                                                                                                                      APPLICANT: Hubert, Rene S.
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582004340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 100.0%;
Local Similarity 100.0%;
hes 4; Conservative 0;
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Pred. No.
                                                          Score 18; DB Pred. No. 20;
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                                                                          DB 1; Length 10;
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     RESULT 11
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Query Match
Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 377
LENGTH: 10
TYPE: PRT
                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/316,664
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 736
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 394
LENGTH: 10
TYPE: PRT
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                                                                        Matches
                                                                                         Query Match
Best Local Similarity
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APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582004340
CURRENT APPLICATION NUMBER: PCT/US02/27760
CURRENT FILING DATE: 2003-07-21
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APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582004340
CURRENT APPLICATION NUMBER: PCT/US02/27760
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 60/316,664
PRIOR FILING DATE: 2001-08-31
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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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APPLICANT: Challita-Eid, Pi
APPLICANT: Raitano, Arthur
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                                    1 GLSI 4
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Pred. No.
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Pred. No.
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RESULT 13
US-10-411-206A-11
(S-10-411-206A-1)
; Sequence 11, Application US/10411206A
; GENERAL INFORMATION:
; APPLICANT: ITVING W. WAINER et al.
; TITLE OF INVENTION: COMPUTER-BASED MODEL FOR IDENTIFICATION AND CHARACTERIZATION FOR TITLE OF INVENTION: MON-COMPETITIVE INHIBITORS OF MICOTINIC ACETYLCHOLINE RECEPTORS
; TITLE OF INVENTION: AND RELATED LIGAND-GATED ION CHANNEL RECEPTORS
; FILE REFERENCE: 1173-1025P
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GENERAL INFORMATION:
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/411,206A CURRENT FILING DATE: 2003-11-04
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TITLE OF INVENTION: Complementary peptide ligands from the human genome FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/10/462,850
CURRENT FILING DATE: 2003-06-17
NUMBER OF SEQ ID NOS: 4203
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APPLICANT:
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CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: US 60/316,664
PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hubert, Rene S.
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582004340
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APPLICANT: Challita-Eic
APPLICANT: Raitano, Art
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                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: sequence located in PMEL17 OR D12S53E at 164-173 and OTHER INFORMATION: Sequence 2167 in this patent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo Sapiens
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nilarity 100.0%;
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Pred. No.
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Pred. No.
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GLSI 10

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RESULT 14
US-10-631-402-2489
Commence 2489, Ap
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CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: US/09/547,599C
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 08/905,223
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION:
; OTHER INFORMATION:
US-10-411-206A-11
                                                      Query Match
Best Local
                                       Matches
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SEQ ID NO 2489
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SOFTWARE: PatentIn version
SEQ ID NO 11
LENGTH: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 08/904,468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Duclert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: Expressed Sequence Tags and Encoded
                                                                                                                           OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: GEN-T119C1
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                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                               LOCATION: -21
                                                                                                                                                                                                NAME/KEY: SIGNAL
                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                    OTHER INFORMATION:
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                                     Conservative
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                                                                                                                       Von Heijne matrix
score 4.50
seq SILFHCSVCLFLC/QY
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                                                    100.0%; Score 18; 100.0%; Pred. No.
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Pred. No. 52;
                                 Mismatches
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                                                      59;
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RESULT 15

US-10-631-441-2489

Sequence 2489, Application US/10631441

CORRENT INCORMATION:
APPLICANT: Dumbs Milne Edwards, Jean Baptiste
APPLICANT: Lacrotx, Bruno
TITLE OF INCORMATION: Expressed Sequence Tags and Encoded Human Proteins
TITLE OF INCORMATION: EXPRESSED Sequence Tags and Encoded Human Proteins
TITLE OF INCORMATION: EXPRESSED Sequence Tags and Encoded Human Proteins
TITLE OF INCORMATION: EXPRESSED Sequence Tags and Encoded Human Proteins
TITLE OF INCORMATION NUMBER: US/20/541,599C

PRIOR APPLICANTON NUMBER: US/20/54,468

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Listing first 45 summaries
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hypothetical prote		-	spa9 protein - Shi	independent	hypothetical proce		≅	ribosomal protein	collagen alpha 1(conserved hypothe	hypothetical proce	-	, 5	pr

ALIGNMENTS

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A; Reference number: S57494
A; Accession: S57519
A; Status: preliminary
A; Molecule type: mRNA
A; Mesidues: 1-17 <BUR>
A; Cross-references: EMBL: Z499
C; Keywords: T-cell receptor
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A;Description: T cell receptor repertoire for a viral epitope in humans is diversifie A;Reference number: S57494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T cell receptor beta chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 10-Oct-1995 *sequence_revision 17-Nov-1995 *te
C;Accession: $57519
A;Experimental source: strain 9a5c
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer Briones, C.; Bleno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.P.; Krieger, J.E.; Kuramae, E.E.; La J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A;Authors: Marrins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C. F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
(82839)
hypothetical protein XF0163 [imported] - Xylella fastidiosa (strain 9a5c)
hypothetical protein XF0163 [imported] - Xylella fastidiosa (strain 9a5c)
hypothetical protein XF0163 [imported] - Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Accession: G82839
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
Nature 406, 151-157, 2000
NayTitle: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Note: for a complete list of authors see reference number A59328 below
N;Accession: G82839
N;Catterior: G82839
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-31 <SIM>
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Pred. No. 1.1e+02;
; Mismatches 0;
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submitted to the EMBL Data L
A; Reference number: Z19189
A; Accession: T19865
A; Status: preliminary; trans
A; Molecule type: DNA
A; Residues: 1-34 <WIL>
A; Experimental source:
C; Genetics:
A; Gene: CESP:H12D21.1;
A; Map position: 5
                                                                               A; Molecule type: DNA
A; Residues: 1-34 <WI
                                                              A; Cross-references:
                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDB.
                                                                                                                         submitted to the EMBL Data Library, A; Reference number: Z20387 A; Accession: T27557
                                                                                                                                                                                                                                                                                                                          hypothetical protein H12D21.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T23074; T27557
                                                                                                                                                                         A; Experimental source: clone H12D21
R; Ainscough, R.
                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-34 <WIL>
A; Cross-references: EMBL: 292849; PIDN: CAB07428.1;
                                                                                                                                                                                                                                              A; Status: preliminary; translated from
                                                                                                                                                                                                                                                               submitted to the EMBL Data
A; Reference number: Z19671
A; Accession: T23074
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T19865
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tc
C;Accession: T19865
R;White, S.
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A;Contents: annotation
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: XF0163
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                                     EMBL:278067; PIDN:CAB01526.1; GSPDB:GN00023; CESP:2C412.7
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             CESP: ZC412.7
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Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                                                March 1997
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Silveir
A.L.; Z
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C;Accession: S68648
R;Calvete, J.J.; Dostalova, Z.;
FEBS Lett. 379, 207-211, 1996
                                                                                   RESULT 7
S68648
                                    major glycoprotein PSP-I - pig (fragments)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 17-Mar-1999
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                                                                                                                                                                                                                                                    A; Gene: CESP: ZC412.6
A; Map position: 5
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A; Residues: 1-34 <WIL>
                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data A; Reference number: Z20387
                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein ZC412.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27560
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T26210
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                                                                                                                                                                                                                                                                                                           A; Cross-references:
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submitted to the EMBL Data
A;Reference number: Z20173
A;Accession: T26210
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A; Map position: 5
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A; Residues: 1-34 <WIL>
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Pred. No. 2.
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             Adermann, K.;
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hypothetical protein ORF35 - Norway spruce chloroplast C: Species: chloroplast Picea ables (Norway spruce) C: Species: chloroplast Picea ables (Norway spruce) C: Attention: T11812 C: Accession: T11812 R: Kluemper, S.; Kanka, S.; Riesner, D.; Etscheid, M. submitted to the EMBL Data Library, March 1997 A; Description: Characterisation of a Norway spruce chloroplast DNA clone: Complete nucl A; Reference number: Z17349 A; Accession: T11812
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A; Genome:
C; Keywords
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A;Residues: 1-35 <KLU>
A;Cross-references: EMBL:U92462; NID:g2959581; PID:g2959588
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A; Residues: 1-7;8-12;13-20;21-27;28-32;33-34
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                                                                                                                                                                                                                                                                                                                                                                                                     probable nitrogen regulation protein II (EC 2.7.3.-) - Xanthomonas campestris
C;Species: Xanthomonas campestris pv. campestris
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 17-Jul-1998
C;Accession: S11913
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RESULT 10
S78726
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A;Title: Use of oligonucleotide probes to identify members of two-component regulatory A;Reference number: S11912; MUID:91042416; PMID:2233675
A;Accession: S11913
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A; Residues: 1-46 < OSB>
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Best Local
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$68648; MUID:96184566; PMID:8603690
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Pred. No.
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Pred. No. 2.3
0; Mismatches
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protein YKL162c-a - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 15-Jan-1999 #sequence_revision 15-Jan-1999 #text_change 15-Jan-1999
C;Accession: S78726
R;Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.
submitted to the Protein_Sequence Database, March 1994
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A; Residues: 1-50 <VA2>
A; Cross-references: EMI
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N;Alternate names: calmodulin-independent protein kinase
C;Species: Avena sativa (oat)
C;Date: 27-Oct-1995 #sequence_revision 19-Jan-1996 #text_cha
C;Accession: S56727
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                                                                                                                                                                                                                                hypothetical protein asr3001 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec C;Accession: AB2181
                                                                                                                                                                                                                                                                                                                             RESULT 12
AB2181
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A; Residues: 1-53 <HUT>
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                                                                                                                                                                            R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, N
DNA Res. 8, 205-213, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
             A;Cross-references: GB:BA000019; PIDN:BAB74700.1; A;Experimental source: strain PCC 7120 C;Genetics:
                                                                                                    A; Reference number: AI
A; Accession: AB2181
A; Status: preliminary
                                                                   A; Molecule type: DNA
A; Residues: 1-55 < KUR>
                                                                                                                                                              A; Title: Complete Genomic
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                                                                                                                                               Sequence of the Filamentous Nitrogen-fixing Cyanobacterium 7; MUID:21595285; PMID:11759840
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                                                      PID:g17132095; GSPDB:GN00179
                                                                                                                                                                                                       M.; Yamada,
                                                                                                                                                                                                       Sasamoto, S.; Watanabe, A.;
M.; Yamada, M.; Yasuda, M.;
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RESULT 15
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H95182
                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-56 < KUR>
                                                                                                                                                                                                                                                                                                                  A;Althors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                      on, J.D.; Umayam, L.A.;
nson, T.; Hickey, E.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein SP1570 [imported] - Streptococcus pneumoniae (strain TIGR4) C;Species: Streptococcus pneumoniae (strain TIGR4) C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001 C;Accession: H95182
                                                                                                                                                                                                                                                                                               A; Status: preliminary
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A:Genome: nucleomorph
C:Superfamily: Escherichia coli ribosomal protein S14
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C90120
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A:Molecule type: DNA
A:Residues: 1-56 <DOU>
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Nature 410, 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40s ribosomal protein S29A [imported] - Guillardia theta nucleomorph C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endos
                                                                                                                                            Query Match
Best Local ;
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91-1096, 2001
                                                                                                                   Conservative
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#sequence_revision 10-May-2001 #text_change 02-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                         K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei
White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
Holt, I.E.
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                                                                                                                                                                      A;Gene: spr1428
                                                                                                                                                                                            A;Cross-references: GB:AE007317; PIDN:AAL00232.1; PID:g15459082; GSPDB:GN00174
                                                                                                                                                                                                                                                                                                                                                                                                       R;HOSKINS, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowltz, E.J.; Lu, J.; Matsushima, P.; McAhren, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein spr1428 [imported] - Streptococcus pneumoniae (strain R6) c;Species: Streptococcus pneumoniae C;Species: 22-Oct_2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
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A; Residues: 1-56 < KUR>
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P21019 vaccinia vi
P29890 vaccinia vi
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ID VX2A_C
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DT 01-NOV
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.

NCBI_TaxID-386;
                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                             Nitrogen fixation; SEQUENCE 70 AA;
                                                                                                                                                                                                                                                                                                     EMBL; X51963; CAB37405.1; PIR; S09281; S09281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Iismaa S.E., Ealing P.M., Scott K.F., Watson J.M.;
"Molecular linkage of the nif/fix and nod gene regions in leguminosarum biovar trifolli.";
Mol. Microbiol. 3:1753-1764(1989).
-1- SIMILARITY: TO K.PNEUMONIAE AND A.VINELANDII NIFT PROT THE N-TERMINAL OF R.MELILOTI MOSB PROTEIN.
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    Porcine
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      gastroenteritis coronavirus
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YKO7_YEAST
YIJD_ECOLI
R811_MYCPN
RL7_MYCPU
YFD3_RHILO
YABR_BACSU
CHHB_BOMMO
LSM1_HUMAN
LSM1_HUMAN
LSM1_MOUSEE
PSP1_PIG
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Pred. No. 2.3
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01-FEB-1991
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MEDLINE=91021027; PubMed=2219722;
Johnson G.P., Perkus
                                                                                                                                                                                                                   "Appendix to 'The complete DNA Virology 179:517-563(1990).
                                                                                                                                                                                                                                                              Goebel S.J., Johnson Paoletti E.;
                                                                                                                                                                                                                                                                                                        COMPLETE
                                                                                                                                                                                                                                                                                                                                             Virology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Orthopoxvirus
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Viruses; dsDNA viruses, no RNA sta
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PIR; S01739; S
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InterPro; IPR006784; Corona_3.
Pfam; PF04694; Corona_3; 1.
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Biochimie 69:591-600(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA Coronaviridae;
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                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                         complete DNA sequence logy 179:247-266(1990).
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SEQUENCE FROM N.A.
STRAIN-UAB CTIP;
MEDLINE=21267165; PubMed=11353084;
MEDLINE=21267165; PubMed=11353084;
Membaud I., Heilig R., Ferris S., Branchambaud T., Heilig R., Wroblewski H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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15-SEP-2003
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       "The complete genome sequence
                                                                                                                                                                   Q98R64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA Orthopoxvirus.
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01-APR-1993
01-APR-1993
                                                                                               Mycoplasma pulmonis.
Bacteria; Firmicutes;
                                                                                                                  Hypothetical
MYPU_1460:
                                                                                      WCBI_TaxID=2107;
                                                                                                                                                                            Y146_MYCPU
                                                                                                                                                                                                                                                                                                      SEQUENCE
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Serpinskii O.I., Blinov V.M., Nikulin A.E., Vasi
                                                                                                                                                                                                                                                                                                                                                                                                            Biotekhnologiya 4:442-449(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=31531;
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F14L OR F4.
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P29890;
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NCE 73 AA; 8307 M
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pulmonis.";
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Pred. No. 2.4
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                           Η.,
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                                     Barbe V.,
                                                                                                                                              update)
        murine respiratory pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                             of segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                            <u>Viari</u>
                                                                                                                                   update)
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                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73
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                                                                                                                                                                          AA
                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                               .4e+02;
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                           Α.,
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                                   Samson
                           Rocha
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                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             vaccinia virus
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                                    Galisson
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O8VBX1:
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Endothelial lipase (EC 3.1.1.3) (Endothelial-derived lipase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 29:2145-2153(2001).
-I- SIMILARITY: BELONGS TO THE UPF0154 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BN-Lx/Cub, and SHR/OlaIpov;

MEDLINE-21913086; PubMed-11924532;

Bonne A.C.M., den Bleman M.G., van Lith H., van Zutphen B.F.M.;

Bonne A.C.M., den Bleman M.G., van Lith H., van Zutphen B.F.M.;

"Sequencing and chromosomal assignment of the rat endothelial-derived lipase gene (Lipg).";

DNA Seq. 12:285-287(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq. 12:285-287(2001).

FUNCTION: Has phospholipase and triglyceride lipase activities.

Hydrolyzes high density lipoproteins (HDL) more efficiently than
                                                                                                                                                                                                                                                             fatty acid anion.
SUBCELLULAR LOCATION: Secreted (By similarity).
MISCELLANDOUS: It is termed endothelial lipse due to the fact
that it is synthesized in endothelial cells, a characteristic that
distinguishes it from other members of the family. However this
protein is also expressed in other cell types.
SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolyzes high density lipoproteins (HDL) more ef other lipoproteins. Binds heparin (By similarity). CATALYTIC ACTIVITY: Triacylglycerol + H(2)0 = diac
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ilarity 100.0%;
Conservative (
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8470 MW;
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Rodentia;
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A92264859CE7E908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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9 0; 'Indels
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    diacylglycerol

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
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Best Local S
Matches
                                  EMBL; M30612; AAA66395.1; -
EMBL; S50936; AAB19564.1; -
PIR; C31684; C31684.
Hypothetical protein.
SEQUENCE 83 AA; 9512 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical protein IORF2.
Bovine coronavirus (strain Mebus) (BCOV) (BCV),
Bovine coronavirus (strain Quebec) (BCOV) (BCV).
Viruses; ssRNA positive-strand viruses, no DNA s
Coronaviridae; Coronavirus.
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P22054;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000734; Lipase, pfam; PF00151; lipase; 1. Hydrolase; Lipid degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                            MEDLINE-89279187; PubMed-2732684; Parker M.D., Cox G.J., Deregt D., Fitzpatrick D.R., E Parker M.D. deregt D., Fitzpatrick D.R., E "Cloning and in vitro expression of the gene for the haemagglutinin glycoprotein of bovine coronavirus."; J. Gen. Virol. 70:155-164(1989).
                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        MEDLINE-91353426; PubMed-2103108;
Kienzle T.E., Abraham S., Hogue B.G.,
"Structure and expression of the bovi
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-90204700; PubMed-2319653;
Kienzle T.E., Abraham S., Hogue B.G., Brian
"Structure and orientation of expressed bovi
hemagglutinin-esterase protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Mebus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=11132,
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  Ādv.
                                                                                                                                                                                                                                                                                                                             protein.";
                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Mebus;
                                                                                                                                                                                                                                                                           STRAIN=Quebec;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    Virol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AY027561; AAK14774.1;
AY027562; AAK14775.1;
                                                                                                                                                                                                                                                                                                                  Exp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 GLSI 19
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                                                                                                                                                                                                                                                                                                                  Med.
                                                                                                                                                                                                                                                                                                                                                                                                                    64:1834-1838(1990).
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80 AA;
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                                                                                                                                                                                                                                                                                                                  Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8791 MW;
                                     9512 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
100.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                           the bovine
                                     7343F2AC9330DAE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
 Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                       Brian D.
                                                                                                                                                                                                                                                                                                                                                                                                                                             bovine coronavirus
                                                                                                                                                                                                                                                                                                                                              coronavirus hemagglutinin
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              DB 1;
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             Length 83;
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                                                                                                                                                                 restrictions
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Query Match Best Local S Matches 4

Similarity 4; Conser

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Mismatches

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Gaps

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GLSI GLSI 46

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RESULT 8

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ID TATE_YERPE

ID TATE_OBJOHI

PAC 082DHI

DT 28-FEB

DT 18-FEB

DT 28-FEB

DT 28-FE
                                                         Transport; Protein transport; Inner membrane; Complete prote
                                                                                                            InterPro; IPR003369; MttA_Hcf106.
InterPro; IPR006312; TatA_E.
Pfam; PF02416; MttA_Hcf106; 1.
TIGRFAMS; TIGR01411; tatAE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of versinia pestis KIM.";

J. Bacteriol. 184:4601-4611(2002).

-I- FUNCTION: Required for correct localization of precursor bearing signal peptides with the twin arginine conserved S/T-R-R-X-F-L-K. This sec-independent pathway is termed T twin-arginine translocation system. This system mainly tr proteins with bound cofactors that require folding prior
                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinfo
the European Bioinformatics Institute,
use by non-profit institutions as la
modified and this statement is not rem
                                                                                                                                                                                                                                                                                     EMBL; AJ414153; CAC92840.1; EMBL; AE013720; AAM84747.1;
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28-FEB-2003
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                               entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blatti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M. Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yersinia pestis.
Bacteria; Proteobacteria;
Enterobacteriaceae; Yersin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=KIM5 / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21470413; PubMed=11586260
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                                                                                                                                                                                                                         L; AE013720; AAM84/4

L; AE013720; AAM84/4

; AI0316; AI0316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (By similarity).
SUBCELLULAR LOCATION: Inner-membrane bound (Probable)
SIMILARITY: BELONGS TO THE TATA/E FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                            d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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           A,
                                                      Complete proteome
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POTENTIAL.
BD7E1533D3865055 CRC64;
                                                                                  Translocation;
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RESULT 9
SPAQ_SHIFL
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Buchrieser C., Glaser P., Rusnick C., Ne
Kunst F., Sansonetti P., Parsot C.;
"The virulence plasmid pWR100 and the re
by the type III secretion apparatus of si
Mol. Microbiol. 38:760-771/2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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P40705; Q55297;
01-FEB-1995 (Rel. 3
01-FEB-1995 (Rel. 3
28-FEB-2003 (Rel. 4
                                                                                                                                                                                                                                                                                                         SPECIES-S. flexneri; STRAIN-301 / Serotype

MEDLINE-22272406; PubMed-12384590;

Jin Q., Yuan Z., Xu J., Wang Y., Shen Y.,

Yang J., Yang F., Zhang X., Zhang J., Yang

Sun L., Xue Y., Zhao A., Gao Y., Zhu J., K

Cheng H., Yao Z., He B., Chen R., Ma D., Q
                       SEQUENCE
                                                                                 requires
                                                                                                      Venkatesan M.M., Buysse J.M., "Surface presentation of Shige
                                                                                                                                           MEDLINE=92193289; PubMed=1312536;
                                                                                                                                                                  SPECIES=S.flexneri;
                                                                                                                                                                                          SEQUENCE OF 1-53
                                                                                                                                                                                                                                  Nucleic
                                                                                                                                                                                                                                                   through
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    J. Bacteriol.

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MEDLINE=93224456; PubMed=8385666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasakawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Intect.
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete DNA sequence and Shigella flexneri.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=S.flexneri; STRAIN=M90T / MEDLINE=21189246; PubMed=11292750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pWR100, Plasmid pMYSH
Bacteria; Proteobacteria; Gam
Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shigella flexneri, and Shigella sonnei.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venkatesan M.M., Goldberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Surface presentation of antigens SPAQ OR SPA9 OR CP0154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invasion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wa C., Komatsu K., Tobe T., Suzuki T.,
genes in region 5 that form an operon
on of epithelial cells by Shigella flex
teriol. 175:2334-2346(1993)
                                                                                                                                                                                                                        sequence of Shigella flexneri 2a: insights into comparison with genomes of Escherichia coli K12 Acids Res. 30:4432-4441(2002).
                     FROM
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                                                         presentation of Shigella flexneri
the products of the spa locus.";
riol. 174:1990-2001(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pMYSH6000,
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31, Last sequence update)
41, Last annotation update)
                                                                                                                                                                STRAIN-M90T /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YYSH6000, and Plasmid Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analysis
                                                                                                                                                                                                                                                                                                       Y., Shen Y., Lu W., War
Zhang J., Yang G., Wu H.
Y., Zhu J., Kan B., Dir
n R., Ma D., Qiang B., V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                         Oaks E.V.;
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Pred. No.
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2.8e+02;
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                                                                                                  invasion
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Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                             Wang
u H.,
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                                                                                                plasmid antigens
                                                                                                                                                                                                                                                                                                         K., Chen
                                                                                                                                                                                                                                                                                                                                               Qu D.,
                                                                                                                                                                                                                                             pathogenicity and 0157.";
                                                                                                                                                                                                                                                                                                                                                                   Liu
                                                                                                                                                                                                                                                                                                                                               Dong J.,
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SPECIES-S

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Best Local
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EMBL; AP348706; AARI8473.1; --
EMBL; D13663; BAA02830.1; --
EMBL; AP3486526; AAL72556.1; --
EMBL; AP346526; AAL72556.1; --
EMBL; M81458; -; NOT_ANNOTATED_CDS.
EMBL; M81458; -; NOT_ANNOTATED_CDS.
EMBL; D50601; BAA09163.1; ALT_INIT.
PIR; H49846; H49846
InterPro; IPR002191; Bac_export_3.
InterPro; IPR006306; Hrp0.
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submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
11- FUNCTION: REQUIRED FOR SURFACE PRESENTATION OF INVASION PLASMID ANTIGENS. COULD PLAY A ROLE IN PRESERVING THE TRANSLOCATION COMPETENCE OF THE IPA ANTIGENS. REQUIRED FOR INVASION AND FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pl1448;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Cytochrome C6 (Soluble cytochrome f) (Cytoc 553).
                                                                                                                                                           SEQUENCE, AND CHARACTERIZATION.

MEDLINE-88139277; PubMed=381367;
Okamoto Y., Minami Y., Matsubara H., Sugimura Y.;

"Studies on algal cytochromes VI: some properties and sequence of cytochrome c6 from a green alga, Bryopsis J. Blochem. 102:1251-1260(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                        Bryopsis maxima (Green alga).
Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpales;
Bryopsidaceae; Bryopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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PRINTS; PR00952; TYPE3IMOPROT.
TIGRFAMs; TIGRO1403; fl1Q_rel_IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYC6_BRYMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid; Virulence; Transmembrane.
-I- SÜBUNIT: Monomer.
-I- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
-I- PTM: Blnds one heme group per molecule.
-I- MISCELLANEOUS: The midpoint redox potential for this protein i
                                                                                                      -!- FUNCTION: Functions as an electron carrier be
cytochrome b6f and photosystem I in oxygenic
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECRETION OF THE THREE IPA PROTEINS.
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: BELONGS TO THE FLIQ/MOPD/SPAQ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GLSI 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 AA;
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE3IMOPROT.
403; fliQ_rel_III; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9429 MW;
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552D3DBCB9C896E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 1;
Pred. No. 2.8e+0;
Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
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                                                                                                                                       carrier between membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.8e+02;
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                                                                                                              photosynthesis.
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Best Local :
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BINDING
METAL
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P22407;
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PRINTS; PR00605; CYTCHROMECIC.
PRINTS; PR00607; CYTCHROMECIE.
PROSITE; PS00190; CYTOCHROME_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003088; Cyt_CI.
InterPro; IPR002329; Cyt_CIC.
InterPro; IPR002323; Cyt_CIE.
InterPro; IPR000345; CytC_heme_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A30021; CCBM6.
                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P08197;
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01-AUG-1991 (Rel.
28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Electron transport;
                                                                                                                     EMBL; M21778; AAA88409.1; PIR; F31844; F31844.
                                                                                                                                                    entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                      "Complete nucleotide sequence of the Streptomyces lividans pIJ101 and correlation of the sequence with genetic propert J. Bacteriol. 170:4634-4651(1988).
                                                                                                                                                                                                                                                                                                 MEDLINE-89008081; PubMed-3170481;
                                                                                                                                                                                                                                                                                                                                  Plasmid plJ101.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

NCBI_TaxID=1916;
                                                                                                                                                                                                                                                                                                                                                                               Streptomyces lividans.
                                                                                                                                                                                                                                                                                                                                                                                            SPDA.
                                                                                       SEQUENCE
                                                                                                            Plasmid
                                                                                                                                                                                                                                           J. Bacteriol. 170:4634-4651(1988).
                                                                                                                                                                                                                                                                                                                                                                                                    Protein spdA
                                                                                                 TRANSMEM
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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83 GLSI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GLSI 4
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                      1 GLSI 4
                                                     Similarity
                                                                                                            Transmembrane.
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nilarity 100.0%;
Conservative 0
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                                                                                       94 AA;
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                                                                                                                                                                                                                                                                                          Cohen
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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19
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                                           100.0%; ;
100.0%; ;
tive 0;
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IRON
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IRON (HEME AXIAL LIGAND).
EFDE2C2680175E01 CRC64;
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Pred. No.
                                           Score 18; DE
Pred. No. 3.1
0; Mismatches
                                                                                       47D80CB57D824656 CRC64;
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. 2.9e+02;
0;
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                                            3.1e+02;
thes 0;
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                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chloroplast; Thylakoid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 88
                                                                Length 94;
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properties.";
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RESULT 13
NULM_CERCA
ID JUMA
AC Q3404
DT 15-JU
DT 15-JU
DT 15-JU
DT 15-JU
OS CERAT
OS CERAT
OS CERAT
OS MITO
OC FURAD
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RN ([1]
RN ([1]
RN SEQU
RC STRA
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RA GASP
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GRP7_DAUCA STANI
ID GRP7_DAUCA STANI
AC P37704;
D1 OCT-1994 (Rel. 30
D1 O1-OCT-1994 (Rel. 31
D1 O1-OCT-1994 (Rel. 31
D2 O1-OCT-1994 (Rel. 31
D3 O1-OCT-194 (Rel. 31
D4 O1-OCT-194 (Rel
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Best Local :
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STRAIN-Guatemala laboratory colony;
MEDLINE-95261546; PubMed-7742977;
Gasparich G.E., Sheppard W.S., Han
                                                                                                                                                                                                                                                                                                034049;
115-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
115-JUL-1998 (Rel. 36, Last annotation updat
NADH-ubiquinone oxidoreductase chain 4L (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _CERCA
                                                                                                                                  Neoptera; Endopterygota; Diptera; Br. Tephritoidea; Tephritidae; Ceratitis NCBI_TaxID=7213;
                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                           Ceratitis capitata (Mediterranean fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NULM_CERCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X15706; CAA33736.1; -. PIR; S35715; S35715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- FUNCTION: MAY BE CONNECTED WITH THE INITIATION OF EMBRYOGENESIS OR WITH THE METABOLIC CHANGES PRODUCED BY THE REMOVAL OF AUXINS.

-i- DEVELOPMENTAL STAGE: TRANSIENTLY EXPRESSED DURING EARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1994 (Rel. 30, Last sequence update) 01-OCT-1994 (Rel. 30, Last annotation updat Clycine-rich protein DC7.1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Daucus carota (Carrot).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; campanulids; Apiales; Apiaceae; Daucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Gene expression during cell suspensions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Asteridae; campanulids; Apiales; Apiaceae; Daucus.
NCBI_TaxID-4039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDUCTION: BY THE REMOVAL OF AUXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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ilarity 100.0%;
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9319 MW;
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7C00D44637B7A364 CRC64;
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GLYCINE-RICH PROTEIN DC7.1.
2 APPROXIMATE REPEATS OF H-H-G(4,6)-H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
     Han H.Y.,
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There are no restrictions
ong as its content is in
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     McPheron
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                                                                                                                                                                                     Muscomorpha;
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     В.А.,
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     Steck G.J.;
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RESULT 14
NULM_DROME
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Matches 4
                        muse by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                             J. MOI. EVOL. 51:48-63(2000).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted by the European Bioinformatics Institute.
                                                                                                                                                                                                                  STRAIN=Oregon-R, and Zimbabwe 53; MEDLINE=20363871; PubMed=10903372;
                                                                                                                                                                                                                                                                                                                               STRAIN=Bretagne;
MEDLINE=88212147; PubMed=3130291;
                                                                                                                                                                      Drosophila melanogaster subgroup.";
                                                                                                                                                                                                      Ballard J.W.O.;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              Genetics
                                                                                                                                                                                                                                                                                            evolutionary
                                                                                                                                                                                                                                                                                                                       Garesse
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            Ephydroidea; Drosophilidae;
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
22-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                       "Comparative genomics of mitochondrial DNA in members
                                                                                                                                                                                                                                                                                                                                                                                                                      Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MT:ND4L OR ND4L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P18934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase; NAD; Ubiquinone; Mitochondrion. SEQUENCE 96 AA; 11346 MW; B743137D69FF2331 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                       "Drosophila melanogaster mitochondrial DNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00420; oxidored_q2; 1.
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InterPro; IPR003214; Oxidred4L.
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-i- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
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118:649-663(1988).
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era; Muscomorpha;
                                      http://www.isb-sib.ch/announce/
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R EMBL; AF200828; AAF77235.1; -.
R EMBL; AF200829; AAF77247.1; -.
R PIR; SC01188; SC01188; mt:ND4L.
R FlyBase; F9gn0013683; mt:ND4L.
R InterPro; IPR001133; Oxidored_4L.
R InterPro; IPR003214; Oxidored_2.1.
R Pfam; PF00420; oxidored_2.1.
R Pfam; PF00420; oxidored_2.1.
R ProDom; PD000359; Oxidred4L; 1.
W Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 96 AA; 11359 MW; D383557D738A175B CRC64;
Query Match
Best Local Similarity
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SEQUENCE FROM N.A., Wolstenholme D.R.;

MEDLINE-84221393; PubMed-6328435;

Clary D.O., Wahleithner J.A., Wolstenholme D.R.;

"Sequence and arrangement of the genes for cytochrome b, URF1, URF4L,

"Sequence and five trNas in Drosophila mitochondrial DNA.";

URF4, URF5, URF6 and five trNas in Drosophila mitochondrial DNA.";

Nucleic Acids Res. 12:3747-3762(1984).

-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                   EMBL; X03240; CAA26994.1; ...
PIR; A30020; A30020.
FlyBase; FBgn0013186; Dyak\mt:ND4L.
InterPro; IPR001133; Oxidored_4L.
InterPro; IPR003214; Oxidred4L.
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STRAIR-2317, 6 Ivory Coast;
MEDLINE-86089137; PubMed-3001325;
MEDLINE-86089137; PubMed-3001325;
Clary D.O., Wolstenholme D.R.;
"The mitochondrial DNA molecular of Drosophila yakuba: nucleotide sequence, gene organization, and genetic code.";
J. Mol. Evol. 22:252-271(1985).
                                                                                   Oxidoreductase; NAD; Ubiquinone; Mitochondrion. SEQUENCE 96 AA; 11386 MW; 59ABEC7D738A174B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                Pfam; PF00420; oxidored_q2; 1.
ProDom; PD000359; Oxidred4L; 1.
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01-APR-1988 (Rel. 07, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4L (EC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Rephydroidea; Drosophilidae; Drosophila.
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P07708;
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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HIV DR super motif	ABP24804	22	15	100.0	20	45
super	477	22	15	100.0	20	44
HIV DR super motif	ABP24682	22	15	100.0	20	43
Fragment of human	AAY76385	21	15	100.0	20	42
ens	AAW41933	19	15	100.0	20	41
o acid sequen	AAY93533	21	14	100.0	20	40
P6'-F	AAB29426	21	14	100.0	20	39
rtin p	AAW61498	19	14	100.0	20	38
indi	AAW05491	17	13	100.0	20	37
Pylartin protein,	AAW61497	19	12	100.0	20	36
binding rar	AAR83335	16	12	100.0	20	ω :
ţij	ABP21023	22	11	100.0	20	34
B58 super mo	ABP18039	22	11	100.0	20	33
B58 super mot	ABP18038	22	11	100.0	20	32
super mot	ABP11838	22	11	100.0	20	31
A01 super	ABP11833	22	11	100.0	20	30
habditis	AAB13309	21	:	100.0	20	29
A24 motif	ABP24208	22	10	100.0	20	28
B58 super	ABP18041	22	10	100.0	20	27
B58 super	ABP18037	22	10	100.0	20	26
A24 super	ABP16087	22	10	100.0	20	25
A24 motif	ABP24209	22	9	100.0	20	24
A24 super	ABP15937	22	9	100.0	20	23
B58 super	ABP18040	22	æ	100.0	20	22
IV B58 super	ABP18036	22	œ	100.0	20	21
s pne	AAW62688	19	&	100.0	20	20
hore-labe	AAY80814	21	7	100.0	20	-
e used to	AAY15650	20	. 7	100.0	20	Б :
taphylococcus	ABR46817	24	σ.	100.0	20	17
Staphylococcus aur	681	24	o	100.0	20	6
Staphylococcus aur	642	24	o	100.0	20	5
Staphylococcus aur	642	24	0	100.0	20	4
Staphylococcus aur	603	24	σ	100.0	20	ຜ
Staphylococcus aur	R46	24	σ	100.0	20	โล โ
taphy	R4564	24	σ.	100.0	20	5 (
Staphylococcus aur	ABR45637	24	9	100.0	20	5

ALIGNMENTS

AAY15748 standard; Peptide; 5

A

Peptide used to make fluorescent reporter molecules

27-JUL-1999 (first entry)

AAY15748;

Fluorogenic; fluorescent reporter molecule; enzyme substrate; apoptosis; protease; peptidase; apoptosis cascade; cancer; chemotherapeutic agent; cell death; viral protease activity. Cai 03-MAR-1998; 10-OCT-1997; 09-OCT-1998; Synthetic. New fluorogenic or fluorescent reporter molecules WPI; 1999-312448/26. 22-APR-1999. WO9918856-A1. (CYTO-) CYTOVIA INC. SX, Drewe JA, Keana JFW, 98US-0033661. 97US-0061582. 98WO-US21231. Weber E, Zhang Ξ,

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RESULT 2
AAA7809020
ID AAA7809020
ID AAA780
AXX AAA78
AXX AAA78
AXX Prot
KW Dloc
KW Meth
AXX Synt
XXX WO2(
XXX WO2(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANY15618-Y15759 represent peptides used to make the fluorogenic or CC fluorescent reporter molecules of the invention. These molecules CC contain a peptide molety (e.g. present sequence) which acts as a CC substrate for enzymes involved in apoptosis or protease or peptidase CC enzymes. The compounds can be used as fluorogenic or fluorescent CC substrates for enzymes. Depending on the peptide molety used, the CC fluorescent molecules can be used for detecting or measuring the CC activity of an enzyme involved in the apoptosis cascade in cells; to CC determine whether a test compound has an effect on an enzyme involved CC in the apoptosis cascade in cells; for determining the sensitivity of CC an animal with cancer to treatment with chemotherapeutic agents or CC enhances cell death of test cells; for determining whether a test substance in cells; for determining whether a test compound has an effect on the activity of a viral protease in cells; CC and for measuring the activity of a protease or peptidase in cells; can defect on the activity of a protease in cells; compound has an effect on the activity of a protease or peptidase in cells.
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Best Local :
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                                                                                                                                                                                                                                                                                                                  (CYTO-) CYTOVIA INC.
(ZHAN/) ZHANG H.
(CAIS/) CAI S X.
(DREW/) DREWE J A.
(YANG/) YANG W.
                                                      Claim
                                                                                              New fluorescently labeled amino for detecting enzymes or their magents, contains a halobenzoyl N
                                                                                                                                                                                                              WPI; 2000-195079/17.
                                                                                                                                                                                                                                                              Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protease substrate;
blocking group; hal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fluorophore-labelled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY80902 standard; peptide; 5 AA
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                                                   Page
                                                                                                                                                                                                                                                              Cai SX,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      roup; halobenzoyl group; cleavage;
aminopeptidase type 2; MetAP-2; d;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ഗ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                              109; 174pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0093642
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                                                                                                                                                                                                                                                                 Drewe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fluorescent label; fluorophore; rhodamine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protease substrate peptide,
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                                                                                                                                                                                                                                                              JA,
                                                English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB
Pred. No. 9.3
); Mismatches
                                                                                                                                                                                                                                                              Yang
                                                                                         o acids or peptides, used as substrates modulators, e.g. anticancer or antiviral N-blocking group
                                                                                                                                                                                                                                                              Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.3e+05;
hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      viral protease;
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The invention

relates

6

fluorescently labelled

peptides

activity of an

enzyme

involved) be used volved in

apoptosis

or measuring cascade in c

substrate for enzymes involved in apoptosis or protease or peptidase enzymes. The compounds can be used as fluorescent or fluorescent substrates for enzymes. Depending on the peptide molety used, the fluorescent molecules can be used for detecting or measuring the

a peptide moiety (e.g. pre te for enzymes involved in

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RESULT 3
AAY15739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local
                                                                  AAY15618-Y15759 represent peptides used to make the fluorogenic or fluorescent reporter molecules of the invention. These molecules contain a peptide molety (e.g. present sequence) which acts as a
                                                                                                                                   Claim
                                                                                                                                                                  New
                                                                                                                                                                                              WPI; 1999-312448/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a halobenzoyl group on the fluorophore. They are of the structure peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking group, Y is a fluorescent or fluorigenic moiety (preferably a rhodamine), and the peptide-Y bond is cleavable by the enzyme being assayed. The labelled peptides are reporters for detecting intracellular proteolytic enzymes, particularly caspases and other enzymes involved in apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human cytomegalovirus and hepatitis C virus proteases); and methionine aminopeptidase type 2 (MetAP-2). The peptides are particularly used to identify modulators of these enzymes which may be potentially useful as
                                                                                                                                                                                                                                                                                     03-MAR-1998;
10-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fluorogenic; fluorescent reporter molecule; apoptosis; protease; peptidase; apoptosis ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agents for treating conditions such as cancer, neurodegeneration, autoimmune diseases, myocardial infarction and virla infection.

Modulators identified may also be used to prolong the life of cells being cultured for recombinant protein production, or to monitor the treatment of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are potential anti- angiogenic or anticancer agents. Sequences

AAY80782-Y80910 represent peptides, some of which are specifically
                                                                                                                                                                                                                                                         (CYTO-) CYTOVIA INC
                                                                                                                                                                                                                                                                                                                                09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                              22-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                           WO9918856-A1
                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     chemotherapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY15739 standard; Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      claimed, which may be used in assay methods according to the invention.
                                                                                                                                                              fluorogenic or fluorescent reporter molecules
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                                                                                                                                                                                                                         Drewe JA,
                                                                                                                                  Page 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to make fluorescent reporter molecules.
                                                                                                                                                                                                                                                                                     98US-0033661
97US-0061582
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                                                                                                                                202pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                               se; apoptosis cascade; death; viral protease
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Pred. No.
                                                                                                                                                                                                                          Weber
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                cascade; cancer;
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Matches
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Best Local
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 The invention relates to fluorescently labelled peptides containing a halobenzoyl group on the fluorophore. They are of the structure peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking group, Y is a fluorescent or fluorigenic moiety (preferably a rhodamine), and the peptide-Y bond is cleavable by the enzyme being assayed. The labelled peptides are reporters for detecting intracellular proteolytic enzymes, particularly caspases and other enzymes involved in apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human cytomegalovirus and hepatitis C virus proteases); and methionine aminopeptidase type 2 (MetAP-2). The peptides are particularly used to identify modulators of these enzymes which may be potentially useful as agents for treating conditions such as cancer, neurodegeneration,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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(CAIS/)
(DREW/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  blocking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protease substrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fluorophore-labelled protease
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                                                                                                                                                                                                            Claim
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                                                                                                                                                                                                                                                                                                                                                                 (YANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                CYTO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an effect on the activity of a protease or peptidase in
                                                                                                                                                                                                                                      fluorescently labeled amino acids or peptides, used as detecting enzymes or their modulators, e.g. anticancer its, contains a halobenzoyl N-blocking group \,
                                                                                                                                                                                                                                                                                                      2000-195079/17.
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ZHANG H.
CAI S X.
DREWE J A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   group; halobenzoyl group; cleavage; caspase; vira
ne aminopeptidase type 2; MetAP-2; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFSF 4
                                                                                                                                                                                                                                                                                                                                    Cai SX,
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                                                                                                                                                                                                          109; 174pp;
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                                                                                                                                                                                                                                                                                                                                     Drewe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fluorescent label; fluorophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                     JA,
                                                                                                                                                                                                            English.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                    Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    substrate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 20;
9.3e+05;
thes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      viral protease;
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or antiviral
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Modulators identified may also be used to prolong the life of cells being cultured for recombinant protein production, or to monitor the treatment of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are potential anti- anglogenic or anticancer agents. Sequences AAY80782-Y80910 represent peptides, some of which are specifically claimed, which may be used in assay methods according to the invention.
                                                                    method is used for the propagation (preferably, seedless propagation) of a plant from a plant starting material in an in vitro culture method. Nucleic acids encoding receptor-like kinases are useful in the method. The present sequence is a fragment of a receptor-like kinase protein.
                                                                                                                     The present invention relates to a culture method for propagating a plant from a plant starting material, where root or shoot initiation is stimulated by introducing a gene into the starting material which allows the reduction or absence of phytochrome addition to the culture. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vegetative propagation; RKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A thaliana receptor kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                       recombinant phytochrome
                                                                                                                                                                                                                 In vitro culture propagation of a plant from plant starting material, comprises stimulating root/shoot initiation by introducing a recombinant gene product into the starting material, thus reducing
                                                                                                                                                                                                                                                                                                                                                                                                             EP1094113-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
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                                                                                                                                                                                 Disclosure;
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                                                                                                                                        Peptide;
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        CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell; inflammation; cardiovascular disease; central nervous system disease;
                                                                         Staphylococcus aureus CHIPS-related peptide #491
                                                                                                                                                                                                                                                                                                                                                                                               cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to peptides (ABR44811-ABR47162 and ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5ax) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include
                                                                                                           10-JUN-2003
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                                                                                                                                                                    ABR45301 standard; Peptide;
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Van Strijp JAG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cerebroprotective; neuroprotective; nootropic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                            100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gosselaar-de Haas CJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                       σ
                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                            Score 20; DF Pred. No. 9.3); Mismatches
                                                                                                                                                                                                                                                                                                            DB 24;
. 9.3e+05;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kruijtzer JAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monocyte; endothelial cell;
                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease;
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIPS)
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RESULT 9
ABR4502
ID ABR4
XX ABR4
XX ABR4
XX ABR4
XX CHII
KW CHII
KW Forn
KW Infl
KW 101
KW J01
KW J01
KW Gyn
XX Star
OS Star
OS Star
OS Star
OS Synn
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                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to peptides (ABR44811-ABR47162 and ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein is from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, is genitourinary diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    joint disease; respiratory disease; HIV infection; antiinflammatory; cardiant; cerebroprotective; neuroprotective; nootropic; dermatologigynecological; immunosuppressive; anti-HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Combination of peptides derived from chemotaxis inhibiting protein from Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus
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                                                                                     CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; formylated peptide receptor; FPR; neutrophil; monocyte; endothelial inflammation; cardiovascular disease; central nervous system disease; gestrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory; cardiant; cerebroprotective; neuroprotective; nootropic; dermatologic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 12; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (JARI-) JARI PHARM BV
                                                                         gynecological;
                                                                                                                                                                                              Staphylococcus aureus CHIPS-related peptide #495.
                                                                                                                                                                                                                              10-JUN-2003
                                                                                                                                                                                                                                                            ABR45305
                                                                                                                                                                                                                                                                                       ABR45305 standard;
                                              Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kessel CPM,
Strijp JAG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2003-247783/25
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                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ξ
                                                                                                                                                                                                                              (first entry)
                                              aureus
                                                                         1mmunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gosselaar-de Haas CJC,
                                                                                                                                                                                                                                                                                       Peptide;
                                                                                                                                                                                                                                                                                          σ
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NO;
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 24;
9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kruijtzer JAW
                                                                                                                                                   monocyte; endothelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dermatological;
                                                                                             dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                        disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    joint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHIPS)
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RESULT 10
ABR45637
ID ABR45637
XX ABR45637
AC ABR45
XX Stapt
XX CHIRE
KW CHIRE
KW Infili
KW Joini
KW Joini
KW Joini
KW Gyne
XX Stap
OS Synt
XX WO20
XX WO20
XX 11-J
XX 11-J
XX 11-J
XX 11-J
XX ABR45637
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Best Local S
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Combination of peptides derived from chemotaxis inhibiting protein Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Van
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kidney diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-247783/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (JARI-) JARI PHARM BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUL-2001;
                                                                                                                                                                                                               formylated peptide receptor; FPR; neutrophil; monocyte; endothelial o inflammation; cardiovascular disease; central nervous system disease; gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                             Synthetic
                                                                                                                                                         Staphylococcus
                                                                                                                                                                                     gynecological;
                                                                                                                                                                                                                                                                           CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
                                                                                                                                                                                                                                                                                                      Staphylococcus aureus CHIPS-related peptide #827.
                                                                                                                                                                                                                                                                                                                                 10-JUN-2003
                                                                                                                                                                                                                                                                                                                                                             ABR45637
                                                                                                                                                                                                                                                                                                                                                                                          ABR45637 standard; Peptide; 6
                               11-JUL-2001;
                                                            11-JUL-2001;
                                                                                        23-JAN-2003
                                                                                                                  WO2003006048-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kessel CPM,
Strijp JAG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFSF 4
                                                                                                                                                                                                      cerebroprotective; neuroprotective; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                  (first entry)
                               2001WO-EP08004
                                                            2001WO-EP08004
                                                                                                                                                             aureus.
                                                                                                                                                                                     immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gosselaar-de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20; DB 24;
Pred. No. 9.3e+05;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          joint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from
                                                                                                                                                                                                                                                                cell;
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(JARI-) JARI PHARM BV

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RESULT 11
ABR45641
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Matches
Combination of peptides derived from chemotaxis inhibiting protein Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
                                                                                                                               11-JUL-2001;
                                                                                                                                                                                                                                                                                         CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; formylated peptide receptor; FPR; neutrophil; monocyte; endoth inflammation; cardiovascular disease; central nervous system d gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases,
                                                                                                                                                        11-JUL-2001;
                                                                                                                                                                                 23-JAN-2003
                                                                                                                                                                                                        WO2003006048-A1
                                                                                                                                                                                                                                            Staphylococcus
                                                                                                       (JARI-) JARI PHARM
                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                     gynecological;
                                                                                                                                                                                                                                                                                  cardiant;
                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus CHIPS-related peptide #831.
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                                                                                                                                                                                                                                                                                                                                                                                                                         ABR45641;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR45641 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to peptides (ABR44811-ABR47162 and ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protei from Staphylococcus aureus. The peptide fragments are useful in prophylaxis or treatment of diseases or disorders involving the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 13; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Combination of peptides derived from chemotaxis inhibiting protein from Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Van
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                                                                  Kessel
Strijp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                          2003-247783/25
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Strijp JAG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFSF
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                                                                  JAG;
                                                                                                                                                                                                                                                                                 cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  respiratory diseases and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                              2001WO-EP08004
                                                                                                                                                       2001WO-EP08004
                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                            aureus
                                                                                                                                                                                                                                                                    immunosuppressive;
                                                                             Gosselaar-de
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                                                                                                      ВV
                                                                                                                                                                                                                                                                                                                                                                                            entry)
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                                                                                                                                                                                                                                                                              neuroprotective;
                                                                             Haas
                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haas
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                                                                                                                                                                                                                                                                    anti-HIV
                                                                             cuc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cuc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 24;
. 9.3e+05;
ches 0;
                                                                            Kruijtzer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kruijtzer
                                                                                                                                                                                                                                                                              nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6;
                                                                                                                                                                                                                                                                                           antiinflammatory;
                                                                                                                                                                                                                                                                                                                            endothelial cell;
                                                                                                                                                                                                                                                                             dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIPS)
              from
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The present invention relat ABR47164-ABR47385) derived from Staphylococcus aureus.

invention relates to peptides (ABR44811-ABR47162 and R47385) derived from the Chemotaxis Inhibitory Protein lococcus aureus. The peptide fragments are useful in

(CHIPS)

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RESULT 12
ABR46029
ID ABR46
XX ABR46
XX ABR46
XX ABR46
XX CHIP
XX CHIP
KW Form
KW Infl
KW Garr
KW Garr
KW Gyn
XX Syn
XX Syn
XX 11
XX
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Best Local
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                                                                                                    Disclosure;
                                                                                                                                                                         Staphylococcus prophylaxis and
                                                                                                                                                                                                                            Combination of
                                                                                                                                                                                                                                                                                                                                                                                                   (JARI-) JARI PHARM BV
                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-2001; 2001WO-EP08004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-2001; 2001WO-EP08004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003006048-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gynecological; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastrointestinal disease; skin disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus CHIPS-related peptide #1219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to peptides (ABR44811-ABR47162 and ABR47164) derived from the Chemotaxis Inhibitory Protein (CHIPS from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       joint disease; respiratory disease; HIV infection; antiin rardiant; cerebroprotective; neuroprotective; nootropic;
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Strijp JAG;
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                                                                                                                                                                 peptides derived from chemotaxis inhibiting protein from aureus (CHIPS) having CHIPS activity, useful in d treatment of inflammation, cardiovascular, skin and
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rotective.
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                            The present invention relates to peptides (ABR44811-ABR47162 and ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial celis or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, joint gastrointestinal diseases, skin diseases, genitourinary diseases, joint
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                                                                                                                                                                                                                                            Combination of peptides derived from chemotaxis inhibiting protein Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and kidney diseases .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         formylated peptide receptor; FPR; neutrophil; monocyte; endothelial inflammation; cardiovascular disease; central nervous system disease gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory;
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gynecological; immunosuppressive; anti-HIV.
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Strijp JAG;
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                   respiratory diseases and HIV infection
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                       The present invention relates to peptides (ABR44811-ABR47162 and ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein is from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, diseases, respiratory diseases and HIV infection.
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                                                                                                                                                                                                                                                                                                                       Van Kessel CPM,
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Van Strijp JAG;
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Search completed: August 20, 2003, 12:33:43 Job time: 9.79518 secs

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Listing first 45 summaries
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/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
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/cgn2_6/ptodata/1/1aa/Packfiles1.pep:*
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US-09-521-650-33
US-09-168-888-33
US-09-168-88-33
US-09-168-88-33
US-09-168-825-369A-1
US-08-630-915A-187
US-08-630-915A-202
US-08-630-915A-202
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US-09-230-225B-13
US-09-230-225B-13
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Sequence 4832, Appr		Sequence 4962,	Sequence 262, A	Sequence 1246, 2	Sequence 5775, 1	Sequence 294, Ap	Sequence 6168, Ap	Sequence 7435, I	Sequence 5188, I	Sequence 29, App	Sequence 367, Ap	Sequence 671, Ap	Sequence 25, App	Sequence 25, App	Sequence 25, App	Sequence 25, App

ALIGNMENTS

GENERAL INFORMATION: Patent No. 6248904

Application US/09357952

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APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
APPLICANT: Yang, Wu
TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for W
TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Prot
TITLE OF INVENTION: Other Enzymes and the Use Thereof
FILE REFERENCE: 1735.0030001
CURRENT APPLICATION NUMBER: US/09/357,952
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: US 60/093,642
EARLIER APPLICATION NUMBER: US 60/093,642
EARLIER FILING DATE: 21-UTL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Patentin Ver. 2.0
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Best Local S
Matches 4
                                                                                                                                                                                       Sequence 131, Application US/09521650 Patent No. 6335429 GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Keana, John A.
APPLICANT: Drewe, John A.
APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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FILE REFERENCE: 1735.0290002 CURRENT APPLICATION NUMBER: US/09/521,650 CURRENT FILING DATE: 2000-03-08

OF INVENTION: Use Thereof

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RESULT 4
US-09-357-952-122
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EARLIER APPLICATION NUMBER: 09/168,888

EARLIER FILING DATE: 1998-10-09

EARLIER FILING DATE: 1997-10-10

EARLIER FILING DATE: 1997-10-10

EARLIER FILING DATE: 1998-03-03

NUMBER OF SEQ ID NOS: 142
                                                                                                                                       Matches
                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                               SEQ ID NO 131
                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735.029002
CURRENT APPLICATION NUMBER: US/09/168,888
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 60/061,582
EARLIER APPLICATION NUMBER: US 99/033,661
EARLIER APPLICATION NUMBER: US 99/033,661
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
SOFTWARE: Datentru Var 2 0
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                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Keana, John F.W. APPLICANT: Drewe, John A. APPLICANT: Zhang, Han-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cai, Sui Xiong
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                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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thes 0;
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2.5e+05;
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CURRENT APPLICATION NUMBER: US/09/521,650
CURRENT FILING DATE: 2000-03-08
EARLIER APPLICATION NUMBER: 09/168,868
EARLIER FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 60/061,582
EARLIER FILING DATE: 1997-10-10
EARLIER FILING DATE: 1998-03-03
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
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APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
APPLICANTION: O. 6248904el Fluorescence Dyes and Their Applications for Who
TITLE OF INVENTION: Cher Enzymes and the Use Thereof
FILE REFERENCE: 1735.003001
CURRENT FILING NUMBER: US/09/357,952
CURRENT APPLICATION NUMBER: US/09/357,952
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: US 60/093,642
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOCTWARE: Patentin Ver. 2.0
SEQ ID NO 122
LENGTH: 6
                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 122
LENGTH: 6
Query Match
Best Local Similarity
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Best Local :
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APPLICANT: Drewe, John A.
APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 122, Application US/09357952 Patent No. 6248904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and TITLE OF INVENTION: Use Thereof FILE REFERENCE: 1735.0290002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Weber, Eckard APPLICANT: Cai, Sui Xiong
                                                                                                    OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                         TYPE: PRT
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                                                                                                    Peptide
                                                                                                                         Description of Artificial Sequence: Synthetic
  100.0%;
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  Score 20; DB 4;
Pred. No. 2.5e+05;
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Pred. No.
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                       Length 6;
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Conservative

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Mismatches

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Gaps

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APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Drewe, John A.
APPLICANT: Chang, Han-Zhong
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: USe Thereof
FILE REFERENCE: 1735.029002
CURRENT APPLICATION NUMBER: US6/09/168,888
CURRENT FILING DATE: 1998-10-99
EARLIER APPLICATION NUMBER: US 60/061,582
EARLIER APPLICATION NUMBER: US 09/033,661
EARLIER APPLICATION DATE: 1998-03-03
INUMBER OF SEQ ID NOS: 142
COCTUBER OF SEQ ID NOS: 142
COCTUBER OF SEQ ID NOS: 142
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US-09-168-888-122
; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-357-952-33
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                                                                                                                                                                                APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
APPLICANT: Yang, Wu
TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications f
TITLE OF INVENTION: Other Enzymes and the Use Thereof
TITLE OF INVENTION: Other Enzymes and the Use Thereof
TILE REFERENCE: 1735.0030001
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: US/09/357,952
CURRENT FILING DATE: 1999-07-21
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEO ID NOS: 139
NUMBER OF SEO ID NOS: 139
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                     FEATURE:
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llarity 100.0%;
Conservative
                     Description of Artificial Sequence:Synthetic Peptide
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Pred. No. 2
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Best Local Similarity
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Patent No. 6342611
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APPLICANT: Cal, Sul Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Keana, John F.W.
APPLICANT: Lrewe, John A.
APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735.0290002
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                                                                                APPLICANT: Weber, Eckard
APPLICANT: Ca1, Sui Xiong
APPLICANT: Ca1, Sui Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Drewe, John A.
APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735.0290002
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SOFTWARE: PatentIn Ver. 2.0
CURRENT APPLICATION NUMBER: US/09/168,888 CURRENT FILING DATE: 1998-10-09 EARLIER APPLICATION NUMBER: US 60/061,582 EARLIER FILING DATE: 1997-10-10
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Pred.
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Pred. No. 2.5e+05;
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US-09-053-941-19
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SEQ ID NO 19
LENGTH: 10
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Best Local 9
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                                           CURRENT APPLICATION NUMBER: US/09/817,413
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/043,380
PRIOR FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 25
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                                                                                                                        APPLICANT: SRINIVISAN, ALGARSAMY
APPLICANT: KOPROWSKI, HILARY
TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS
FILE REFERENCE: Chimeric Viral Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/09053941 Patent No. 6271354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Human immunodeficiency virus type 1 PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: 60/043,380 EARLIER FILING DATE: 1999-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/CURRENT FILING DATE: 1998-04-02
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TYPE: PRT
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OTHER INFORMATION: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: Peptide
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Pred. No.
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                                                  Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                              TELEFAX: (516) 822-358 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAGES: 299-
DATE: 1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL: Meth. VOLUME: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human immunodeficiency virus type 1
                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pepi
                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: O'Dea, Sean W.
REGISTRATION NUMBER: 376
                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 822-3550
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Moore TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/8 FILING DATE: March 28, 1997 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM con
OPERATING SYSTEM:
SOFTWARE: WordPel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 350 Je
CITY: Jericho
                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
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                         1 SFSF 4
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                                                                                                                                                                                                                                                                                                                                         US/08/825,369A
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                                                                   Score 20;
Pred. No.
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Pred. No.
                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                             1.44 Mb storage
                                                                                DB 3;
                                                                              Length 12;
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RESULT 13
US-08-630-915A-187
; Sequence 187, Application
; Patent No. 6309820
; Patent No. 6309820

GENERAL INFORMATION: APPLICANT: SPARKS,

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 13 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                       tent No.
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TITLE OF INVENTION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                     NUMBER OF SEQUENCES:
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STATE: New York
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                                   COUNTRY: USA
ZIP: 10036-2711
                                                               CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                  STREET:
                                                                                                  ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
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X: (212) 869-8864/9741
66141 PENNIE
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                        Application US/08630915A
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                                                                                                                                                                                 MCCONNELL, Stephen J.

VENTION: POLYPEPTIDES HAVING A FUNCTIONAL

VENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
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                                                                                                                                                                                                                                    KAY, Brian K.
FOWLKES, Dana M.
                                                                                                                                                                                                                                                                     HOFFMAN, No. 6309820h
                                                                                                                                                                                                                                                                                     SPARKS, Andrew B
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N: 536
Floppy disk
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: 227
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227
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Pred. No.
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US-08-825-369A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08825369A
Patent NO. 6084060
GENERAL INFORMATION:
APPLICANT: MOORE
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Best Local Similarity
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                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                           REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: O'Dea, Sean W.
REGISTRATION NUMBER: 37690
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                      SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES
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OTHER INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                      APPLICATION NUMBER: US/08/6 FILING DATE: March 28, 1997 CLASSIFICATION: 514
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OPERATING SYSTEM:
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ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                  350 Jericho Turnpike
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                                                (516)
                                                                                                                                                                                                                                                                                                                   USA
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                                              822-3582
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/630,915A
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                                                                                                                                                                                                                                                                                                                                                                                 & Baron, LLP
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                                                                                              381-21 CIP
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Page 6

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Search completed: August 20, 2003, 12:44:20 Job time : 4.77108 secs
                                                                      Дb
                                                                                          VQ
                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-825-369A-2
                                                                                                                          Query Match 100.0%; Score 20; DB 3; Length 14; Best Local Similarity 100.0%; Pred. No. 55; Matches 4; Conservative 0; Mismatches 0; Indels
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5 SFSF 8
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Title:
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Maximum Match 100%
Listing first 45 summaries
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No.
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Maximum DB
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                 Score
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seq length: 2000000000
        protein search, using sw
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1: /ggn2_6/ptodata/1/pubpaa/Pi
2: /cgn2_6/ptodata/1/pubpaa/Pi
3: /cgn2_6/ptodata/1/pubpaa/Pi
4: /cgn2_6/ptodata/1/pubpaa/Pi
6: /cgn2_6/ptodata/1/pubpaa/Pi
6: /cgn2_6/ptodata/1/pubpaa/Pi
7: /cgn2_6/ptodata/1/pubpaa/Pi
7: /cgn2_6/ptodata/1/pubpaa/Pi
9: /cgn2_6/ptodata/1/pubpaa/Pi
10: /cgn2_6/ptodata/1/pubpaa/Pi
11: /cgn2_6/ptodata/1/pubpaa/Pi
13: /cgn2_6/ptodata/1/pubpaa/Pi
14: /cgn2_6/ptodata/1/pubpaa/Pi
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11: /cgn2_6/ptodata/1/pubpaa/Pi
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121.698 Million cell updates/sec
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Gapop 10.0 ,
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: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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/cgn2_6/ptcdata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptcdata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptcdata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptcdata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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US-09-934-251A-2
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US-09-947-387-131
US-09-947-387-122
US-09-947-387-33
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Sequence 30, Appl
Sequence 131, App
Sequence 33, Appl
Sequence 23, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 202, Appl
Sequence 202, Appl
Sequence 46, Appl
Sequence 413, Appl
Sequence 413, Appl
Sequence 413, Appl
Sequence 3, Appli
Sequence 158, Appli
Sequence 158, Appli
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Sequence 306, App	9	100.0	
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Sequence 42675, A	9	100.0	
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Sequence 431, App	15	100.0	5 20
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•	15	100.0	
Sequence 850, App	49 10 US-09-764-847-850	100.0	
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Sequence 450, App	12	100.0	20
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Sequence 894, App	15	100.0	
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25,	1 15 US-10-059-585	100.0	
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e 670,	6 15 US-10-091	100.0	
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619	5 11 US-09-809-3	100.0	
Sequence 882, App	1 15 US-10-	0 100.0 3	
153,	0 9 US-09-739-907-1	100.0	
624	5 11 US-09-983-	100.0	
Sequence 142, App	4 15 US-10-144-	100.0	.7 20
Sequence 44483, A	4 9 US-09-864-761-44483	0 100.0 2	•

ALIGNMENTS

US-09-300-425B-30

Sequence 30, Application US/09300425B Publication No. US20030045681A1

GENERAL INFORMATION:

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SEQ ID NO 30
LENGTH: 4
TYPE: PRT
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Best Local S
Matches 4
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APPLICANT: TARLI, Lorenzo
APPLICANT: VIII, Francesca
APPLICANT: BIRCHLER, Mantired
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
TITLE OF INVENTION: ANGIOGENESIS
FILE REFERENCE: SCH-1733P1
CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28
CURRENT FILING DATE: 1999-04-28
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/0
PRIOR FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B OTHER INFORMATION: antibody clone
                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                            FEATURE:
                                         1 SFSF 4
                                                                                                            Similarity
                                                                                       Conservative
                                                                                     100.0%; Score 20; DB 11;
100.0%; Pred. No. 4.4e+05;
Live 0; Mismatches 0;
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                                                                                                               SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 122
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Best Local
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                                                                                                                                                            NUMBER OF SEQ ID NOS: 142
                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/145,746
PRIOR FILING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: US 09/168,888
PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/947,387
CURRENT FILING DATE: 2001-09-07
                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Screening Assays TITLE OF INVENTION: Use Thereof FILE REFERENCE: 1735.0290005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/947,387
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/061,582
PRIOR FILING DATE: 1997-10-10
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Keana, John F.W.
APPLICANT: Drewe, John A.
APPLICANT: Drewe, John A.
APPLICANT: Zhang, Han-Zhong
TITILE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecul
TITILE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITILE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITILE OF INVENTION: Use Thereof
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TITLE OF INVENTION: Use The
FILE REFERENCE: 1735.0290005
                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/061,582 PRIOR FILING DATE: 1997-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/145,746
PRIOR FILING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: US 09/168,888
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 142
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                                                                                               ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LICANT: Zhang, Han-Zhong
LE OF INVENTION: No. US20020150885Alel Fluorogenic or Fluorescent Reporter Molecu-
LE OF INVENTION: Their Applications for Whole-Cell Fluorescence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
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o. US20020150885A1
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. 4.4e+05;
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US-09-205-658-293
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                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     Sequence 293, Application US/09205658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. SEQ ID NO 33
                                                                                                                                                                                                                                                                                   Patent No. US20010029617A1
                                                             EARLIER APPLICATION NUMBER: 08/
EARLIER FILING DATE: 1997-05-15
                                                                                                                                                                       TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE
                                                                                                                                                                                                               APPLICANT: Ruvkun, Gary APPLICANT: Ogg, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/061,582
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/145,746
PRIOR FILING DATE: 1998-03-03
                                                                                                                                                     FILE REFERENCE: 00786/351004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/168,888 PRIOR FILING DATE: 1998-10-09
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CURRENT FILING DATE: 2001-09-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: No. US20020150885Alel Fluorogenic or Fluorescent Reporter
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 1735.0290005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence:Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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nes 4; Conserv
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                    APPLICATION NUMBER: 08/888,534 FILING DATE: 1997-07-07
                                                                                                       APPLICATION NUMBER: US/09/205,658 FILING DATE: 1998-12-03
APPLICATION NUMBER: US98/10080
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SFSF 4
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Pred. No.
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TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-205-658-293
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                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-09-879-957-187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 328
'SOFTWARE: FastSEQ for Windows Version SEQ ID NO 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09934251A patent No. US20020132017A1 GENERAL INFORMATION:
APPLICANT: Moore, Jeffrey G.
                                                                                                                                                                                                                                                                                            Sequence 187, Application US/09879957
Patent No. US20020034755A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Composition and Method for Preserving Progenitor Cells FILE REFERENCE: 108236.136
CURRENT EDUCATION NUMBER: US/09/934,251A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/368,607
PRIOR PILING DATE: 1999-08-05
PRIOR PILING DATE: 1999-08-05
PRIOR FILING DATE: 1996-12-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                             TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                       NUMBER OF SEQUENCES: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 SFSF 11
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                                                                   CITY: New York
STATE: New York
                                  ZIP: 10036-2711
                                                        COUNTRY:
                                                                                                                                                                                                                                               KAY, Brian K.
FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                 HOFFMAN, No. US20020034755A1h
                                                                                                                                                                                                                                MCCONNELL,
                                                        USA
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                                                                                                                                                                             USING SAME
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Pred. No. 1.2e+02;
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Pred. No. 1.3e+02;
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APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                              COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 187:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
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PRIOR APPLICATION DATA:
                   APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                              APPLICATION NUMBER: US/09/879,957
ETLING DATE: 13-Jun-2001
CLASSIFICATION: cUNKnown>
PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
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                                                                                                                                                                                                                                                                                                                                                  STATE: New York
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REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 9; ilarity 100.0%; Pred. No. 1.4e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPARKS, Andrew B.
HOFFMAN, NO. US20020034755Alh
KAY, Brian K.
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FOWLKES, Dana M.
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1155 Avenue of the Americas
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US-09-775-052-46

: Sequence 46, Application US/09775052

: Publication No. US20030054000A1
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                                                                                                                        GENERAL INFORMATION:
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Best Local Similarity
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PATENT NO. US20020132017A1
GENERAL INFORMATION:
APPLICANT: Moore, Jeffrey G.
TITLE OF INVENTION: Composition and Method for Preserving Progenitor Cells
FILE REFERENCE: 108236.136
CURRENT APPLICATION NUMBER: US/09/934,251A
CURRENT FILING DATE: 2001-08-21
                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2
LENGTH: 14
TYPE: PRI
ORGANISM: Artificial Sequence
CURRENT APPLICATION NUMBER: US/09/775,052
CURRENT FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 09/208,966
PRIOR FILING DATE: 1998-12-10
                                                                APPLICANT: Dowdy, Steven F.
TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS
FILE REFERENCE: 48881/1742
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Best Local :
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PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: US 08/762,537
PRIOR FILING DATE: 1996-12-09
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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Pred. No.
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                                                                                                                                                                                                                                                                                                                  1.5e+02;
thes 0;
                                                                                                                                                                                                                                                                                                                                                       DB 10;
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                                                                                   OF USE THEREOF
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Query Match
Best Local Similarity
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            PRIOR APPLICATION NUMBER: 09/892,877
PRIOR FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: 09/437,658
PRIOR APPLICATION NUMBER: PCT/US99/09847
PRIOR APPLICATION NUMBER: PCT/US99/09847
PRIOR APPLICATION NUMBER: 60/085,093
PRIOR APPLICATION NUMBER: 60/085,093
PRIOR APPLICATION NUMBER: 60/085,093
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
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US-09-892-877-413
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                                                                                                                                                                                                                                                                                                              Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       Sequence 413,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 413
LENGTH: 15
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Publication No. US20030077809A1
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Best Local Similarity
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                                                                                                                                                                        CURRENT FILING DATE: 2001-09-10 PRIOR APPLICATION NUMBER: 60/231,846 PRIOR FILING DATE: 2000-09-11
                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/948,783
CURRENT FILING DATE: 2001-09-10
                                                                                                                                                                                                                                                 APPLICANT: Ruben et. al.
TITLE OF INVENTION: 97 Human secreted proteins
FILE REFERENCE: PZ028P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 461
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ORGANISM: human
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APPLICATION NUMBER: 60/085,094
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FILING DATE: 1998-05-

NUMBER: 60/085,105

FILING DATE: 1998-05-1 APPLICATION NUMBER: 60 FILING DATE: 1998-05-1

APPLICATION NUMBER:

60/085,906 60/085,927 60/085,180

APPLICATION NUMBER:

1998-05-12

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; TYPE: PRT ; ORGANISM: Homo sapiens US-09-948-783-413
RESULT 14
US-09-983-802-158
; Sequence 158, Application US/09983802
; Publication No. US20030022185A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
                                                                                                                                                                                                                                     SOFTWARE: Patentin version 3.1; SEO ID NO 3; LENGTH: 22; TYPE: PRT ORGANISM: Coffee erabica US-10-260-212-3
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US-10-260-212-3
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publication No. US20030131380A1
GENERAL INFORMATION:
APPLICANT: SOCIETE DES PRODUITS NESTLE S.A.
TITLE OF INVENTION: Coffee Mannanase
FILE REFERENCE: 88265-6783
CURRENT APPLICATION NUMBER: US/10/260,212
CURRENT FILING DATE: 2002-08-27
CURRENT FILING DATE: 2002-08-27
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Best Local Similarity
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SEQ ID NO 413
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NUMBER OF SEQ ID NOS: 25
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; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 345
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-065-345
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PRIOR APPLICATION NUMBER: PCT/US98/27059
PRIOR FILING DATE: 1998-12-17
PRIOR PPLICATION NUMBER: PCT/US98/27059
PRIOR APPLICATION NUMBER: 60/070, 923
PRIOR FILING DATE: 1997-12-18
PRIOR PPLICATION NUMBER: 60/068,007
PRIOR PPLICATION NUMBER: 60/068,007
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,006
PRIOR APPLICATION NUMBER: 60/068,369
PRIOR PILING DATE: 1997-12-18
PRIOR PPLICATION NUMBER: 60/068,369
PRIOR PILING DATE: 1997-12-19
PRIOR PILING DATE: 1997-12-19
PRIOR PILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068,367
PRIOR PILING DATE: 1997-12-19
PRIOR PILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068,668
PRIOR APPLICATION NUMBER: 60/068,668
PRIOR APPLICATION NUMBER: 60/068,668
PRIOR APPLICATION NUMBER: 60/068,053
PRIOR PILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,054
PRIOR PILING DATE: 1997-12-18
PRIOR PILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,064
PRIOR PILING DATE: 1997-12-18
PRIOR PILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,064
PRIOR PILING DATE: 1997-12-18
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, NAME/KEY: SITE
; LOCATION: (23)
; OTHER INFORMATION: Xaa equals stop translation
US-09-983-802-158
                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                   Matches · 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Publication No. US20030055236A1
GENERAL INFORMATION:
APPLICANT: MOORE, Paul A. et al.
TITLE OF INVENTION: 110 Human Secreted Proteins
FILE REFERENCE: PZ021P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 20; DB 11; Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 4; Conservative 0; Mismatches 0;
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SEQ ID NO 158
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/068,365 PRIOR FILING DATE: 1997-12-19
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TYPE: PRT
ORGANISM: Homo sapiens
11, SFSF 14
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17 SFSF 20
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                                                                                                             100.0%; Score 20; DB 15;
100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0;
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Search completed: August 20, 2003, 13:16:46 Job time: 5.33735 secs

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Title:
Perfect score:
Sequence:
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length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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100.0
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/cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:
/cgn2_6/ptodata/1/paa/US06_COMB.pep:*
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Listing first 45 summaries
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/ cgn2_6/ptodata/1/paa/US101_COMB.pep: *
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                                                         Length DB
  US-09-075-338C-30
US-09-300-425B-30
                                                                                                                       SUMMARIES
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equence 6524,	equence 6523,	e 323	equence 318,	equence 29	guence 293,	e 12693,	equence 6526,	equence 6522,	equence 4572, A	equence 12693,	equence 6526, A	equence 6522	equence 4572, A	equence 46, App	equence 46, App	equence 13945,	equence 12694,	e 4422, A	equence 13	equence 12694,	equence 4422, A	equence 6525, A	equence 6521, A	equence 6525,	equence 6521, A	equence 5651, A	equence 33, App	e 33, App	Sequence 33, App	e 33, App	equence 33, Ap	equence 122	122,	Sequence 122,	_	equence 122, 1	e 131	equence 131,	ce 131	quence 131,	equence 131	30,	

ALIGNMENTS

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RESULT 1
US-09-075-338C-30
US-09-075-338C-30
; Sequence 30, Application US/09075338C
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WERL, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: TARLI, Lorenzo
APPLICANT: BIRCHLER, Manifred
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY
FILE REFERENCE: SCH-1733
; CURRENT APPLICATION NUMBER: US/09/075,338C
; CURRENT FILING DATE: 1998-05-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
LENGTH: 4
TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B
; OTHER INFORMATION: antibody clone
US-09-075-338C-30

Query Match
Best Local Simikarity 100.0%; Pred. No. 5.2e+06;
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US-09-512-082-30
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NUMBER OF SEQ ID NOS:
SOFTWARE: PATENTIN VE
SEQ ID NO 30
LENGTH: 4
TYPE: PRT
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; OTHER INFORMATION: antibody clone
US-09-300-425B-30
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     Query Match
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Best Local Similarity
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                                                                                                                                                                                                                          CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 09/300,425
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
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CURRENT APPLICATION NUMBER: US/09/512,082
CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF TITLE OF INVENTION: ANGIGGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TARLI, Lorenzo
APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfred
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CURRENT FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
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APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfred
                                                        OTHER INFORMATION:
                                                                                               ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF TITLE OF INVENTION: ANGIOGENESIS FILE REFERENCE: SCH-1733P1
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                        Description of Artificial Sequence: anti-ED-B antibody clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 20;
100.0%; Pred. No.
tive 0; Mismatc!
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; FEATURE:
; OTHER INFORMATION:
; OTHER INFORMATION:
PCT-US99-16423-131
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Best Local Similarity
Yatches 4; Conserve
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; Sequence 131, Application PC/TUS9821231
                                                                                                                                           SEQ ID NO 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                         APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
APPLICANT: Yang, Wu
TITLE OF INVENTION: Novel Fluorescence Dyes and Their Applications for Whole-Cell
TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protea
TITLE OF INVENTION: Other Enzymes and the Use Thereof
FILE REFERENCE: 1735.003PC01
CURRENT APPLICATION NUMBER: PCT/US99/16423
CURRENT FILING DATE: 1999-07-21
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EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cytovia, Inc.
APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
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                                                               LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                               SOFTWARE: PatentIn Ver.
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TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the TITLE OF INVENTION: Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: US 60/061,582
EARLIER FILING DATE: 1997-10-10
EARLIER APPLICATION NUMBER: US 09/033,661
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
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CURRENT FILING DATE: 1998-10-09
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ORGANISM: Artificial Sequence
FEATURE:
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Conservative (
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                   Description of Artificial Sequence:Synthetic Peptide
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Pred. No. 5.
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100.0%;

Score

20;

DB 1;

Length

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APPLICANT: Keana, John F.W.

APPLICANT: Drewe, John A.

APPLICANT: Drewe, John A.

APPLICANT: Drewe, John A.

APPLICANT: Drang, Han-Zhong

TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and

TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence

TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the

TITLE OF INVENTION: Use Thereof

FILE REFERENCE: 1735.029005

CURRENT APPLICATION NUMBER: US/09/947,387

CURRENT FILING DATE: 2001-09-07

PRIOR APPLICATION NUMBER: US 60/061,582

PRIOR APPLICATION NUMBER: US 60/145,746

PRIOR FILING DATE: 1998-03-03

PRIOR FILING DATE: 1998-03-03

PRIOR FILING DATE: 1998-03-03

PRIOR FILING DATE: 1998-01-09

NUMBER OF COTT NOSC. 143-
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Best Local Similarity
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                                                            NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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CURRENT FILING DATE: 2000-05-30
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APPLICANT: Zhang, ma..
Trant: Cai, Sui Xiong
Trawe, John A.
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PRIOR FILING DATE: 21-JUL-1999
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 5
TYPE: PRT
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APPLICANT: Yang, Wu
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ORGANISM: Artificial Sequence
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Pred. No. 5.2e+06;
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; OTHER INFORMATION: Description of Artificial Sequence:Synthetic; OTHER INFORMATION: Peptide US-09-947-387-131
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; OTHER INFORMATION:
US-10-138-375-131
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Best Local
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                                                        SOFTWARE: PatentIn Ver. SEQ ID NO 122
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CURRENT FILING DATE: 2002-05-06

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952

PRIOR TILING DATE: EARLIER FILING DATE: 1999-07-21

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642

PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998

NUMBER OF SEQ ID NOS: 139
                                                                                             APPLICANT: Cytovia, Inc.
TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735.029pC02
CURRENT APPLICATION NUMBER: PCT/US98/21231
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 60/061,582
EARLIER APPLICATION NUMBER: US 09/033,661
EARLIER APPLICATION NUMBER: US 09/033,661
EARLIER FILING DATE: 1997-10-10
EARLIER TILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Novel Fluorescence Dyes and Their Applications for Whole-Cell TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Prote TITLE OF INVENTION: Other Enzymes and the Use Thereof FILE REFERENCE: 1735.0030001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 5
TYPE: PRT
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ORGANISM: Artificial Sequence
                   TYPE: PRT
                                       ENGTH:
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Drewe, John A.
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Pred. No.
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US-09-583-225-122
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; OTHER INFORMATION:
PCT-US98-21231-122
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                                                    SEQ ID NO 122
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Best Local
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                                                                                         TITLE OF INVENTION: Novel Fluorescence Dyes and Their Applications for Whole-Cell TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Prote TITLE OF INVENTION: Other Enzymes and the Use Thereof FILE REFERENCE: 1735.003001

CURRENT APPLICATION NUMBER: US/09/583,225

CURRENT FILING DATE: 2000-05-30

PRIOR APPLICATION NUMBER: 09/357,952

PRIOR PELICATION NUMBER: 09/357,952

PRIOR FILING DATE: 21-JUL-1999

NUMBER OF SEQ ID NOS: 139
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CURRENT APPLICATION NUMBER: PCT/US99/16423
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: US 60/093,642
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
                                                                             SOFTWARE: PatentIn Ver.
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APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
                                                                                                                                                                                                                                                                            APPLICANT:
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ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
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; OTHER INFORMATION:
US-09-583-225-122
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CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/061,582
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/145,746
PRIOR FILING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: US 09/168,888
PRIOR APPLICATION NUMBER: US 09/168,888
PRIOR FILING DATE: 1998-10-09
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Best Local :
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SEQ ID NO 122
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CURRENT APPLICATION NUMBER: US/10/138,375
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
                                                                                                                                                                                      APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
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APPLICANT: Drewe, John A.
APPLICANT: Drewe, John A.
APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
TITLE REFERENCE: 1735.0290005
                                                                                                       TITLE OF INVENTION: Novel Fluorescence Dyes and Their Applications for Whole TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, TITLE OF INVENTION: Other Enzymes and the Use Thereof FILE REFERENCE: 1735.0030001
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TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the TITLE OF INVENTION: Use Thereof FILE REFERENCE: 1735.029FC02 CURRENT APPLICATION NUMBER: PCT/US98/21231 CURRENT FILING DATE: 1998-10-09 EARLIER APPLICATION NUMBER: US 60/061,582 EARLIER APPLICATION NUMBER: US 60/061,582 EARLIER APPLICATION NUMBER: US 09/033,661 EARLIER APPLICATION NUMBER: US 09/033,661 EARLIER FILING DATE: 1998-03-03 NUMBER OF SEQ ID NO 33 LENGTH: 7
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PCT-US99-16423-33
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Best Local Similarity 100.0%;
Matches 4; Conservative (
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GENERAL INFORMATION:
APPLICANT: Cytovia, Inc.
                                                                                                                                                                                                                                                     Sequence 33, Application PC/TUS9916423 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 139
SOFTWARE: Patentin Ver. 2.0
JEO ID NO 122
                                                      APPLICANT: Cytovia, Inc.
APPLICANT: Chang, Han-Thong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.

APPLICANT: Yang, Wu
TITLE OF INVENTION: Novel Fluorescence Dyes and Their Applications for Whole-Cell
TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protes
TITLE OF INVENTION: Other Enzymes and the Use Thereof
FILE REFERENCE: 1735,003PC01
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE: OTHER INFORMATION: Description of Artificial Sequence:Synthetic OTHER INFORMATION: Peptide
EARLIER APPLICATION NUMBER: US 60/093,642
               CURRENT APPLICATION NUMBER: PCT/US99/16423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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Search completed: August 20, 2003, 13:13:40 Job time : 41.9398 secs
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; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
PCT-US99-16423-33
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NUMBER OF SEQ ID NOS: 139
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
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ORGANISM: Artificial Sequence
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26647, A
262497, A
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Appl
Sequence 88, Application US/10389674
GENERAL INFORMATION:
APPLICANT: HENNICHS, VOLKER
APPLICANT: CHEN, TEDDY
APPLICANT: CHEN, TEDDY
ITTLE OF INVENTION: IFN-ALPHA HOMOLOGUES
FILE REFERENCE: 02-101510/0140,002
CURRENT APPLICATION NUMBER: US/10/389,674
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: US/09/685,189
PRIOR FILING DATE: 2000-10-06
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US-10-389-674-88
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ALIGNMENTS	US-10-603-113-24061	US-10-603-113-25632	US-10-603-113-24293	US-10-603-113-21184	US-10-631-441-1780	US-10-631-402-1780	US-10-603-113-26215	US-10-603-113-24912	US-10-617-320-4732	US-10-603-113-27444	US-10-603-113-21888	US-10-612-783-5219	US-10-603-113-25759	US-10-603-113-23802	US-10-617-320-4664	US-10-273-573-8204	US-10-603-113-25419	US-10-603-113-22184	US-10-291-265-902
	Sequence 24061, A		Sequence 24293, A	Sequence 21184, A		Sequence 1780, Ap	~	_		-	Sequence 21888, A		-	•		Sequence 8204, Ap	-	Sequence 22184, A	Sequence 902, App

RESULT 1 US-09-963-693A-293 US-09-963-693A-293 SEQUENCE 293, Application US/09963693A GENERAL INFORMATION: APPLICANT: Ogg, Scott APPLICANT: Ogg, Scott TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS FILE REFERENCE: 00786/351004 CURRENT APPLICATION NUMBER: US/09/963,693A CURRENT FILING DATE: 2001-09-25 CURRENT FILING DATE: 2001-09-25 PRIOR APPLICATION NUMBER: 09/205,658 PRIOR FILING DATE: 1998-12-03 PRIOR FILING DATE: 1997-05-15 PRIOR FILING DATE: 1997-05-15 PRIOR APPLICATION NUMBER: 08/888,534 PRIOR FILING DATE: 1997-07-07 PRIOR APPLICATION NUMBER: US98/10080 PRIOR APPLICATION NUMBER: US98/10080 PRIOR FILING DATE: 1998-05-15 NUMBER OF SEO ID NOS: 328 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 293 LENGTH: 11 TYPE: PRT ORGANISM: Caenorhabditis elegans US-09-963-693A-293

y Match 100.0%; Score 20; DB Local Similarity 100.0%; Pred. No. 24; hes 4; Conservative 0; Mismatches

DB 5; Length 11;

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                                                                                                                                                                                                                                                                              Sequence 3325, Application US/10631402 GENERAL INFORMATION:
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APPLICANT: JACKSON, MARY
APPLICANT: GICOTE'
TITLE CT
                                         PRIOR APPLICATION NUMBER: US 08/905,223
PRIOR TILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,135
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,051
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LENGTH: 52
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                                                                                                                            PRIOR APPLICATION NUMBER: US/09/547,599C PRIOR FILING DATE: 2000-04-11
                                                                                                                                                              TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins FILE REFERENCE: GEN-1119C1
CURRENT APPLICATION NUMBER: US/10/631,402
CURRENT FILING DATE: 2003-07-30
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NUMBER OF SEQ ID NOS: 34
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TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM TUBERCULOSIS
FILE REFERENCE: 05394.0009-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/IB97/00923 PRIOR FILING DATE: 1997-07-25
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EQ ID NO 88
LENGTH: 26
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TYPE: PRT
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PRIOR FILING DATE: 1999-10-07
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ORGANISM: Artificial Sequence
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APPLICATION NUMBER: US 08/905,144 FILING DATE: 1997-08-01
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Lacroix, Bruno
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CURRENT FILING DATE: 2003-07-30
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                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins FILE REFERENCE: GEN-T119C1
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EQ ID NO 3325
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                                                                                                 APPLICATION NUMBER: US 08/905,144
FILING DATE: 1997-08-01
APPLICATION NUMBER: US 08/905,279
FILING DATE: 1997-08-01
APPLICATION NUMBER: US 08/904,468
             APPLICATION NUMBER: US 08/905,133 FILING DATE: 1997-08-01
                                                FILING DATE: 1997-08-01
APPLICATION NUMBER: US 08/905,134
FILING DATE: 1997-08-01
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APPLICATION NUMBER: US 08/905,051
FILING DATE: 1997-08-01
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Pred. No. 1.1e+02;
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SOFTWARE: Patent.pm SEQ ID NO 3325 LENGTH: 52

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OTHER INFORMATION: Xaa - Leu, Trp
US-10-631-441-3325
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PRIOR APPLICATION NUMBER: US 08/905,135
PRIOR APPLICATION NUMBER: US 08/905,135
PRIOR APPLICATION NUMBER: US 08/905,051
PRIOR APPLICATION NUMBER: US 08/905,051
PRIOR APPLICATION NUMBER: US 08/905,144
PRIOR APPLICATION NUMBER: US 08/905,144
PRIOR APPLICATION NUMBER: US 08/905,279
PRIOR APPLICATION NUMBER: US 08/905,279
PRIOR APPLICATION NUMBER: US 08/904,468
PRIOR APPLICATION NUMBER: US 08/905,134
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Sequence 3330, Application US/10631402
                                                                                         SOFTWARE: Patent.pm
SEQ ID NO 3330
LENGTH: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/631,402
CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: US/09/547,599C
PRIOR FILING DATE: 2000-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dumas Milne Edwards, Jean Baptiste APPLICANT: Duclert, Aymeric APPLICANT: Lacroix, Bruno TITLE OF INVENTION: Expressed Sequence Tags and FILE REFERENCE: GEN-T119C1
                                                                                                                                                      PRIOR APPLICATION NUMBER: US 08/905,133 PRIOR FILING DATE: 1997-08-01 NUMBER OF SEQ ID NOS: 3475
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OTHER INFORMATION:
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OTHER INFORMATION: Substantia nigra
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                             TYPE: PRT
ORGANISM: Homo Sapiens
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FEATURE:
OTHER INFORMATION: Cerebellum
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; OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: SCORE 7.60
; OTHER INFORMATION: SEG CLATLTLEHTSFS/FQ
US-10-631-402-3330
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Best Local S
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SOFTWARE: Patent.pm
SEQ ID NO 3330
LENGTH: 58
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Best Local Similarity
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PRIOR FILING DATE: 1997-08-01
PRIOR PRIOR PRIOR NUMBER: US 08/905,135
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,051
PRIOR PILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,144
PRIOR APPLICATION NUMBER: US 08/905,144
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CURRENT APPLICATION NUMBER: US/10/631,441
CURRENT FILING DATE: 2003-07-30
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PRIOR APPLICATION NUMBER: US 08/905,134
PRIOR FILING DATE: 1997-08-01
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PRIOR APPLICATION NUMBER: US 08/905,279
PRIOR FILING DATE: 1997-08-01
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OTHER INFORMATION: Cerebellum
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Similarity 100.0%;
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score 7.60
seq CLATLTLFHTSFS/FQ
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Pred. No. 1.2e+02;
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RESULT 8 US-10-603-113-24077 ; Sequence 24077, Application US/10603113 ; GENERAL INFORMATION:

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US-10-603-113-24772
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US-10-603-113~23238
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                                                                                                                   CURRENT APPLICATION NUMBER: US/10/603,113
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
SEQ ID NO 24772
EXECUTE: 61
                                                                                                                                                                                                                                                                                                                                  Sequence 24772, Appl GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
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                                                                 TYPE: PRT ORGANISM: Candida albicans FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
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CURRENT FILING DATE: 2003-06-24
OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
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PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
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CURRENT FILING DATE: 2003-06-24
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                         NAME/KEY: UNSURE LOCATION: (7)
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                                                                                                     SEQ ID NO 150
LENGTH: 62
TYPE: PRT
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LENGTH: 61
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Best Local
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APPLICANT: Keith Weinstock et al
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/291,128
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: PCT/US01/10484
PRIOR FILING DATE: 2001-03-30
                                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/PRIOR FILING DATE: 2000-08-23
                                                                                                                                                        SOFTWARE: Custom
                                                                                                                                                                         NUMBER OF SEQ ID
                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/808,701
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/668,680 PRIOR FILING DATE: 2000-09-22
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CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBI
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
                                                                                                                                                                                                                                                            PRIOR FILING DATE:
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                                                                                     ORGANISM: Homo sapiens
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100.0%; Score 20; DB 6; ilarity 100.0%; Pred. No. 1.3e+02; Conservative 0; Mismatches 0;
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SOFTWARE: Custom
SEQ ID NO 151
LENGTH: 62
TYPE: PRT
ORGANISM: Homo sapiens
US-10-291-128-151
                                                                                                                                                                                                                                                                                                                                                               US-10-603-113-21539, Application US/10603113; Sequence 21539, Application US/10603113; GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS; FILE REFERENCE: 107196.132
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Best Local S
Matches 4
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CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
SEQ ID NO 21539
LENGTH: 62
TYPE: PRT
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APPLICANT: Nuvelo,
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Best Local
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PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/695,618
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 09/728,711
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PRIOR APPLICATION NUMBER: PCT/US01/10484
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
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  58 SFSF 61
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                                                                              100.0%; Score 20; DB 6; ilarity 100.0%; Pred. No. 1.3e+02; Conservative 0; Mismatches 0;
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Search completed: August 20, 2003, 12:45:13 Job time: 1.15663 secs
                                                                                                                                                                                                                           ; ORGANISM: Candida albicans
US-10-603-113-23627
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US-10-603-113-23627
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBI
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
                                                                                                                                                                                                                                                                                SEQ ID NO 23627
LENGTH: 62
                                                                                                                                                                    Query Match
Best Local :
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PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
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                                                                                                                                                                                                                                                                TYPE: PRT
                                                                          13 SFSF 16
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                                                                                                                                                Similarity 100.
4; Conservative
                                                                                                                                                                    100.0%;
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Pred. No. 1.3e+02;
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                                                                                                                                                                                     Length 62
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
August 20, 2003, 12:25:56; Search time 2.79518 Seconds
(without alignments)
137.621 Million cell updates/sec

Title: US-09-512-082-30 Perfect score: 20 Sequence: 1 SFSF 4

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

228 228 238 248 258 268 268 268 268 268 268 268 268 268 26	ω ω ν μ	Result
222222222222222222222222222222222222222	200	Score
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C75415	T29674	AE3247	AH1609	AD1247	T06963	B96574	JQ1822	C42525	D85803	G90954	T17809	C47188	S26991	T42000	D82182
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ALIGNMENTS

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Db 5 SFSF 8 RESULT 3 A03367 lectin - Macrotyloma axillare (fragment)	Query Match 100.0%; Score 20; DB 2; Length 24; Best Local Similarity 100.0%; Pred. No. 78; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1 SFSF 4 Qy 1 SFSF 4	llaume, J.L.; Hoebeke, J. cta 1033, 210-213, 1990 oup A specific lectin from the seeds of (\$08292; MUID:90167102; PMID:2306467 otein GUP is designated as Crotalaria striata	RESULT 2 \$08292 S08292 lectin - smooth rattlebox (fragment) C; Species: Crotalaria pallida (smooth rattlebox) C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993 C; Accession: \$08292	Qy 1 SFSF 4 Db 5 SFSF 8	Query Match 100.0%; Score 20; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 32; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 1 \$33905 lectin GNL2 alpha chain - kidney bean (fragment) C;Species: Phaseolus vulgaris (kidney bean) C;Species: Phaseolus vulgaris (kidney bean) C;Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997 C;Accession: \$38305 C;Accession: \$38305 R;Kamemura, K.; Furuichi, Y.; Umekawa, H.; Takahashi, T. Bjochim. Biophys. Acta 1158, 181-188, 1993 A;Title: Purification and characterization of novel lectins from Great Northern A;Reference number: \$38304; MUID:94002183; PMID:8399319 A;Accession: \$38304; MUID:94002183; PMID:8399319 A;Accession: \$38304; MUID:94002183; PMID:8399319 A;Accession: \$38304; MUID:94002183; PMID:8399319 A;Rocession: \$38305

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C; Genetics: A; Gene: BH3
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1993
C;Accession: A03367
R;Haylett, T.; Swart, L.S.
S. Afr. J. Chem. 35, 33-36, 1982
A;Reference number: A03367
A;McCession: A03367
A;McCession: A03367
A;McCeule type: protein
A;Residues: 1-32 <HAY>
C;Comment: This lectin from legume seeds is a tetramer of noncovalently bound identical e carbohydrates galactose, glucosamine, mannose, and fucose. It agglutinates erythrocyte C;Comment: This fragment is related to the amino end of the lentil lectin beta chain. C;Comment: Dolichos axillaris (Macrotyloma axillare) is an African legume, also now grow C;Superfamily: plant lectin
                                                                                                            A;Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BAB06788.1; A;Experimental source: strain C-125
                                                                                                                                                    A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-42 <STO>
                                                                                                                                                                                                      A;Reference number: A83650; MUID:20512582; PMID:11058132 A;Accession: E84033
                                                                                                                                                                                                                                                                                                                   hypothetical protein BH3069 [imported] C:Species: Bacillus halodurans C:Date: 01-Dec-2000 #sequence_revision
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E84033
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C; Superf
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R; Takami, H.; Nakas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoconj. J. 7, 311-322, 1990
A; Title: Structural requirements for the binding A; Reference number: A48431; MUID: 92361170; PMID: 2
                                                                                                                                                                                                                                                                 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, Nucleic Acids Res. 28, 4317-4331, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
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A48431
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       100.0%;
llarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                      Score 20;
Pred. No.
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Pred. No.
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Pred. No.
     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                     01-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inding of oligosaccharides to PMID:2136348
                     1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3e+02;
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                                      Length 42;
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                                                                                                                                                                                                                                          Bacillus halodurans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-Sep-1998
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                                                                                                          RESULT 8
G97539
                            hypothetical protein AGR_C_2731 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-C;Accession: G97539
R;Goodner, B.;
A.; Liu, F.; V
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                                                                                                                            A; Genome: ch
C; Keywords:
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                                                                                                                                                                                                                                                                                                                hypothetical protein 50 - Chlorella vulgaris chloroplast
C;Species: chloroplast Chlorella vulgaris
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07306
                                                                                                                                                           C; Genetics:
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A; Residues: 1-50 <WAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Heddelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein VCA0733 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae (c;Cace: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: H82423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
H82423
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A;Experimental source: serogroup
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A; Residues: 1-50 <HEI>
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llarity 100.0%;
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                                                          Score 20; DE Pred. No. 1.7); Mismatches
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Pred. No. 1.7
); Mismatches
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                                                            1.7e+02;
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1.7e+02;
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El Tor
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H.; Dragoi,
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Hinkle,

G.;

; Gattung, Allinger,

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30-Sep-2001 #text_change 18-Nov-2002 Miller, N.; Blanchard, M.; Qurollo, Doughty, D.; Scott, C.; Lappas, C.;

(strain C58,

B.; Goldı Markelz,

Goldm

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early protein gp6 - phage PZA
C:Species: phage PZA
A:Note: host Bacillus subtilis
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 23-Jul-1999
C:Accession: B29004
R:Paces, V.; Vlcek, C.; Urbanek, P.; Hostomsky, Z.
Gene 44, 115-120, 1986
A:Title: Nucleotide sequence of the right early region of Bacillus subtilis phage PZA cc A:Reference number: A91551; MUID:87031575; PMID:3095189
A:Accession: B29004
A:Molecule type: DNA
A:Residues: 1-54 <PAC>
A:Cross-references: GB:M11813; GB:M13904; GB:M13905; NID:g216046; PIDN:AAA88495.1; PID:g
C:Genetics:
A:Gene: 16.6
C:Superfamily: phage PZA early protein gp6
C:Keywords: early protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein NMB0517 [imported] - Neisseria meningitidis (strain MC58 serogroup C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: G81188
C:Accession: G81188
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fileischmann, R.D.; Dougherty, B.A.; Cience 287, 1809-1815, 2000
A:A; Olin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V.
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Ccossion: G81188
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-51 <TET>
A;Cross-references: GB:AE002408; GB:AE002098; NID:g7225740; PIDN:AAF40949.1; PID:g72257
A;Cross-references: GB:AE002408; GB:AE002098; NID:g7225740; PIDN:AAF40949.1; PID:g72257
A;Coss-references: GB:AE002408; GB:AE002098; NID:g7225740; PIDN:AAF40949.1; PID:g72257
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A;Title: Genome Sequence of the Pi.
A;Reference number: A97359; MUID:2
A;Accession: G97539
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <KUR>
A;Cross-references: GB:AE007869; Pi
C;Genetics:
A;Gene: AGR_C_2731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:AE002098; NID:g7225740; PIDN:AAF40949.1; PID:g722574
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1.7e+02;
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A;Title: Nucleotide sequence of the right earl A;Reference number: J80192; MUID:89232766; PMI A;Accession: J50196
A;Molecule type: DNA
A;Residues: 1-54 <BEN>
A;Cross-references: GB:M28830; NID:g215438; PI C;Genetics:
A;Gene; 16.6
C;Superfamily: phage PZA early protein gp6
C;Keywords: early protein
hypothetical immunity region protein 11 C; Species: Bacillus phage phi-105 A; Note; host Bacillus subtilis C; Date: 20-Aug-1999 #sequence_revision C; Accession: A27234 R; Cully, D. F.; Garro, A. J. Gene 38, 153-164, 1985
                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                  R;Garvey, K.J.; Yoshikawa, H.; Ito, J. Gene 40, 301-309, 1985
A;Title: The complete sequence of the Bacillus phage phi-29
A;Reference number: JN0030; MUID:86165872; PMID:3007295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             early protein gp6 - phage phi-29
N,Alternate names: ORF 16.6 protein
C;Species: phage phi-29
A;Note: host Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Benes, V.; Arnold, L.; Smrt, J.; Paces, V. Gene 75, 341-347, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: phage phi-15
A;Note: host Bacillus subtilis
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990
C;Accession: JS0196
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A; Residues: 1-54 <GAR>
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                                                                                                                                                                                                            A; Map
                                                                                                                                                                                                                                                                                                                                                A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84839
                                                                                                                                                                                                                                                                                                                                                                                                                     R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhken, S.E.; Umayam, L.; Tallon, Leuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein At2g41230 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: D84839
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Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlq
A;Reference number: Z15985; MUID:97303241; PMID:9159184
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C;Species: chloroplast Chlorella vulgaris
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
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A;Residues: 1-60 <WAK>
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A;Accession: T07328
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YIGC4_YEAST
Y465_AQUAE
CU05_HOMAM
YJ57_YEAST
POL_HY1C4
GTRA_BPSF2
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             EMBL; AF137379; AAD54818.1; HAMAP; MF_00522; -; 1.
                                           entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A.
-!- FUNCTION: May help in the subunits (By similarity).
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28-FEB-2003
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   InterPro;
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                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
Chlorodendrales; Chlorodendraceae; Nephroselmis.
NCBI_TaxID=31312;
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S. Afr. J. Chem. 35:33-36(1982).
-i- FUNCTION: METALLOGIYCOPROTEIN, CONTAINING CA, MG, J. THE CARBOHYDRATES GALACTOSE, GLUCOSAMINE, MANNOSE, AGGLUTINATES ERYTHROCYTES OF BLOOD GROUP Al.
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InterPro; IPR001220; Lectin_legB.
Pfam; PF00139; lectin_legB; 1.
PROSITE; PS00307; LECTIN_LEGUME_BETA; IPROSITE; PS00308; LECTIN_LEGUME_ALPHA;
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HSSP; P05045; 1LU1.
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RESULT 5
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Viruses; dsDNA viruses, phi-29-like viruses. NCBI_TaxID=10755;
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                                          Bacteriophage phi-15
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SEQUENCE FROM N.A.
MEDLINE=86165872; PubMed=3007295;
Garvey K.J., Yoshikawa H., Ito J.;
Garvey K.J., Sequence of the Bacillus
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Viruses; dsDNA viruses,
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Benes V., Arnold L.
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Viruses; dsDNA viruses,
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RESULT 8
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Viruses; dsDNA viruses, n Lambda-like viruses. NCBL_TaxID-10717;
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P41505;
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01-NOV-1995
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 Albani D., Robert L.S., Donaldson P.A., Altosaar Fabijanski S.F., "Characterization of a pollen-specific gene famil mapus which is activated during early microspore plant Mol. Biol. 15:805-622(1990).

-I- TISSUE SPECIFICITY: Pollen-specific.
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L.S., Donaldson
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                                                                                Hypothetical protein. sequence 89 AA; 9909
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Viruses; dsDNA viruses, no RNA stag
Orthopóxvírus.
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16-OCT-2001 (Rel. 40, Last annotation
Hypothetical 9.9 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the Swiss Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family.
63 AA;
                                                Conservative
                                                                                                                                                                                                                              Johnson G.P.,
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                              4
            13
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                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                   G.P.,
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tute of Bioinformatics and the EMBL outset
ics Institute. There are no restrictions
titutions as long as its content is in
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                                                                                                                                                                                                                            Perkus M.E.,
                                                                                                                                                                                                                                                                                 Perkus M.E.,
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                                                                                399EA9270DF3E75A CRC64;
                                             Score 20; DB 1;
Pred. No. 1.4e+02;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                         update)
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                                                                                                                                                                                                                           Davis S.W., Winslow J
                                                                                                                                                                                                                                                                                 Davis S.W.,
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                                                              Length 89;
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                                                                                                                                                                                                          virus'.";
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RESULT 11
POL_HV1J3
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YCXF_CYAPA
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Best Local S
Matches 4
                                                                                                                                                                                        POL_HV1J3
P12498;
01-OCT-1989
01-OCT-1996
28-FEB-2003
 MEDLINE=89352108; Pu
Komiyama N., Hattori
                                     SEQUENCE FROM
                                                                  Human immunodeficiency Viruses; Retroid viruse Viruses; Retroid viruse VICBI_TaxID=11694;
                                                                                                                                                        Reverse transcriptase
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PIR; ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-UTEX LB 555 / Pringsheim;
Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella
Farley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C.,
Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
"The complete sequence of the cyanelle genome of Cyanophora
the genetic complexity of a primitive plastid.";
(In) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,
Schwemmler W. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YCXF_CYAPA
P48336;
01-FEB-1996
01-FEB-1996
16-OCT-2001
                                                                                                                                                                        POL polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Cyanelle. SEQUENCE 91 AA; 11166 MW; 6
                                                                                                                                        (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotism and Symbiosis, pp.40-48,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bryant D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=UTEX LB 555 / Pringsheim;
Stirewalt V.L., Michalowski C.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel.
Hypothetical 11.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Glaucocystophyceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyanelle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequence of the cyanelle DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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T06963; T06963.
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J3 (Rel. 41, Lau
J3 (Rontains: F
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(Rel. 34, Last seq
(Rel. 41, Last ann
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                                                                                       viruses;
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PubMed=2669897;
ori N., Inoue J.
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40,
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                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                     virus type 1 (JH3 isolate) (HIV-1)
es; Retroviridae; Lentivirus.
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Last annotation updat
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Michalowski C.B., Annarella
nung S., Newmann-Spallart C.,
Sakuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Loeffelhardt W., Bohnert H.J.,
                                                                                                                                                        (Retropepsin); Ribonuclease
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Kurimura
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 91;
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Ξ.
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3.1.26.4)]
Yoshida M.;
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RESULT 12
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Best Local
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Y067_METJA
Q60371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997
01-NOV-1997
16-OCT-2001
           STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MIDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Button G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Strain G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kalne B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00141; ASP_PROTEASE; 1.
PROSITE; PS50175; ASP_PROT_RETROV; 1.
AIDS; Polyprotein; Hydrolase; Aspartyl protease; Endonuclease;
Nuclease; Transferase; RNA-directed DNA polymerase.
CHAIN
57 > 100 PROTEASE.
CHAIN
57 > 100 PROTEASE.
B1 B1 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Met
Methanocaldococcaceae; Methanocaldococcus
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InterPro; IPR001969; Aspprotease_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV; M21137; POL$JH3.
MEROPS; A02.001; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical MJ0067.
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                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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DETERMINED.
SIMILARITY: THE PROTEASE BELONGS
KNOWN AS THE RETROPEPSIN FAMILY.
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CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N + (DNA)(N).
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
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RESULT 13
Y123_METJA
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01-NOV-1997
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.E., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR;
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-I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein;
TRANSMEM 6 21
TRANSMEM 34 5.
TRANSMEM 79 9.
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Q57587;
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                         TIGR;
                                                   EMBL; U67469; PIR; C64315;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Archaea; Euryarchaeota; א
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2190;
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                            MJ0123;
                                                                                U67469; AAB98111.1;
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4; Conserv
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ilarity 100.0%;
Conservative 0
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Pred. No. 1.6
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13187 MW;

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RESULT 14
YGCA_Y
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RP SEQUEN
RA HEDLIN
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Y465_AQUAE
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16-OCT-2001
16-OCT-2001
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Y465_AQUAE
MEDLINE=98196666; PubMed=9537320; Deckert G., Warren P.V., Gaasterl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
SEQUENCE
                                                          STRAIN-VF5
                                                                                                                          Bacteria; Aquificae;
NCBI_TaxID=63363;
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                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                         Hypothetical
                                                                                                                                                                             Aquifex aeolicus
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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical 12.2 kDa protein in PGD1-STT3 int
YGL024W.
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TRANSMEM 22 4;
TRANSMEM 48 68
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
[1]
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S64026; S64026.
S0002992; YGL024W.
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(Rel. 40, Last sequence.update)
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protein AQ_465.
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68 P
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the EMBL/GenBank/DDBJ databases.
       Gaasterland
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Pred. No. 1.7e+02;
Mismatches 0;
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Pred. No. 1.7e+02;
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       Young W.G.,
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                                                                                                                                                                       EMBL; AE000691; AAC06729.1; -. PIR; C70342; C70342.
                                                                                                                                                                                                                                                                                                                                                               Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                        Hypothetical protein;
TRANSMEM 7 29
                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                Nature 392:353-358(1998).
73 SFSF
                               1 SFSF 4
                                                              Similarity
4; Conserv
                                                                                                                           113 AA;
                                                              Conservative
 76
                                                                                                                         29 F
13252 MW;
                                                                           100.0%;
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                                                              0;
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Pred. No.
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                                                                         1.8e+02;
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Search completed: August 20, 2003, 12:34:56 Job time: 4.62918 secs

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Maximum Match 100%
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Q9S8B2
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Q49491 mycoplasma
Q9k8d7 bacillus ha
Q8ezr7 leptospira
Q8sm41 spatoglossu
O60031 aspergillus
Q8kb18 chlorobium
Q9fb83 helicobacte
Q9fk10 vibrio chol
                                                                                                                                                                                                            Q9s8j5 psophocarpu
Q9s8b2 phaseolus v
Q96g12 homo sapien
Q45547 bacillus su
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Q9s8x8 erythrina v
Q91fb5 chilo iride
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ALIGNMENTS

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Query Match
Best Local S
Matches 4
Q9S8B2
Q9S8B2;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2002
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Q9S8J5; O1-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                                                                                        Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheor
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                          tetragonolobus (L.) DC.";
Plant Cell Physiol. 35:1087-1095(1994).
SEQUENCE 20 AA; 2363 MW; 1BF1B347020D3DCE CRC64;
                                                                                                                                                                                                                                                                                                    MEDLINE-95120285; PubMed-7820375;
Yagi F., Sawada R., Imada T., Toyonaga S., ?
"Two isolectins from leaves of winged bean,
                                                                                                                                                                                                                                                                                                                                                                               Psophocarpus .
NCBI_TaxID=3891;
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(TrembLrel. 21, Last ann
                                                            PRELIMINARY;
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Last sequence update)
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Pred. No.
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                                                                                                                                                                                                                                                                                                       Psophocarpus
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RESULT Q45547
ID 45547
AC Q4
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Best Local S
Matches 4
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Q45547;
01-NOV-1996
STRAIN-W23;
Harry E.J., Partridge S.R.,
"divIB region of Bacillus li
Submitted (NOV-1993) to the
EMBL; L25649; AAA72410.1; -.
                                                                                                                                                                                                      Bacillus subtilis.
Bacteria; Firmicutes;
NCBI_TaxID=1423;
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01-DEC-2001
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-2001) to the EMBL; BC010062; AAH10062.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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Phaseolus vulgaris (Kidney bean) (French bean).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
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Homo sapiens (Human).
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2399 MW; B09E883F93CCD833 CRC64;
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2476 MW;
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                                                                  "Structural requirements for the binding of oligosaccharides to immobilized lectin of Erythrina variegata (Linn) var. orientalis ISSP, P16404; 1AX2.
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Delius H., Daral G.;
"Molecular cloning and physiridescent virus type 6: fi
the viral genome.";
Virology 160:66-74(1987).
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"Identification and characterization of the repetitive
the genome of insect iridescent virus type 6.";
Virology 167:485-496(1988).
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MEDLINE=86174607; PubMed=3959991;

Lorbacher de Ruiz H., Gelderblom H., Hofmann

"Insect iridescent virus type 6 induced toxion mice.";
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Delius H., Darai G., Fluegel R.M.;

"DNA analysis of insect iridescent virus

permutation and terminal redundancy.";
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SEQUENCE FROM N.A.

MEDILINE-94167241; PubMed-8121799;
Schnitzler P., Hug M., Handermann
Dellus H., Darai C.;

"Identification of genes encoding
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                                                                                                                       Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.; "Identification of the gene encoding the major capsid protein insect iridescent virus type 6 by polymerase chain reaction."; J. Gen. Virol. 74:873-879(1993).
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MEDLINE-94353641; PubMed-8073636;

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Iridovirus: Coding Strategy of the Genome of
Virology 286:182-196(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98141693;
Bahr. U., Tidona C
                                               Jakob N.J., Mueller K., Bahr
Submitted (SEP-2000) to the I
EMBL; AF303741; AAK82269.1; '
SEQUENCE 41 AA; 4991 MW;
                                                                                                                                                                                                    virus Genes 18:243-264(1999).
                                                                                                                                                                                                                                 Muller K., Tidona C.A., Darai G., "Identification of a gene cluster within the irridescent virus encoding enzymes involved in
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Q8EZR7;
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01-MAR-2003
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STRAIN-C-125 / JCM 9153;
MEDLINE-0512582; PubMed-11058132;
MEDLINE-0512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G.
Fuji F., Hirama C., Nakamura Y., Ogasawara
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01-OCT-2000
01-OCT-2000
01-MAR-2002
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Nucleic Acids Res. 19:6027
                                                                                                                                                                                                                                                                                                               *Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtili; Nucleic Acids Res. 28:4317-4331(2000).
EMBL; AP001517; BAB06788.1:
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Random genomic sequence MG44 (Fragment).
Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae;
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Nucleic Acids Res. 19:602
EMBL; X61539; CAA43751.1;
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01-AUG-1998 (TREMBLIREL 07, 01-AUG-1998 (TREMBLIREL 07, 01-DEC-2001 (TREMBLIREL 19, Hypothetical 5.7 kDa protein Aspergillus niger.
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01-JUN-2002 (TIEMBLIEL 2
01-MAR-2003 (TIEMBLIEL 2
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STRAIN=56601 / Serogroup
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39 MW; B3374E64EBE8AlD6 CRC64;
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21, Last sequence update)
23, Last annotation update)
23 carboxylase small subunit (Fragment).
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X MEDLINE-22103685; PubMed-12093901;

A Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

A Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,

A Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

A Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,

A Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,

A Nierman W.C., Feldblyum T.V., Hansen C.L., Ketchum K.A.,

Venter J.C., Tettelin H., White O., Gruber T.M., Ketchum K.A.,

The complete genome sequence of Chlorobium tepidum TLS, a

photosynthetic, anaerobic, green-sulfur bacterium.";

photosynthetic, anaerobic, green-sulfur bacterium.";

PTOC. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).

RR EMBL; AE011948; AAM73198.1; -.
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Q8KB18;
Q1-QCT-2002 (TrEMBLrel. 22, Cr
Q1-QCT-2002 (TrEMBLrel. 22, La
Q1-QCT-2002 (TrEMBLrel. 22, La
Q1-QCT-2002 (TrEMBLrel. 22, La
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MEDLINE-20309321; PubMed-10852481;

Wan den Bink J.M., Punt P.J., Van Gorcom R.F.M.,

Van den Hondel C.A.M.;

Van den Hondel C.A.M.;

Regulation of expression of the Aspergillus niger benzoate |
hydroxylase cytochrome P450 system.";
hydroxylase cytochrome P450 system.";
Mol. Gen. Genet. 263:601-609(2000).

EMBL; AJ005117; CAA06381.1; -.
Hypothetical protein.

Hypothetical protein.

BYDOTHETICAL PROTECTION.

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EB85F2B8CAOB1CDD CRC64;
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
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SEQUENCE 48 AA; 5801 MW; 4A3D5E7EE14A77DD CRC64;
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"A M(r) 34,000 proinflammatory outer membrane pr
Helicobacter pylori.";
Proc. Natl. Acad. Sci. U.S.A. 97:7533-7538(2000)
EMBL; AF233670; AAG00390.1; -.
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"A M(r) 34,000 proinfilammatory outer membrane protein (oipA) of
Helicobacter pylori.";
Proc. Natl. Acad. Sci. U.S.A. 97:7533-7538(2000).
EMBL; AF233660; AAG00380.1; -.
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Bacteria; Proteobacteria; Epsilonproteobact
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Bacteria; Proteobacteria; Epsilonproteobact
Helicobacteraceae; Helicobacter.
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D.H., Graham D.Y.;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

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Human secretory po Staphylococcus epi Human ORFX protein Human digestive sy Human liver associ		Q.	-fungal and -fungal and -fungal and n histatin nR-13 pepti nR-13 pepti n brain exp ide #12385	Human BLyS binding NE-dlg SEQ ID NO:6 Human colon cancer Human INTERCEPT 29 Anti-fungal and an Anti-fungal and an pr-s export signal Streptococcus poly Arabidopsis thalia Group B Streptococ Full length human

ALIGNMENTS

RESULT 1 AAB10067

AAB10067 standard; peptide; 9

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UlA protein; tryptic peptide; functional site; Unidentified. UlA protein derived tryptic peptide #6 03-NOV-2000 AAB10067; WO200031544-A1 WPI; 2000-400193/34. (XERI-) XERION PHARM GMBH. 24-NOV-1998; 23-NOV-1999; 02-JUN-2000 LL, Ng (first entry) 98DE-1054196 99WO-EP09052 detection

Identifying functional sites in proteins, useful for detecting epitopes and ligand binding sites, by complexing with tagged binding partner, then laser irradiation to alter the protein close to the tag

Example

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                                                                                                                                                                                    Identifying functional sites in proteins, useful for detecting epitopes and ligand binding sites, by complexing with tagged binding partner, then laser irradiation to alter the protein close to the tag
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               irradiating the complex (II) radicals that alter bound (I) identifying the altered region
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                                                              It can identify non-linear or discontinuous epitopes, and deprotein function without inactivation of (I) (since the tag
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and ligand binding sites, by complexing with tagged binding partner,
then laser irradiation to alter the protein close to the tag .
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Pred. No.
                             Score 26;
Pred. No.
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Matches 4; Query Match Best Local

Similarity

100.0%;

Score 26; DB Pred. No. 54; D; Mismatches

54; В 21; 0;

Length 13;

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Gaps

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Conservative

0;

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cc infection by an acid-resistant microorganism (A) by treating a faccal comple with at least two different monoclonal antibodies (MAb) (or their fragments or derivatives) or aptamers (collectively (I)) and detecting cc formation of a complex (C) between (I) and the corresponding antigen of CC (A). The first and second (I) bind to epitopes of different antigen of CC (A). These epitopes are present, after passage through the intestines, CC in at least some mammals, and have either: (1) their native structure; CC infected or immunized with (A), or its extract, lysate, derived protein CC infected or with a synthetic peptide. Practically all mammals display or fragment, or with a synthetic peptide. Practically all mammals display at least one of the specified epitopes. The method is used to detect complexive and campylobacter, specifically H. pylori, H. hepaticus, Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, CC witherapeutically. The method is direct and non-invasive, and provides an inexpensive and easily standardizable diagnosis, despite possible degradation of antigens during passage through the intestines. This complementarity determining region CDR3 which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H. pylori 26 kDa protein-binding antibody heavy chain CDR3 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acid-resistant microorganism; detection; faecal; intestine; infection
monoclonal antibody; heavy chain; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel method for the detection of a mammallan
                                                                                                                                                                                                                                                                                                                                                                                                                                                             petecting infection by acid-fast microbes for diagnosis of Helicobacter pylori, comprises reacting a faecal sample with two binding reagents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAB10003
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06-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                          Claim 22; Page 21; 84pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                            antigens that survive intestinal passage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-365747/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reiter C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CONN-) CONNEX GMBH.
 Sequence
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98EP-0120687
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RESULT 6
AABHOO71
ID AABH
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XX AAB
XX U1A
XX U
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AAE02857
ID AAEC
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                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel method for identifying one or more C functional sites in a target protein (I) which comprises: (1) complexing C(I) with a binding partner (A) that carries a laser-activatable tag; (ii) cradiating the complex (II) formed with laser light to generate free CC radicals that alter bound (I) selectively at the binding sites; and (iii) C identifying the altered region by a combination of protein cleavage and CC mass spectrometry (MS). The method is used to identify any type of CC functional site in any type of protein but particularly ligand-binding CC sites and epicopes. It can also be used to investigate pathologically CC altered proteins or oncogenic proteins, and to inactivate target three-dimensional structure of (I), and is simple, rapid and automatable. CC tran identify non-linear or discontinuous epitopes, and determines CC protein function without inactivation of (I) (since the tag is bound to CC (A) not to (I) itself). The method may be used in vitro or in vivo for Studying intra- or extra-cellular proteins. This sequence represents a complete continuous determines of the invention derived tryptic peptide which is used to illustrate the
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Best Local (
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        AAE02857;
                                          AAE02857 standard; peptide;
                                                                                                                                                                                                                                                                                                               Sequence
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Pred. No. 54;
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10-AUG-2001

(first entry)

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RESULT 8
AAE02910
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
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17-DEC-1999;
27-JAN-2000;
03-MAY-2000;
10-NOV-2000;
AAE02910;
                                                AAE02910 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel breast cancer-associated proteins and nucleic acids encoding proteins useful for diagnosing, treating breast cancer and as indicators for monitoring the efficacy of breast cancer therapy -
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2000US-0178860.
2000US-0201721.
2000US-0172170.
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Pred. No. 54;
D; Mismatches
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Tryptic peptide #1

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human U2 small nuclear ribonucleoprotein

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RESULT 9
AAO26562
ID AAO2
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AC AAO2
AC AAO2
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                                                                                                                                                                                                                                                                                                                                          The present invention relates to marker molecules indicative of disease in mammals which are identified using a new method in which an abundant protein is removed from a sample to enable less abundant molecules to be evaluated as possible markers, the sample is then fractionated and if fractions analysed by known mass spectroscopy techniques and results compared between individuals with and without the disease. The method is useful for identifying disease markers in mammals, especially humans, cespecially markers for cancer, such as breast, lung, prostate, bladder, cervical, ovarian, colon or colorectral cancer. Once identified, the markers can be used as targets in assays for detecting the disease and in disease treatment e.g. administration of antibodies binding to and celiminating/reducing activity of the target protein in vivo. The present sequence is a tryptic peptide of human U2 small nuclear ribonucleoprotein B (U2 snRNP B) which is used in the invention. The peptide is obtained from U2 snRNP B by proteolysis with trypsin.

Note: The present sequence is also shown in sequence listing of the specification, but lacks an amino acid in the N-ternimal end and in the
                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 4
                 Threonine synthetase 13.75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spectroscopy based methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identification of disease markers in mammals, especially cancer markers useful as targets in methods for detecting or treating cancer, by removing an abundant protein from a sample and analyzing by mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watkins
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03-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example
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17-DEC-1999;
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                                             06-MAR-2003
                                                                          AA026562;
                                                                                                      AAO26562 standard;
                                                                                                                                                                                                                                                                                                   Sequence
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2000US-0172170.
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Mismatches
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RESULT 10
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Best Local (
                                                                                                                                                                                                                                           BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention also relates to the polynucleotide for coding it, the process for preparing the polypeptide by DNA recombination technique, the application of the polypeptide in treating send as cancer, HIV infection, the antagonist against this polypeptide and its therapeutic action, and the application of said polynucleotide to coding this new threonine synthetase 13.75. This sequence represents an N-terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the threonine synthetase 13.75 protein of the terminal peptide region of the terminal pe
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16-JUN-2000; 17-OCT-2000; 16-MAR-2001;

2000US-212210P. 2000US-240816P. 2001US-276248P.

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RESULT 11
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Human discs large 1 gene family - useful in,
composition(s) for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 repretible antibodies and fragments of the antibodies described in the met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibodies against B Lymphocyte Stimulating the diagnosis and treatment of cancers and :
                                                                                                          (SUME ) SUMITOMO ELECTRIC IND
                                                                                                                                                    23-AUG-1996;
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                                                                                                                                                                                                                                     10-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                               internal secretion tissue
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Best Local
                                             cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletion in a patient's genome that affect the activity of P by expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a NE-dlg molecule. The present invention describes human discs large 1 gene (dlg) family expressible in nerve tissue. Also described are: (1) a polynucleotide (PN) encoding dlg and comprising a 3100 (I) or 3213 bp (II) sequence; (2) RNA corresponding to PN having sequences (I) and (II), (3) RNA having a base sequence translated by dlg; (4) an antisense PN having a t least 15 bp sequence and which is a part of PN of (1); (5) a derivative of the antisense PN; (6) an antibody specific for dlg, and (7) an antibody specific for a polypeptide having a 817 or 849 as sequence. The polypeptide, RNA's and antibodies can be used for detection of dlg. The antisense PN can be used as a therapeutic composition for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                            Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
  inactive proteins or to supplement the patients own production Additionally, N may be used to produce the colon cancer-associa
                                                                                                                                                                                                                                                           AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human
                                                                                                                                                                                                                                                                                                              Claim 11; Page 9724; 9803pp; English.
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03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                               ; acids encoding for preventing,
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r treating colorectal cancers -
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and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TANGO protein; INTERCEPT protein; neurological disorder; central nervous system; focal brain disorder; bipolar affective disorder; global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease; senile dementia; Huntington's disease; amyotrophic lateral sclerosis; Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep;
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N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                 The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see ARF45121-F45136 and ARF45138-F45139 and ARB66031-B66057, ARB66064-B66083 and ARB66085). The TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders, CNS-related disorders, focal brain disorders global-diffuse cerebral disorders and other neurological and cerebrovascular disorders. The CNS disorders include Alzhelmer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome, autonomic function disorders such as hypertension and sleep disorders, autonomic function disorders such as hypertension and sleep disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McCarthy SA,
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                               neuropsychiatric disorders, psychoactive substance use anxiety, and bipolar affective disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurological diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens.
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prevention, diagnosis
AAH37196 to AAH37204
ification of the
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RESULT 14
AAW19473
CC D-amino acid histatin 2, found in human paratiol secretion, where at CC least one amino acid in the peptide is in the D-configuration. The CC peptide is preferably modified by an acetyl or carbamyl addition at the C-terminus and/or amidation at the C-terminus. The novel D-amino CC acid-containing peptide, based on the naturally occurring histidine-CC rich human histatins, have anti-fungal and anti-bacterial activity and CC are useful in compositions for the treatment of oral, vaginal, urethral, CC mucosal, respiratory, skin, ear and ophthalmic fungal or bacterial cC canida albicans infection, against oral bacterial diseases such as CC caries and periodontitis (by inhibiting e.g. Streptococcus mutans and CC porphyromonas gingivalis) and against Clostridium histolyticum. The D-CC amino acid-containing peptide has superior anti-fungal (especially canti-candidal) and anti-bacterial activity, particularly on a weight basis, compared to the natural L-amino acid forms of histatins and CC histatin-based peptides. The presence of D-residues also makes the
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                                                                                                                                                                                                                                                                                                                                                             The present sequence represents an anti-fungal and anti-bacterial
                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                  histatin-based peptide(s) - useful endingerions, periodontitis and caries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-fungal and anti-bacterial D-amino histatin-based peptide(s) - useful esp
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ophthalmic infection;
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treating Candidal
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RESULT 15
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Best Local
The present sequence represents histatin 2, found in human paratoid secretion, where at least one amino acid is in the D-configuration. The peptide preferably is modified by an acetyl or carbamyl addition at the N-terminus and/or amidation at the C-terminus. The peptide, based on the naturally occurring histidine-rich human histatins, have anti-fungal and anti-bacterial activity and are useful in compositions for the treatment of oral, vaginal, urethral, mucosal, respiratory, skin, ear and ophthalmic fungal or bacterial infections. It is particularly effective against local and systemic Candida albicans infection, against oral bacterial diseases such as caries and periodontitis (by inhibiting e.g. Streptococcus mutans and Porphyromonas gingivalls) and against Clostridium histolyticum. The peptide has
                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
01-NOV-1991;
28-OCT-1993;
09-AUG-1994;
                                                                                                                                                                                                     Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for treating Candidal infections, periodontitis and caries.
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptides more resistant to degradation than corresponding L-amino acid versions.
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91US-0786571.
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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3: /cgn2_6/ptodatta/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodatta/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodatta/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/Dackfiles1.pep:*
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US-08-441-914-14
US-08-481-888A-2
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US-08-481-888A-1
US-08-485-273A-1
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US-08-973-553A-1
US-09-103-352-1
US-09-103-352-1
US-09-104-476-439
US-09-104-373-4-001C-4702
US-09-083-352-19
US-09-083-352-19
US-09-083-352-19
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                                          US-09-107-532A-6005
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US-08-287-717-14
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            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative (
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                                                                              TOPOLOGY:
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ALIGNMENTS

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; MOLECULE TYPE: peptide US-08-287-717-14
                                                                                                                                                                                                                                                              CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US/08/145,030

APPLICATION NUMBER: US/07/786,571

FILING DATE: 01-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                        TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: BU TELECOMMUNICATION INFORMATION: 617-861-6240
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                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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CITY: Lexington
STATE: Massachus
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/287,717 FILING DATE:
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Score 26; DB 1;
Pred. No. 2.5e+05;
; Mismatches 0;
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US-08-441-914-14
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                                                                              Sequence 2, Application US/08481888A Patent No. 5631228
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Best Local (
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                                                                GENERAL
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Sequence 14, App...
                    APPLICANT:
APPLICANT:
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      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 28-OCT-1
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/287,717
FILING DATE: 09-AUG-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Oppenner
APPLICANT: Xu, Tao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: David E. Brook
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: BU
                                                                                                                                                                                                                               Local Similarity tes 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07 FILING DATE: 01-NOV-91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
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                                               Oppenheim, Frank G.
Roberts, F. Donald PARTI-BACTERIAL AND ANTI-BACTERIAL
                                    Xu, Tao
                                                                                                                                                                                                                                 Conservative
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RESULT 4
US-08-485-273A-2
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                                                                                                                                                                                                                                                                             Sequence 2, Application US/08485273A Patent No. 5646119
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                           APPLICANT: Oppenheim, Frank G.
APPLICANT: Xu, Tao
APPLICANT: Spacciapoli, Peter
TITLE OF INVENTION: D-Amino Acid i
TITLE OF INVENTION: Anti-Fungal ar
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                GENERAL
COUNTRY: US
ZIF: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                CORRESPONDENCE ADDRESS:
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LENGTH: 27 amino acids
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TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                       STATE:
                                                                                                      CITY:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 09-AUG-1994
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CLASSIFICATION:
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                                                                                                                .E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
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                                                                                                                                                                           D-Amino Acid Histatin-Based Peptides as Anti-Fungal and Anti-Bacterial Agents
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Pred. No. 28;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 07-JUN

07-JUN-1995

US/08/485,273A

ASSIFICATION:

OPERATING SYSTEM: SOFTWARE: Patent

PatentIn

PC-DOS/MS-DOS
n Release #1.0, Version #1.30

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US-08-973-563A-2
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                   ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  tent No.
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                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
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                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     APPLICANT: Friden, Philip M.
TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based
TITLE OF INVENTION: Peptides
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                                                                                                                                                        STREET: Two Mil.
CITY: Lexington
STATE: MA
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                                                                                                                          COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECULE TYPE: peptide
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OR APPLICATION DATA:
PPLICATION NUMBER.
LING DATA:
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                PPLICATION NUMBER:
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                                                                                                                                                                                      E: Hamilton, Brook, Smith & Reynolds, P.C. Two Militla Drive
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07-JUN-1996
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              US/08/973,563A
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US-08-973-559-2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 27 amino acids
                                                FILING DATE: 07-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,888
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
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REFERENCE/DOCKET NUMBER: PER95-01A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SPACCIAPOLI, PETER
APPLICANT: FRIDEN, PHILIP M.
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
TITLE OF INVENTION: Histatin-Based Peptides
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OTHER INFORMATION:
OTHER INFORMATION:
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                             Lexington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROBERTS, F. D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "At least one amino acid must have a D configuration"
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RESULT 8
US-08-287-717-9
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US-08-973-559-2
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Patent No. 6555650
GENERAL INFORMATION:
APPLICANT: Lajoie, Gilles A.
TITLE OF INVENTION: Cyclic Analogs of Histatins
FILE REFERENCE: 36555-0002
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Best Local Similarity
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Best Local
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PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 40
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                                                       COUNTY OF THE PROPERTY OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Oppenheim,
APPLICANT: Xu, Tao
TITLE OF INVENTION: N
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
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                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                            STATE:
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   APPLICATION NUMBER:
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TOPOLOGY: 11
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Xu, Tao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 5486503el Anti-Fungal Peptides and Uses
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US/08/287,717
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Pred. No.
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US-08-481-888A-1
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            REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/287,717
FILING DATE: 09-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                              APPLICATION NUMBER: US 08/145,030
FILING DATE: 28-OCT-1993
PRIOR APPLICATION UDATA:
APPLICATION UDATA:
US 07/786,571
FILING DATE: 01-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                            ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08 FILING DATE: 07-JUN-1995
                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
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ZIP: 02173
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REGISTRATION NUMBER: 32,
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                                                                              Brook, David E.
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Two Militia Drive
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617-861-9540
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                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                             22,592
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SEQUENCE CHARACTERISTICS: LENGTH: 38 amino acids

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Best Local Similarity 100.0%;
Matches 4; Conservative 0
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                                                                                                                      TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
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                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
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APPLICATION NUMBER: US 07/786,571
FILING DATE: 01-NOV-1991
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                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                         OLECULE TYPE:
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OTHER INFORMATION: /product- "PSE"
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CITY: Lexington
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                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 07-JUN CLASSIFICATION: 514
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                                            TOPOLOGY:
                                                       STRANDEDNESS:
                                                                                                                                                                                                  REGISTRATION NUMBER:
NAME/KEY: Modified-site
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                                                                         amino acid
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                   US 08/287,717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brook, Smith & Reynolds, P.C
                                                                                                                                                                                            22,592
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. Pred. No.
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                                                       ; MOLECULE TYPE: US-08-441-914-9
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Patent No. 5696078
GENERAL INFORMATION:
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 Matches
          Query Match
Best Local Similarity
                                                                                                                               TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/1
FILING DATE: 28-CCT-93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/7
FILING DATE: 01-NOV-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08,
FILING DATE: 09-AUG-94
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CURRENT APPLICATION DATA:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
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                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                 LENGTH:
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                                                                                                    amino acid
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Conservative
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               100.0%;
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               Score 26;
Pred. No.
   Mismatches
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               DB 1; Length 38; 39;
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RESULT 13
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US-08-973-563A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tent No.
                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/485,273
FILING DATE: 07-JUN-1995
ATTORREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                   NAME/KEY:
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                                                                                                                                                                                         LOCATION: 1..38
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                   NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                ENGTH:
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                                                                                                                                      Similarity
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                            peptide
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                                                                                                                                     100.0%; Score 26; 100.0%; Pred. No.
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must have a D configuration."
                                                                                                                                                                                                                                                         /product= "PSE"
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                                     GENERAL INFORMATION:
APPLICANT: Lajoie, Gilles A.
TITLE OF INVENTION: Cyclic Analogs of Histatins
FILE REFERENCE: 36555-0002
CURRENT APPLICATION NUMBER: US/09/693,822B
CURRENT FILLING DATE: 2000-10-23
                                                                                                                                          Sequence 28, Application US/09693822B Patent No. 6555650
                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                    Best Local Similarity
PRIOR APPLICATION NUMBER: CA 2,285,673 PRIOR FILING DATE: 1999-10-21 NUMBER OF SEQ ID NOS: 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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JENTION: Anti-Fungal and Anti-Bacterial
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Pred. No.
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SOFTWARE: PatentIn version 3.1 SEQ ID NO 28

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ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Lesile

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-155

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090

TELEFAX: 212 869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEO ID NO: 143:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 amino acid

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-189-331-143
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NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: phosphoserine
US-09-693-822B-28
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US-08-189-331-143
Search completed: August 20, 2003, 12:44:21 Job time: 3.77108 secs
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PATENT NO. 5747334
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTRY: U.S.A.
2IP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNUMBER: US/08/189,331
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
CLASSIFICATION: 435
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Best Local Similarity 100.0%;
Matches 4; Conservative 0
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TYPE: PRT
ORGANISM: Homo sapiens
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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121.698 Million cell updates/sec
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Match
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US-10-042-431-56

US-09-864-761-46278

US-09-904-615-88

US-09-904-615-88

US-10-055-098-88

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1 US-09-895-298-161

1 US-09-895-298-161

1 US-09-764-887-237
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Sequence 31, Appl
Sequence 262, App
Sequence 8476, App
Sequence 426, App
Sequence 56, Appl
Sequence 46278, A
Sequence 88, Appl
Sequence 88, Appl
Sequence 88, Appl
Sequence 88, Appl
Sequence 439, App
Sequence 439, App
Sequence 237, App
Sequence 237, App
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189	189	189	189	189	189	189	189	189	189	189	189	189	189	177	177	177	147	147	146	118	118	118	117	98	93	89	89	78.	70
15 US-10-175-737-126	15 US-10-176-758-126	US-10-17	us-10-05	US-10-19	US-10-18	US-10	US-09-87	US-10-199-672	US-10-006-130#	US-10-015-387A-			9 US-09-765-205-4		11 US-09-988-067B-62	-608-60-SD	~	US-09-764-847-97		9 US-09-867-550-198		US-09-815-242-			us-09-995-		US-09-925-301-1	10 US-09-764-877-1056	11 US-09-764-891-4300
Sequence 126, App				Sequence 126, App	120	Sequence 8, Appli	356	126	Sequence 8, Appl1			Sequence 356, App		38,	Sequence 62, Appl	565,	`	Sequence 972, App	Sequence 188, App	198,	Sequence 11560, A	11401	61,	176,	Sequence 108, App	.7	Sequence 1058, Ap	Sequence 1056, Ap	Ç

ALIGNMENTS

Sequence 31, Application US/09300425B Publication No. US20030045681A1

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SEQ ID NO 31
LENGTH: 4
                                                                 Query Match
Best Local S
Matches 4
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PRIOR APPLICATION NUMBER: U9/V
PRIOR FILING DATE: 1998-05-11
PRIOR FILING DATE: 34
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF TITLE OF INVENTION: ANGIGGENESIS FILE REFERENCE: SCH-1733P1 CURRENT APPLICATION NUMBER: US/09/300,425B CURRENT FILING DATE: 1999-04-28 DELICATION NUMBER: 1999-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NERI, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: VITI, Francesca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B OTHER INFORMATION: antibody clone
                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                 TYPE: PRT
                                                                                     Similarity
                                 FPFY 4
                                                                                                                                                                                                                                                                                   PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIRCHLER, Manfred
                                                                      Conservative
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                                                                                     100.0%;
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                                                                    0;
                                                                   ; Score 26; DB; Pred. No. 4.4
0; Mismatches
                                                                                     DB 11;
4.4e+05;
                                                                                                      Length 4;
                                                                      Indels
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RESULT

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US-09-912-672A-10

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RESULT 4
US-10-106-698-8476
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US-09-880-748-2262
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US-09-880-748-2262
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                                    GENERAL INFORMATION:
APPLICANT: Ruben et
                                                                       Sequence 8476, Application US/10106698 Publication No. US20030109690A1
                                                                                                                                                                                                                                                                          Query Match
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SOFTWARE: FastSEQ for
SEQ ID NO 10
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Best Local Similarity
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                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
BEIOR ETITIN NUMBER: 60/212,210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ruben et al. TITLE OF INVENTION: Ant FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2001-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/475,541 PRIOR FILING DATE: 1999-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/912,672A CURRENT FILING DATE: 2001-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: CLASS II CYTOKINE RECEPTOR-LIKE PROTEINS
TITLE OF INVENTION: AND NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 07334-184001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/276,248 FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/240,816 FILING DATE: 2000-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/277,379 FILING DATE: 2001-03-21
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et al.
ON: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
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)S: 3239
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Pred. No.
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US-09-759-130B-426
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LENGTH: 22
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Best Local
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                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/479,249 PRIOR FILING DATE: 2000-01-07
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/759,130B CURRENT FILING DATE: 2002-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE,
TITLE OF INVENTION: USES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/106,69
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
                                                                                                                                                                                           PRIOR
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
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                                                                                            APPLICATION NUMBER: US 09/608,452 FILING DATE: 2000-06-30
                                                                                                                                  APPLICATION NUMBER: US 09/342,364 FILING DATE: 1999-06-29
                                                                        APPLICATION NUMBER: US 09/393,996
                                                                                                                                                                                       APPLICATION NUMBER: US 09/596,194
                                                                                                                                                                                                             FILING DATE: 1999-06-14
                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/333,159
                                     APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wrighton, Nicolas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser, Christ
Sharp, John D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goodearl, Andrew
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                                                       1999-09-10
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09/420,707
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Pred. No.
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PRIOR FILING DATE: 2000-10-04

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CURRENT APPLICATION NUMBER: US/10/042,431
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 56
LENGTH: 23
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US-09-759-1308-426
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; ORGANISM: Homo sapiens
US-10-042-431-56
         FILE REFERENCE: AGOMICA-Y-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
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SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 426
LENGTH: 23
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                 Sequence 46278, Application US/09864761 Patent No. US20020048763A1
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APPLICANT: BARNES, Thomas M
APPLICANT: FRASER, Christopher C
APPLICANT: SHARP, John D
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
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TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
                                                                                                                                                                              TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                      APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
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Chen, Wensheng
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NUMBER: GB 24263.6
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100.0%; Pred. No. 55,
tive 0; Mismatches
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CURRENT FILING DATE: 2000-12-19
EARLIER APPLICATION NUMBER: 09/511,554
EARLIER FILING DATE: 2000-02-23
EARLIER APPLICATION NUMBER: 09/519330
EARLIER FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 60/97,917
EARLIER APPLICATION NUMBER: 60/98,634
EARLIER FILING DATE: 1998-08-25
EARLIER APPLICATION NUMBER: 60/08,634
EARLIER FILING DATE: 1998-08-31.
NUMBER: 05/078,634
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US-09-739-254-88
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
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EXPRESSED IN BRAIN, SIGNAL = 2.1
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; OTHER INFORMATION:
US-09-739-254-88
                                                                                                              Sequence 88, Application US/10055098 Publication No. US20030139954A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  Best
APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PZ032P1
CURRENT APPLICATION NUMBER: US/10/055,098
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/511,554
PRIOR FILING DATE: EARLIER FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                                                        Matches
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Best Local
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NUMBER OF SEQ ID NOS: 170
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PRIOR FILING DATE: 2000-02-23
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TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PZ032P1
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OTHER INFORMATION: Xaa equals stop
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NAME/KEY: SITE
LOCATION: (34)
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TYPE: PRT
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ORGANISM: Homo sapiens
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/904,615
PRIOR FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/511,554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -10-054-988-88
                                                                                                                                                                                                        FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn Ver. 2
                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1998-08-31
                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/098,634
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/097,917 PRIOR FILING DATE: 1998-08-25
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/054,988
CURRENT FILING DATE: 2002-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
                                                                                                                                                                         LOCATION: (34)
OTHER INFORMATION:
                                                                                                                                                                                                                                 LENGTH: 47
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PZ032P1
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                                                                                                                                OTHER INFORMATION:
                                                                                                                                              NAME/KEY: SITE LOCATION: (47)
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LOCATION: (47)
OTHER INFORMATION: Xaa equals stop translation
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NAME/KEY: SITE
LOCATION: (34)
OTHER INFORMATION: Xaa equals
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TYPE: PRT
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                                                       Conservative
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No.
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                                                                                                                                                                       occurring L-amino acids
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RESULT

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Query Match
Best Local Similarity
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                                                                                    RESULT 14
US-09-764-887-237
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                                                                                                                                                                                                                                                                                             ; NAME/KEY: SITE ; LOCATION: (24) ; LOCATION: (74) ; OTHER INFORMATION: Xee equals any of the naturally occurring L-amino acids US-09-809-391-439
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NUMBER OF SEQ ID NOS: 761
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 439
LENGTH: 53
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Sequence 237, Application US/09764887
Patent No. US20020042099A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 439, Application US/09809391 Publication No. US20030049618A1 GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILING DATE: 2001-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen et al. TITLE OF INVENTION: 47
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US99/29950 PRIOR FILING DATE: 1999-12-16
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p. US20030078405A1
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Pred. No. 1.2e+02;
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SEQ ID NO 237
LENGTH: 68
TYPE: PRT
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CURRENT FILING DATE: 2001-01-17
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CURRENT FILING DATE: 2002-03-05
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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                                                                                                                                                                                 OR APPLICATION NUMBER: 60/225,757
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/226,868
OR FILING DATE: 2000-08-22
OR APPLICATION NUMBER: 60/216,647
OR FILING DATE: 2000-07-07
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                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/225,447
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/2210,290
FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/217,487
FILING DATE: 2000-07-11
APPLICATION NUMBER: 60/225,758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/180,628 FILING DATE: 2000-02-04 APPLICATION NUMBER: 60/214,886 FILING DATE: 2000-06-28
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                                                   APPLICATION NUMBER: 60/251,869
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                                                                                                                                               APPLICATION NUMBER: 60/225,267 FILING DATE: 2000-08-14
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                                                                                           APPLICATION NUMBER: 60/225,270
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D. US20030077602A1
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2000-09-27
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                 60/235,834
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Pred. No. 1.5e+02;
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APPLICATION NUMBER: 60/234,223 FILING DATE: 2000-09-21

PRIOR EPILING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: 60/249,210 PRIOR APPLICATION NUMBER: 60/225,759 PRIOR APPLICATION NUMBER: 60/225,759 PRIOR APPLICATION NUMBER: 60/225,759 PRIOR APPLICATION NUMBER: 60/225,759 PRIOR APPLICATION NUMBER: 60/225,213 PRIOR APPLICATION NUMBER: 60/225,213 PRIOR APPLICATION NUMBER: 60/225,214 PRIOR APPLICATION NUMBER: 60/225,214 PRIOR APPLICATION NUMBER: 60/225,214 PRIOR APPLICATION NUMBER: 60/225,216 PRIOR APPLICATION NUMBER: 60/225,216 PRIOR APPLICATION NUMBER: 60/225,266 PRIOR FILING DATE: 2000-08-14 PRIOR FILING DATE: 2000-05-16 PRIOR APPLICATION NUMBER: 60/249,218 PRIOR FILING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: 60/249,218 PRIOR APPLICATION NUMBER: 60/249,218 PRIOR APPLICATION NUMBER: 60/249,218 PRIOR APPLICATION NUMBER: 60/249,218 PRIOR APPLICATION NUMBER: 60/249,219 PRIOR APPLICATION NUMBER: 60/249,219 PRIOR APPLICATION NUMBER: 60/249,211 PRIOR APPLICATION NUMBER: 60/249,215 PRIOR APPLICATION NUMBER: 60/249,216 PRIOR APPLICATION NUMBER: 60/249,216 PRIOR APPLICATION NUMBER: 60/249,217 PRIOR APPLICATION NUMBER: 60/249,217 PRIOR APPLICATION NUMBER: 60/249,217 PRIOR APPLICATION NUMBER: 60/249,214 PRIOR APPLICATION NUMBER: 60/249,214 PRIOR APPLICATION NUMBER: 60/231,240 PRIOR APPLICATION NUMBER: 60/231,240 PRIOR APPLICATION NUMBER: 60/231,240 PRIOR APPLICATION NUMBER: 60/233,063 PRIOR APPLICATION NUMBER: 60/233,063 PRIOR APPLICATION NUMBER: 60/233,063 PRIOR APPLICATION NUMBER: 60/233,063 PRIOR APPLICATION NUMBER: 60/232,3064 PRIOR APPLICATION NUMBER: 60/232,3064 PRIOR APPLICATION NUMBER: 60/232,3064 PRIOR APPLICATION NUMBER: 60/232,3064 PRIOR APPLICATION NUMBER: 60/232,3	·		· · · · · · · · · · · · · · · · · · ·
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IOR APPLICATION NUMBER: 60/22, 514
IOR APPLICATION NUMBER: 60/224, 518
IOR APPLICATION NUMBER: 60/224, 519
IOR APPLICATION NUMBER: 60/22, 519
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IOR APPLICATION NUMBER: 60/25, 268
IOR FILING DATE: 2000-09-29
IOR APPLICATION NUMBER: 60/25, 368
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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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and is derived by analysis of the total score distribution.
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6: //ggn2_6/ptodata/1/paa/VCSO81_COMB.pep:*

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US-09-075-338C-31
US-09-300-425B-31
                                     Description
Sequence 31, Appl
Sequence 31, Appl.
                                                                                                                                                                                             RESULT 1

US-09-075-338C-31.

US-09-075-338C-31.

Sequence 31, Application US/09075338C

GENERAL INFORMATION:

APPLICANT: NERI, Dario

APPLICANT: TARLI, LOTENZO

APPLICANT: BIRCHLER, Manified

APPLICANT: BIRCHLER, Manified

TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY

FILE REFERENCE: SCH-1733

CURRENT APPLICATION NUMBER: US/09/075,338C

CURRENT FILING DATE: 1998-05-11

NUMBER OF SEQ ID NOS: 34
                                               SEQ ID NO 31
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: antibody clone
US-09-075-338C-31
   Query Match
Best Local Similarity
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23 US-09-856-285-9
16 US-09-224-669-10
18 US-09-224-669-11
23 US-09-912-672A-10
24 US-09-912-672A-10
24 US-09-912-672A-10
25 US-09-912-672A-10
26 US-09-867-819B-86
3 US-07-867-819B-86
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23 US-09-867-819B-86
24 US-09-912-776A-1
25 US-09-867-819-110-2262
26 US-10-29-412A-6
27 US-09-880-748-2262
28 US-10-29-412A-6
29 US-09-259-412A-6
20 US-09-259-412A-6
21 US-09-259-412A-6
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23 US-09-259-412A-6
24 US-09-259-412A-6
25 US-10-042-431-56
26 US-10-042-431-56
27 US-09-333-159-56
28 US-10-042-431-56
29 US-09-259-130B-426
29 US-09-259-130B-426
20 US-10-042-431-56
21 US-09-578-063-672
21 US-09-578-063-672
21 US-09-578-063-672
22 US-09-59-130B-426
23 US-09-35-052-14634
24 US-09-513-996A-77180
25 US-10-042-431-56
26 US-10-095-10-793-56152
31 US-60-1424-599-266152
31 US-60-453-050-10630
      Score
Pred.
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      26;
      DB 14;
5.1e+06;
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sequence 31, Appl
sequence 10, Appl
sequence 86, Appl
sequence 86, Appl
sequence 11, Appl
sequence 13, Appl
sequence 1, Appl
sequence 1262, Ap
sequence 2262, Ap
sequence 2262, Ap
sequence 2262, Ap
sequence 2662, Appl
sequence 6, Appl
sequence 56, Appl
sequence 672, Appl
sequence 56, Appl
sequence 57, App
sequence 672, App
sequence 672, App
sequence 673, App
sequence 77180, A
sequence 77180, A
sequence 77180, A
sequence 34, Appl
sequence 36, Appl
sequence 77180, A
sequence 77180, A
sequence 77180, A
sequence 17495, A
sequence 17495, A
sequence 17495, A

Length 4;

anti-ED-B

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; OTHER INFORMATION: ; OTHER INFORMATION: US-09-512-082-31
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Query Match
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                                                                                                                                                                     SEQ ID NO 31
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                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                  FILE REFERENCE: SCH-1733P2

GURRENT APPLICATION NUMBER: US/09/512,082

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: 09/300,425

PRIOR TILING DATE: 1999-04-28

PRIOR APPLICATION NUMBER: 09/075,338

PRIOR FILING DATE: 1998-05-11
                                                                                                                                                                                                                                                                                                                                 APPLICANT: NERI, Dario
APPLICANT: TARLI, LOTENZO
APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfred
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGAT
TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT
TITLE OF INVENTION: ANGIGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: SCH-1733P1
CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B OTHER INFORMATION: antibody clone
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VITI, Francesca
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                                                        Description of Artificial Sequence: anti-ED-B antibody clone
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Pred. No. 5.1e+06;
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US-09-475-541-10

(Sequence 10, Application US/09475541); SEQUENCE INFORMATION:

(APPLICANT: BUSFIELD, Samantha J.

(TITLE OF INVENTION: CLASS II CYTOKINE RECEPTOR-LIKE PROTEINS)
                                                                                                                                                                                                                                                                                                                              US-09-224-669-10
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US-09-224-669-10
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US-09-856-285-9
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                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/09224669 GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
                                                                                                                                                                                                                                                                  Query Match
Best Local S
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APPLICANT: 11ag, Leodevico L.
APPLICANT: Ng, Jocelyn, H.
APPLICANT: Ng, Jocelyn, H.
TITLE OF INVENTION: Method for Modifying and Identifying
TITLE OF INVENTION: Functional Sites in Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/224,669
CURRENT FILING DATE: 1998-12-31
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 09404/069001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: CLASS II CYTOKINE RECEPTOR-LIKE PROTEINS AND NUCLEIC ACIDS TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: DE 19854196.1
PRIOR FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/EP99/09052 PRIOR FILING DATE: 1999-11-23
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CURRENT FILING DATE: 2001-05-18
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                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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4; Conserv
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Similarity 100.0%;
4; Conservative 0
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                                                                                                                                                                                                                                          100.0%; Score 26; DB 16; 100.0%; Pred. No. 4.5e+02; ... wismatches 0;
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5.1e+06;
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TITLE OF INVENTION:

AND NUCLEIC ACIDS ENCODING THEM

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Sequence 10. Application US/09856285

GENERAL INFORMATION:

APPLICANT: 11ag, Leodevico L.

APPLICANT: 10g, Jocelyn, H.

APPLICANT: 10g, Jocelyn, H.

TITLE OF INVENTION: Method for Modifying and Identifying

TITLE OF INVENTION: Functional Sites in Proteins

FILE REFERENCE: 50125/024001

CURRENT APPLICATION NUMBER: US/09/856,285

CURRENT FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: PCT/EP99/09052

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: DE 19854196.1

PRIOR FILING DATE: 1998-11-24

NUMBER OF SCT IN NOTE: 19854196.1
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CURRENT FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: 09/224,669
PRIOR FILING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 27
SOPTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 10
LENGTH: 10
TYPE: PRT
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US-09-475-541-10
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; ORGANISM: Homo sapiens
US-09-856-285-10
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                                                                                                                    Sequence 10, Application US/09912672
GENERAL INFORMATION:
APPLICANT: BUSfield, Samantha J.
TITLE OF INVENTION: CLASS II CYTOKINE RECEPTOR-LIKE PROTEINS
TITLE OF INVENTION: AND NUCLEIC ACIDS ENCODING THEM
TILE REFERENCE: 0734-184001
CURRENT APPLICATION NUMBER: US/09/912,672
CURRENT APPLICATION NUMBER: US/09/912,672
PRIOR APPLICATION NUMBER: 09/475,541
PRIOR FILING DATE: 1998-12-31
NUMBER: 05 550 T. 1000
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Best Local
                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10 LENGTH: 10 TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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Pred. No.
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-672A-10
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US-09-856-285-11
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Best Local Similarity
Matches 4; Conserv
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GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
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                                                                                                                                                                                                   SEQ ID NO 11
                                                                                 Query Match
Best Local
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PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FASTSEQ for Windows Versio
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TITLE OF INVENTION: CLASS II CYTOKINE RECEPTOR-LIKE PROTEINS
TITLE OF INVENTION: AND NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 07334-184001
                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                  LENGTH: 11
TYPE: PRT
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Pred. No. 4.5
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Pred. No.
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Pred. No.
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RESULT 11

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US-07-867-819A-86
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Best Local (
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                        CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 07
FILING DATE: 31-JAN-1991
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 13-APR-199
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/472,947 FILING DATE: 31-JAN-1990 ATTORNEY/AGENT INFORMATION:
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                            COUNTRY: USA
ZIP: 30309-3450
                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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    Patrea L. Pabst
    2800 One Atlantic Center, 1250 West Peachtree Street

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1100 Péachtree Street
                                                                                                                                                                                     Harley, John
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                                                                                                                                        METHODS AND REAGENTS FOR DIAGNOSIS AUTOANTIBODIES 122
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Pred. No. 5
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                                  Matches
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PRIOR FILING DATE: 1990-01-31
PRIOR APPLICATION NUMBER: 07/648,205
                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 122 SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/07/867,819B CURRENT FILING DATE: 1992-04-13
                                                                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Harley, John TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies FILE REFERENCE: OMRF 114 CIP (2)
                                                                                                         LOCATION: (4)..(11)
OTHER INFORMATION: Binding site
                                                                                                                                                                          TYPE: PRT
ORGANISM: homo sapien
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                                                                                                                                           NAME/KEY: MISC_FEATURE
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                                                                                                                                                                                                             ENGTH:
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LENGTH: 12 amino acids
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
(404)-873-8794
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APPLICATION NUMBER: US 07/648,205
FILING DATE: 31-JAN-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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TOPOLOGY: lir
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 1 FPFY 4"
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                                                 Similarity
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Pred. No. 5.
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; NAME/KEY: MISC_FEATURE
; LOCATION: (4). (11)
; OTHER INFORMATION: Binding site
US-07-867-819D-86
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US-08-475-955-86
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APPLICANT: Harley, John
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LENGTH: 12
TYPE: PRT
ORGANISM: homo sapien
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GENERAL INFORMATION:
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Best Local
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TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
FILE REFERENCE: OMRF 114 CIP (2)
CURRENT APPLICATION NUMBER: US/07/867,819D
CURRENT FILING DATE: 1992-04-13
PRIOR APPLICATION NUMBER: 07/472,947
PRIOR FILING DATE: 1990-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 07/648,205
PRIOR FILING DATE: 1991-01-31
NUMBER OF SEQ ID NOS: 161
                                                                                                                                                 APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: APILI 13, 1992
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                          ZIP: 30309-3450

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: 07/472,947 FILING DATE: January 31, 1990 ATTORNEY/AGENT INFORMATION:
                                                                  PRIOR APPLICATION DATA:
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Local Similarity 100.0%; Pred. No. 5.3e+02;
nes 4; Conservative 0; Mismatches 0;
                                                                               APPLICATION NUMBER: 07/648,205 FILING DATE: January 31, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Patrea L. Pabst
2800 One Atlantic Center, 1250 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                               LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                              NAME/KEY: Binding-site LOCATION: 4..11
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Pred. No. 5.3e+02;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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US-10-603-113-27257
US-10-612-783-5205
US-10-612-783-5205
US-10-612-783-5216
US-10-612-783-5229
US-10-612-783-5219
US-10-612-783-5219
US-10-612-783-6421
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US-10-612-783-6421
US-10-612-783-6421
US-10-612-783-6421
US-10-612-783-64817
US-10-612-783-6880
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US-10-286-897-1962
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US-10-603-113-19356
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86, Appl
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                                                             MOLECULE TYPE: FEATURE:
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ALIGNMENTS

RESULT 1 US-10-376-121A-86 US-10-376-121A-86 ; Sequence 86, Application US/103761zin ; GENERAL INFORMATION: APPLICANT: Harley, John APPLICANT: Harley, John AUTOANTIBODIES TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF AUTOANTIBODIES NAME: Pabst, Patrea L. REGISTRATION NUMBER: 31,284 REFERENCE/DOCKET NUMBER: OM TELECOMMUNICATION INFORMATION: TELEPHONE: (404)-817-8473 TELEFAX: (404)-817-8588 INFORMATION FOR SEQ ID NO: 86: SEQUENCE CHARACTERISTICS: LENGTH: 12 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear TOPOLOGY: linear COUNTRY: USA ZIP: 30309-3400 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/376,121A FILING DATE: 27-War-2003 CLASSIFICATION -CURRENT -CURRENT APPLICATION NUMBER: 07/867,819 FILING DATE: APPLICATION NUMBER: 07/867,819 FILING DATE: January 31, 1991 APPLICATION NUMBER: 07/448,205 FILING DATE: January 31, 1991 APPLICATION NUMBER: 07/472,947 FILING DATE: January 31, 1990 ATTORNEY/AGENT INFORMATION: NAMME: Pabst. Patter 1. CORRESPONDENCE ADDRESS: ADDRESSEE: Patrea L. Pabst STREET: Suite 2000, 1201 West Peachtree STREET: Suite CITY: Atlanta peptide OMRF114CIP(2)DIV(2)

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RESULT 4
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
                                                                                                                                             Query Match
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4565, Application US/10612783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8043, Application US/10273573
                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/612,783
CURRENT FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 7098
                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(53373)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 10994
SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                       ENGTH: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                                                     ID NO 4565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity es 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100. es 4; Conservative
                                                        53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FPFY 4
                                                                                                                               Similarity
                                                                                    FPFY 4
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                                                                                                              100.0%; S
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tive 0;
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Pred. No.
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Pred. No. 5
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                                                                                                                              DB 6; Length 59; 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Candida albicans US-10-603-113-23128
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; ORGANISM: Candida albicans
JS-10-603-113-27267
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US-10-603-113-25825
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GENERAL INFORMATION:
GENERAL INF
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PRIOR APPLICATION NUMBER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
SEQ ID NO 23128
LENGTH: 67
                                                                                                                                                          SEQ ID NO 27267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23128, Appl GENERAL INFORMATION:
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LENGTH: 62
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Best Local
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Best Local
                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/603,113
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEO ID NOS: 28206
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CURRENT APPLICATION NUMBER: US/10/603,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBITITIE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/603,113
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                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 FPFY 49
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Pred. No.
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Pred. No.
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NAME/KEY: misc_feature;
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LOCATION: (B) LOCATION 1...75;
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SEQUENCE DESCRIPTION: SEQ ID NO: 3303:
US-10-617-320-3303
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                           TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3303:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/617,320
FILING DATE: 10-Jul-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           ORIGINAL SOURCE:
ORGANISM: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
39
                                1 FPFY 4
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OPERATING SYSTEM: <Unknown>
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 FPFY 42
                                                                                                                                                                                                                                                                                           TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: <Unknown>
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ilarity 100.0%;
Conservative (
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Pred. No.
                                                                                Score 26; DB Pred. No. 29;
                                                                Mismatches
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RESULT 8

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; ORGANISM: Candida albicans US-10-603-113-27139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT ; ORGANISM: Proteus mirabilis US-10-603-114-8012
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US-10-603-114-8012
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US-10-612-783-5205
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBI
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 8012
LENGTH: 77
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SEQ ID NO 27139
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GENERAL INFORMATION:
APPLICANT: GARY BRETON
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                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                         Sequence 5205,
CURRENT APPLICATION NUMBER: US/10/612,783
CURRENT FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 7098
SEQ ID NO 5205
LENGTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRA TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/10/603,114
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/543,681
PRIOR FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/248,796
PRIOR FILING DATE: 1999-02-12
                                                                                            TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53373)A
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                                                                                                                                                               APPLICANT:
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TYPE: PRT
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Cao, Yongwei
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nilarity 100.0%;
Conservative 0
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Pred. No.
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; OTHER INFORMATION:
US-10-631-402-2116
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                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 3475
SOFTWARE: Patent.pm
SEQ ID NO 2116
LENGTH: 94
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 08/905,133
PRIOR FILING DATE: 1997-08-01
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CURRENT FILING DATE: 2003-07-30
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                                                                                                                                                                                                               OTHER INFORMATION:
                                                                                                                                                                                                                                                                          NAME/KEY: SIGNAL LOCATION: -24.'.-1 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Hypertrophic prostate
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/904,468 FILING DATE: 1997-08-01 APPLICATION NUMBER: US 08/905,134
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APPLICATION NUMBER: US 08/905,279
FILING DATE: 1997-08-01
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APPLICATION NUMBER: US 08/905,051
FILING DATE: 1997-08-01
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        54 FPFY 57
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                                     1 FPFY 4
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1997-08-01
THATHER: US 08/905,135
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Pred. No. 35;
0; Mismatches
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Pred. No.
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В
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Best Local Similarity
Thes 4; Conserve
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SEQ ID NO 2116
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                APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
                                                                       APPLICANT:
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PRIOR FILING DATE: 1997-08-01
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TITLE OF INVENTION: Expressed Sequence Tags
FILE REFERENCE: GEN-T119C1
'ILE REFERENCE: 38-21(53373)A
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APPLICATION NUMBER: US 08/905,051
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                                                                                                           La Rosa, Thomas
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                                                    Zhou, Yihua
Cao, Yongwei
                                                                                          Kovalic, David
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APPLICANT: Wong, James F. H.

TITLE OF INVENTION: Orally Active Pesticidal Biopeptides
FILE REFERENCE: 35718/260673
CURRENT APPLICATION NUMBER: US/10/617,978
CURRENT FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: 60/395,428
PRIOR FILING DATE: 2002-07-12
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 103
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COTHED TUPORMATION: DR1 signal peptide linked to VC1
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                Sequence 576, Application US/10612783

Sequence 576, Application US/10612783

SERVERAL IMPORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53373)A

CURRENT APPLICATION NUMBER: US/10/612,783

CURRENT FILING DATE: 2003-07-02
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Best Local 9
SEQ ID NO 5576
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CURRENT FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 7098
SEQ ID NO 5529
LENGTH: 99
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NAME/KEY: unsure
LOCATION: (1)..(99)
OTHER INFORMATION: unsure at all xaa locations
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Local Similarity 100.0%;
hes 4; Conservative 0
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7 FPFY 10
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McCutchen, Billy Fred
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ALIGNMENTS

A;Molecule type: DNA A;Residues: 1-45 <HEI; A;Cross-references: GB:AE004284; GB:AE003852; NID:g9656649; PIDN:AAF95248.1; GSPDB:GN A;Experimental source: serogroup O1; strain N16961; blotype El Tor C;Genetics: R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; chardson, D.; Ermolaeva, M.D.; Vanathevan, J.; Bass, S.; Qin, H.; Dragoi, I., R.R.; Mckalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio ch A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: E82117
A;Status: preliminary hypothetical protein VC2102 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: E82117 RESULT E82117 A; Gene: VC2102 A; Map position: 1 Matches Best Local Similarity Query Match 26 FPFY 29 1 FPFY 4 4. Conservative 100.0%; 0 Score 26; Pred. No. Mismatches 38; 2 0 Length 45 Indels pathogen Vibrio cholerae 0; Gaps Dodson, R. I.; Sellers 0 2

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RESULT D90403

hypothetical protein SSO10228 [imported] - Sulfolobus solfataricus transposon ISC1058 C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C;Accession: D90403

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redcarrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.

.J.; Ch Redder

A; Reference number: A99139 A; Accession: D90403

A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-50 < KUR>

A;Cross-references: C;Genetics: GB:AE006641; NID:g13815629; PIDN:AAK42483.1; GSPDB:GN00155

A; Gene: SS010228

100.0%; Score 26; DB <u>ب</u> Length 50;

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Risabatini, L.M.; Azen, E.A.

Blochem. Blophys. Res. Commun. 160, 495-502, 1989

Blochem. Histatins, a family of salivary histidine-rich

A; Reference number: A90156; MUID:89246491; PMID:2719677

A; Accession: A32541
                            R; vanderSpek, J.C.; Offner, G.D.; Troxler, R.F.; Oppenheim, Arch. Oral Biol. 35, 137-143, 1990
A; Title: Molecular cloning of human submandibular histatins A; Reference number: A60659; MUID:90262442; PMID:2344289
                                                                                                                                                                                                               J. Dent. Res. 69, 2-6, 1990
A;Title: Structural relationship between human salivary
A;Reference number: A60742; MUID:90154430; PMID:2303595
A;Accession: A60742
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 20-57 <SUS>
R;Oppenheim, F.G.; Xu, T.; McMillian, F.M.; Levitz, S.M.; Diamond
J. Biol. Chem. 263, 7472-7477, 1988
J. Title: Histatins, a novel family of histidine-rich proteins in
A;Reference number: A94685; MUID:88227937; PMID:3286634
A;Accession: A28164
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A;Title: Nucleotide sequence analysis of the human salivary
A;Reference number: 157425; MUID:93330039; PMID:8336540
A;Accession: 157425
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C;Date: 31-Dec-1993 *sequence_revision 31-Dec-1993 *text_change 08-Dec-2000
C;Accession: I57425; A3254; A32987; A25661; A60664; A28164; A60742; A60659
R;Sabatini, L.M.; Ota, T.; Azen, E.A.
Mol. Biol. Evol. 10, 497-511, 1993
                                                                                                                                                    A; Molecule type: protein A; Residues: 31-57 < TRO>
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A;Residues: 20-57 <0Pp. A;Residues: 20-57 <0Pp. A;Residues: 20-57 <0Pp. A;Residues: 20-57 <0Pp. A;Residues: 20-57 <0Pp. A;Residues: 20-57 <0Pp. A;Risugiyama, K.; Ogino, T.; Ogata, K.
A;Rich. Oral Biol. 35, 415-419, 1990
A;Title: Rapid purification and characterization of histatins (histidine-rich polypepti A;Reference number: A60664; MUID:90321151; PMID:2372245
A;Accession: A60664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 261, 1177-1182, 1986
A;Title: The primary structure and functional characterization of A;Reference number: A25661; MUID:86111755; PMID:3944083
A;Accession: A25661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M26664; NID:g292143; PIDN:AAA58645.1; PID:g292144 R;vanderSpek, J.C.; Wyandt, H.E.; Skare, J.C.; Milunsky, A.; Oppenheim, F. Am. J. Hum. Genet. 45, 381-387, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181-887, 181
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A;Residues: 14-57 <VAN>
R;Oppenheim, F.G.; Yang, Y.C.; Diamond,
J. Biol. Chem. 261, 1177-1182, 1986
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A32541
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                                                                                                                                                                                                                                                                                                                                    R;Troxler, R.F.; Offner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-57 <SAB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:L04132; NID:g184051; PIDN:AAA02745.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N; Alternate names: histidine-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Status: translated from GB/EMBL/DDBJ
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Matches
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4; Conserv
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                                                                                                                                                                                                                                                                                                                                    G.D.; Xu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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; Mismatches
                                                                                                                                                                                                                                                                                                                                 T.; Vanderspek, J.C.; Oppenheim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F.M.; Levitz, S.M.; Diamond, R.D.; Offner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.D.; Hyslop, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                           R;Gattung; S.

Rigattung; S.

submitted to the EMBL Data Library, Februa
                                                                                                                                                                                                                                                                                                                                                             hypothetical protein K10B3.1 - Cae
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_rev
C;Accession: T16615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
C70246
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A; Introns: 17/3; 24/3; 34/3
C; Superfamily: histatin precursor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: C70246
                                                                                                                 A; Molecule type: DNA
A; Residues: 1-73 <GAT>
                                                                                                                                                                                                         A; Accession: T16615
                                                                                                                                                                                                                                            A; Description: The sequence A; Reference number: Z18546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T16615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-68 < KLE>
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C; Genetics:
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A; Residues: 'VML', 14-57 <VA2>
                                                        A; Experimental source:
                                                                                        A; Cross-references:
                                                                                                                                                                             A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Genome:
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                               Genetics
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CESP: K10B3.1
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                                                     EMBL:U49941; NID:g1206038; PID:g1206042; ce: strain Bristol N2; clone K10B3
                                                                                                                                                                                                                                                                                                                                                                                                #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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    Caenorhabditis elegans

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Pred. No.
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Pred. No.
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legans cosmid
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                                                                                                                                                                                GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                20-Sep-1999 #text_change 18-Feb-2000
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                                                                                        PIDN: AAB53870.1;
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GSPDB:G

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hypothetical protein BBJ10 - Lyme disease spirochete plasmid J/lp38 C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999 C;Accession: C70246
                                                                                                                                                                                                                                                                                                                                                                                                                                R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
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                                                                                                                                                                                                     PIDN: AAC66097.1;
                                                        Length 68
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                                                                                                                                                                                                                                                                                                                                                                          Borrelia
                                                                                                                                                                                               PID:g2690189;
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A;Gene: GDB:FKHL10; FREAC6
A;Cross-references: GDB:45(3
A;Map position: 5q34-5q34
C;Superfamily: unassigned i
F;6-76/Domain: fork head DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Pierrou, S.; Hellqvist, M.; Samuelsson, L.; Enerbaeck, S.; CEMBO J. 13, 5002-5012, 1994
A;Title: Cloning and characterization of seven human forkhead A;Reference number: S51624; MUID:95045392; PMID:7957066
A;Accession: S51629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FREAC-6 protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 24-Sep-1999
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A; Introns: 25/3
                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-77 - KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73598.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: asr1899
                                                                                                                                                                                                                           A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Accession: AE2043
                                                                                                                                                                                                                                                                                                                   hypothetical protein asr1899 [imported] - Nostoc sp. (strain PCC C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. sC;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change C;Accession: AE2043
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                                                                                                                                                                                                                                                         Nakazaki, N.; Shimpo, S.;
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic
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                                                                                                                                                                                                                                                                                         S.; Sugimoto, M.; Takazawa, M.; Yamada,
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A; Molecule type: mRNA
A; Residues: 1-97 <KNO>
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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M. Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; The arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: A99427
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                                                                                                                                            fork head homolog XFD-2' - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 31-Oct-1997
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A; Residues: 1-92 < KUR>
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A; Accession: E90483
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C; Species: Sulfolobus solfataricus
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               A; Title: Activin A induced expression of a A; Reference number: A56556; MUID: 93041288; A; Accession: C56556
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A; Residues: 1-97 < KUR>
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C; Species: Sulfolobus solfataricus
                                                                                   R;Knochel, S.; Lef, J.; Clement, J.; Klocke, B.; Hille, S.; Mech. Dev. 38, 157-165, 1992
A;Status: preliminary;
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  with conceptual translation
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                                          fork head related PMID:1358174
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Redder
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brain factor-3 - rat (fragment)
C; Species: Rattus norvegicus (N
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C:Species: Homo sapiens (man)
C:Date: 10-May-1996 #sequence_revision 10-May-1996 #text_change 12-Sep-1997
C:Accession: A47450
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A; Residues: 1-101 <RES>
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A;Title: Identification of nine tissue-specific transcription A;Reference number: A47450; MUID:93248207; PMID:7683413
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R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, F.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
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Pred. No.
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A; Residues: 1-105 < KUR>
A; Cross-references: GB:
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A; Accession: F90335
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A; Residues: 1-101 < RES>
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R;Clevidence, D.E.; Overdier, D.G.; Tao, W.; Qian, X.; Pani, L.; Lai, Proc. Natl. Acad. Sci. U.S.A. 90, 3948-3952, 1993
A;Fitle: Identification of nine tissue-specific transcription factors A;Reference number: A47450; MUID:93248207; PMID:7683413
A;Accession: I60919
A;Accession: I60919
                                                                                                                                                                                                                                                                                                            R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Al
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng,
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: F90335
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A;Title: Identification of nine tissue-specific transcription fac A; Reference number: A47450; MUID:93248207; PMID:7683413
A; Accession: I60918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein SSO1745 [imported] - C; Species: Sulfolobus solfataricus
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
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R;Clevidence, D.E.; Overdier, D.G.; Tao, W.; Qian, X.; Pani, L.; Lai, E.; C
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Peng, X.; Thi-Ngoc, H.P.; Redder
                        Length 105;
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SRY_CAPHI
SRY_SHEEP
Y382_METJA
PLSC_BORBU
ELLR_AQUAE
ED5_DROME
Y103_AQUAE
MED1_HUMAN
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ALIGNMENTS

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191 SEQUENCE OF 20-57. TISSUE-Parotid gland; MEDLINE-88227937; PubMed-3286634;	c. Natl. Acad. Sci. U.S.A.	ration and	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,		Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Honking R F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,	F.S., Wagner L.,	MEDLINE=22388257; PubMed=12477932;		SEQUENCE FROM N.A.		HIS1 and HIS2, and evolution of the STATH/HIS gene family.";	tvaru	MEDLINE=93330039; PubMed=8336540;	[2]	Biochem. Biophys. Res. Commun. 160:495-502(1989).	"Histatins, a tamily of salivary nistigine-rich proteins, are encoded by at least two loci (HIS1 and HIS2).";		MEDLINE-89246491; PubMed-2719677;	[1] SEQUENCE FROM N.A.	I_TaxID=9606;	EURATYOLA; Metazoa; Chordata; Ciantata, Veitebiata, Hattitobiomi, Mammalla: Entheria: Primates: Catarrhini: Hominidae: Homo.	sapiens (Human).	HTN1 OR HIS1.	Histatin 1 precursor (Histidine-rich protein 1) (Post-PB protein) (PPB) [Contains: Histatin 2].	: :	(Rel. 14, Created)	P15515;	MAN CTANANT CT

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                                                                                                     SEQUENCE
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Sugiyama K., Ogino T., Ogata K.;
"Rapid purification and characterization
polypeptides) from human whole saliva.";
Arch. Oral Biol. 35:415-419(1990).
                                                                                                                                            PEPTIDE
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J. Biol. Chem. 263:7472-7477(1988).
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tissue distribution of the
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MEDLINE-86111755; PubMed-3944083;
Oppenheim F.G., Yang Y.C., Diamond
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                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: HISTATINS ARE SALIVARY PROTEINS THAT ARE CONSIL BE MAJOR PRECURSORS OF THE PROTECTIVE PROTEINACEOUS STRUCTOOTH SURFACES (ENAMEL PELLICLE). IN ADDITION, HISTATINS ANTIBACTERIAL AND ANTIFUNGAL ACTIVITIES.

PTM. HISTATIN 2 IS A PROTECLYTIC PRODUCT OF HISTATIN 1: SIMILARITY: TO HISTATIN 3.
                                                                                                                                                            GO:0005576; C:extracellular; NAS.
GO:0003797; F:antibacterial peptide activity; NAS.
GO:0006952; P:defense response; NAS.
mineralization; Fungicide; Antibiotic; Signal; Phos
                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                             ; L04132; AAA02745.1; -.; BC017835; AAH17835.1; -. 157425; A32541.
 43
                                                                                                                                                                                                                                                                                   M26664; AAA58645.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ization of the genes for histatins distribution of the mRNAs."; Hum. Genet. 45:381-387(1989).
                                                                                                                                                                                                                                 HGNC:5283; HTN1.
                                                               Similarity
                . FPFY
FPFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F.G., Xu T., McMillian F.M., Levitz D., Troxler R.F.;
                                                100.
nilarity 100.
Conservative
                                                                                                      57
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31
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                                                 0;
                                               Score 26; DE
Pred. No. 25;
Mismatches
                                                                                                   F3532BD1DCE23D83
                                                                                                                             HISTATIN 2.
                                                                                                              PHOSPHORYLATION
                                                                                                                                        HISTATIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.C.,
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                                                                          DB
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                                                                                                                                                              Signal; Phosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human chromosome
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                                                                      Length 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primary structure,
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S STRUCTURE
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EXHIBIT
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                                             Gaps
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RESULT 2
FXL2_MOUSE

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                                                                                                                                                                                                                        Matches
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Best Local
                                       30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
FOrkhead box protein C2 (Brain factor-3) (BF-3)
FOXC2 OR HFHBF3.
                                Rattus norvegicus (Rat).
                                                                  Q63246;
30-MAY-2000 (Rel. 39,
30-MAY-2000 (Rel. 39,
30-MAY-2000 (Rel. 39,
                                                                                                                 FXC2
                                                                                                                                                                                                                                                                              DNA_BIND NON_TER
NCBI_TaxID=10116;
            Mammalia;
                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fentities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001
16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00053; FORKHEAD.
ProDom; PD000425; TF_Fork_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1349428; Fox12.
InterPro; IPR001766; TF_Fork_head.
Pfam; PF00250; Fork_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Multistep signaling requirements for pituitary organogenesis vivo.";
                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                      NON_TER
                                                                                                                                                                                                                                                                                                            PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
DNA-binding; Nuclear protein; Transcription
                                                                                                                                                                                                                                                                                                                                                             SMART; SM00339; FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes Dev. 12:1691-1704(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treier M., Gleiberman A.S., McMahon A.P., Rosenfeld M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98283916; PubMed=9620855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Fragment).
FOXL2 OR PFRK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 fork-head domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MESENCHYME OF DEVELOPING EYELIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Q63245;
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          Eutheria; Rodentia;
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ilarity 100.0%;
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                     Chordata;
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Rodentia;
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L, Last
L L2 (Pi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ast sequence update)
ast annotation update)
(Pituitary forkhead f
                                                                                                                                                                                                                                                                   MW.
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                                                                                                                                                                                                                   Score 26; DB Pred. No. 38; ); Mismatches
        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                         FORK-HEAD
                                                                                                                PRT;
                                                                                                                                                                                                                                                                 03CE0DEC6BA84BEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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                                                      (HFH-BF-3)
                                                                                                                                                                                                                                          Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OVARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D.P., McMahon J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
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FX11_RF

ID 11_RF

ID 12_RF

ID 12_R
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Best Local S
Matches 4
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PRODOM; PD000425; TF_Fork_head; 1.

SMART; SM00339; FF; I; SM0239; FF; I; I; PROSITE; PS00657; FFORK_HEAD_1; 1.

PROSITE; PS00658; FORK_HEAD_2; 1.

PROSITE; PS50039; FORK_HEAD_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come entitles requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Sprague-Dawley;
MEDLINE-93248207; PubMed-7683413;
Clevidence D.E., Overdier D.G., Tao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FXI1_RAT STANDARD; PRT; 101 AA.
063248;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Forkhead box protein I1 (Forkhead-related protein FKHLI0) (Forkhead-related transcription factor 6) (FREAC-6) (Hepatocyte nuclear factor 3 forkhead homolog 5) (HFH-5) (Fragment).
FOXI1 OR FKHL10 OR FREAC6 OR HFH-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <del>+</del> <del>+</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Sprague-Dawley;
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SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001766; TF_Fork_head. Pfam; PF00250; Fork_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; 160918; 160918.
HSSP; Q63245; 2HFH.
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                                                                                                                                  hepatocyte nuclear factor 3/forkhead Proc. Natl. Acad. Sci. U.S.A. 90:3946-1- SUBCELLULAR LOCATION: Nuclear.-1- SIMILARITY: Contains 1 fork-head
                                                This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription
                                                                                                                                                                                                                                                                                  "identification of nine tissue-specific transcription for the state of the second of t
                                                                                                                                                                                                                                                                                                                                                                              Costa R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116
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SIMILARITY: Contains 1 fork-head domain.
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    the Swiss
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101 AA;
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12098 MW;
    Institute
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Pred. No. 43;
0; Mismatches
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   EMBL; AE001535; AAD06654.1; PIR; G71851; G71851. HAMAP; MF_00402; -; 1.
                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genomic sequence comparison of two unrelated gastric pathogen Helicobacter pylori."; Nature 397:176-180(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alm R.A., Ling L.-S.L., Moir D.T., Smith D.R., Noonan B., Guild B.C., Tummino P.J., Caruso A., Uria-Nick
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TRANSFAC; T102480; -.
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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                                                                                                                                         or send an email to license@isb-sib.ch).
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SIMILARITY: BELONGS TO THE L19P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., D.R., Noonan B., Gulid B.C., dedonge B.L., Carmel G to P.J., Caruso A., Uria-Nickelsen M., Mills D.M., To P.J., Caruso A., Uria-Nickelsen M., Mills D.M., To P.J., Caruso A., Uria-Nickelsen M., Mills D.M., To P. C., Merberg D., Mills S.D., Jiang Q., Taylor D.E.,
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Best Local
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STRAIN-26695 / AFCC 700392;

MEDLINE-97394467; PubMed-9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Glodek A., Nelson K., Chardson D., Dodson R., Khalak H.G., Glodek A., KritzGerald L.M., Lee N., Adams M.D., Hickey E.K., WcKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., HitzGerald J.M., Fujii C., Bowman C., Watthey L., Wallin E. Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E. Cotton M.D., Weidman J.M., Karp P.D., Smith H.O., Fraser C.M.,
                                                 PRINTS; PR00061; RIBOSOMALLI9.
ProDom; PD002979; Ribosomal_L19; 1.
TIGREAMS; TIGR01024; rp1S_bact; 1.
PROSITE; PS01015; RIBOSOMAL_L19; 1.
                                                                                                                                                        TIGK; HP114/; -.
HAMAP; M=00402; -; 1.
InterPro; IPR001857; Ribosomal_L19.
Pfam; PF01245; Ribosomal_L19; 1.
                                                                                                                                                                                                                                                                                        EMBL;
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                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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Nature 388:539-547(1997).
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Batteria; Proteobacteria; Epsilonproteobacteria;
Helicobacteraceae; Helicobacter.
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01-NOV-1997
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50S ribosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: THIS PROTÉIN IS LOCATED AT THE 30S-50S RIBOSOMAL SI INTERFACE AND MAY PLAY A ROLE IN THE STRUCTURE AND FUNCTION (AMINOACYL-TRNA BINDING SITE (BY SIMILARITY).

SIMILARITY: BELONGS TO THE L19P FAMILY OF RIBOSOMAL PROTEINS
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A151AD3A165A233F CRC64;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsithe European Bioinformatics Institute. There are no restrictions
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ
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"Molecular cloning of
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CAPALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
acylglycerophosphocholine + a fatty acid andon.

COPACTOR: Binds I calcium ion per subunit (By similarity).

SUBCELLULAR LOCATION: Secreted (By similarity).

TISSUE SPECIFICITY: Expressed by the venom gland.

SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP 1
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(Rel. 41, Last sequence update)

(Rel. 42, Last annotation update)

se, A2 5 precursor (EC 3.1.1.4) (Phosphatidylcholine 2-
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erpentes; Colubroidea;
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braum M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurite K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurite K., Lapidus A., Lardinois S., Mauel C., Medigue C.,
RA Kurite K., Lapidus A., Lardinois S., Mauel C., Medigue C.,
RA Noone D., O'Reilly M., Ogswa K., Oglwara A., Oudega B., Park S.H.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Rakedin M., Tanakoshi A., Tanaka T., Tarabashi H., Takemaru K.,
RA Sato T., Scanlan E., Takaji T., Takahashi H., Takemaru K.,
RA Sato T., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Winters P., Wipat A., Yanamoto H., Yamane K., Yasumoto K., Yata K.,
The Complete genome sequence of the Gram-positive bacterium Bacillus
The complete genome sequence of the Gram-positive bacterium Bacillus
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Trach K., Hoch J.A.;
Trach R., Hoth J.A.;
The Bacillus subtilis spoOB stage 0 sporulation operon encodes essential GTP-binding protein.
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                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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EMBL; Z99118; CAB14751.1;
PIR; D32804; D32804.
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or send an
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
1- FUNCTION: FORMS A COMPLEX WITH THE HEAVY CHAIN OF THE CL.
TRANSPLANTATION ANTIGENS DURING AN ADENOVIRUS INFECTION,
REDUCING CLASS I EXPRESSION ON THE CELL SURFACE.
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MEDILINE-81053687; PubMed-6253880;
Herisse J., Courtois G., Galibert F.;
"Nucleotide sequence of the EcoRI D fragment of adenovirus 2 genome.";
Nucleic Acids Res. 8:2173-2192(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human adenovirus type 2, and
Human adenovirus type 6.
Viruses; dsDNA viruses, no RN
NCBI_TaxID=10515, 10534;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Early E3 18.5 kDa glycoprotein precursor (G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-Human adenovirus type 6;
Reichmann H., Schaarschmidt E., Geisler B.,
                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                  EMBL; J01917; AAA92221.1; EMBL; Y16037; CAA75990.1;
                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: TO OTHER ADENOVIRUSES GP19K.
                                                                                                                                                                                                                                                                                                                                                                                                                                            reticulum.
                                                                                                                                                                                 A03821; Q6ADE
                                                                                                                                         PF04881; Adeno_GP19K;
                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FPFY 4
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an email to license@isb-slb.ch).
                                                                                                                                                            IPR006965; Adeno_GP19K
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    18
18
124
124
145
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Transmembrane; (1) 17 PP 18 159 E. 18 123 L. 144 PP 159 C. 29 N
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2; ACT.
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W; 4D11D222BAB20E27 CRC64;
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Pred. No.
  LUMENAL (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .)
                                                                                 EARLY E3
                                                                                                      POTENTI
                                                                                                                       Glycoprotein;
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precursor (GP19K).
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                                                                                   kDa GLYCOPROTEIN
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      .) (POTENTIAL).
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SOCCERTAR RANGER                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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Interpro; IPRO06965; Adeno_GP19K.
Pfam; PF048B1; Adeno_GP19K; 1.
Early protein; Transmembrane; Glyco
SIGNAL 1 18 POTENT
CHAIN 19 160 EARLY
DOMAIN 19 124 LUMENA
TRANSMEM 125 145 POTENT
DOMAIN 146 160 CYTOPL
CARBOHYD 79 79 N-LINK
SEQUENCE 160 AA; 18502 MW; B1FC
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDITINE-2007470; PubMed=1727603;
Chroboczek J., Bieber F., Jacrot B.;
"The sequence of the genome of adenovirus type 5 and its compari with the genome of adenovirus type 2.";
VITOLOGY 186:280-285(1992).
-1-FUNCTION: FORMS A COMPLEX WITH THE HEAVY CHAIN OF THE CLASS TRANSPLANTATION ANTIGENS DURKING AN ADENOVIRUS INFECTION, THE REDUCING CLASS I EXPRESSION ON THE CELL SURFACE.

REDUCING CLASS I EXPRESSION ON THE CELL SURFACE.
                                                                                                                                                                                                                                                                     EMBL; M73260; -; NOT_ANNOTATED_CDS.
EMBL; M30002; CAA26783.1; -.
EMBL; M12406; AAA426782.1; -.
PIR; A03822; ERADA5.
                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P04494;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Early E3 18.5 kDa glycoprotein precursor (GP19K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=85130985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=85092388; Pubmed=
Cladaras C., Wold W.S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLETE GENOME.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID-28285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human adenovirus type 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: TO OTHER ADENOVIRUSES GP19K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LINE=85130985; PubMed=3882694;

d W.S.M., Cladaras C., Deutscher S.L., Kapoor Q.S.;
e 19-kDa 91ycoprotein coded by region E3 of adenovirus.
ification, characterization, and structural analysis.";
Biol. Chem. 260:2424-2431(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140:28-43(1985).
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159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=2981456;
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18438
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                      POTENTIAL.

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...)
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                                                                                                                     LUMENAL (POTENTIAL).
                                                                                                                                             EARLY E3 18.5 kDa GLYCOPROTEIN
                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                          Glycoprotein; Signal.
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Pred. No. 66;
D; Mismatches
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  BlF0D2AC4D6330E0 CRC64;
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                      (POTENTIAL).
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Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., "Whole-genome random ran
                DP1_HUMAN STANDARD; PRT; 000765; Q04198; Q9BMH9; 01-APR-1993 (Rel. 25, Created) 28 FEB-2003 (Rel. 41, Last sequence uplication (Rel. 42, Last annotation (Rel. 42) (Rel. 43) (Rel. 44) (Rel. 44) (Rel. 44) (Rel. 45) (Rel. 46) (Rel. 47) (Rel. 47) (Rel. 48) (Re
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01-NOV-1995
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Fleischmann R. D., Adams M.D., White O., Kerlavage A.R., Bult C.J., Tomb J.-F., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole-genome random sequencing and assembly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus
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32, Last sequence up
41, Last annotation
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protein

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RA Strausberg R.D., Felngold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., McGrey K.C., Hale S., Garcia A.M., Gay L.J., Hulhy S.W.,
RA Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski N.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length
RT Tencr Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

C. -- SIMILARITY: TO C. ELEGANS T19C3.4.
   Transmembrane.
TRANSMEM 3
TRANSMEM 8
CONFLICT 11:
CONFLICT 15:
                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                        Pfam;
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Kinzler K.W., Nilbert M.C., Su L.K., Vogelstein B., Bryan T.M.,
Levy D.B., Smith K.J., Preisinger A.C., Hedge P., McKechnie D.,
Finniear R., Markham A., Groffen J., Boguski M.S., Altschul S.F.,
Horii A.K., Ando H., Miyoshi Y., Miki Y., Nishisho I., Nakamura Y.,
"Identification of FAP locus genes from chromosome 5q21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Joslyn G., Carlson M., Thliveris A., Albertsen H., Gelbe Samowitz W., Groden J., Stevens J., Spirio L., Robertson Sargeant L., Krapcho K., Wolff E., Burt R., Hughes J.P., Warrington J., McPherson J.D., Wasmuth J.J., le Paslier Abderrahim H., Cohen D., Leppert M., White R.; "Identification of deletion mutations and three new gene familial polyposis locus.", Cell 66:601-613(1991).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                 GO:0016021; C:integral to erPro; IPR004345; TB2_DP1_Im; PF03134; TB2_DP1_HVA22;
                                                                                                                                                      L; M73547; AAA60136.1; L; M74090; AAA66351.1; L; BC000232; AAH00232.1; A39658; A39658.
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111
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A39658.
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POTENTIAL.
POTENTIAL.
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REF.
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Robertson M.,
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RC STRAIN=Berkeley;
RX MEDLING-2019606; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beleson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Benos P.V., Berman B.P., Davenport L.B., Davies P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Docison K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Docison K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Docison K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeqwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeqwam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nanda M.V., Moshry C., Morris J., Moshrefi A.,
RA Nanda M.V., Moshry C., Morris J., Moshrefi A.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
                      RESULT 13
RU1A_DROME
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Best Local
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MEDLINE-95011590; PubMed-7926776;
Flickinger T.W., Salz H.K.;
"The Drosophila sex determination with sequence and functional simil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        determination protein SNF).

SNF OR D25 OR LIZ OR FS(1)1621 OR CG4528.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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P43332; O9W4D7;
O1-NOV-1995 (Rel. 32, Created)
O1-NOV-1995 (Rel. 32, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
O1 small nuclear ribonucleoprotein A (
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Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).

-i- FUNCTION: BINDS STEM LOOP II OF US INRNA. IT IS THE FIRST SN-RNP

-i- FUNCTION: BINDS STEM LOOP II OF US INRNA. IT IS THE FIRST SN-RNP

-i- FUNCTION: BINDS STEM LOOP II OF US INTERACTION IS REQUIRED FOR THE

SUBSEQUENT BINDING OF UZ SN-RNP AND THE U4/U6/U5 TRI-SN-RNP (BY

SIMILARITY). PLAYS A ROLE IN REGULATING SEX-LETHAL SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stapleton M., Carlson J., George R.A., Guarin H., F
Rubin G.M., Celniker S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0003449; snf. GO; GO:0030532; C:small nuclear ribonucleoprotein complex; GO; GO:0007539; P:primary sex determination, soma; NAS. InterPro; IPR000504; RNA_rec_mot. Pfam; PF00076; rrm; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-22426066; PubMed-12537569;
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PROSITE; PS00030; RRM_RNP_1; 1.
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3L; L29521; AAA28903.1; -.
3L; AE003433; AAF46017.1; -.
3L; AY061491; AAL29039.1; -.
3L; AY061491; AA129039.1; -.
8; A54279; A54279
SP; P09012; 3UTR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE U1 A/B" FAMILY. SIMILARITY: Contains 2 RNA recognition motif (RRM)
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RNA-BINDING (RRM) 1.
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b J.M., Park S.,
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RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
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RA Halley J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Halley J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Cheys J., Barlow K.F., Bates K.N., Beard L.M., Brown A.J.,
RA Clays S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Cleys S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Cleys S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Collson A., G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Collson A., G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
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RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Holden J.L., Howden P.J.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Mickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Mickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Mickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Mickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Mickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Mickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Mickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature [3]
                                                                                                                                                                                                                                            MEDIINE-98379985; PubMed-9716128;
Price S.R., Evans P.R., Nagai K.;
"Crystal structure of the spliceosomal U2B'-U2A'
bound to a fragment of U2 small nuclear RNA.";
Nature 394.645-650(1998).
This SWISS-PROT entry is copyright. between the Swiss Institute of Bio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coleman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22079017; PubMed=12084575; Chung S., Zhou Z., Huddleston K.A.
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                                                                                                                                                             associated with sn-RNP U2. It binds stem loop IV of in presence of the A' protein.

-i- SUBUNIT: Present in a spliceosome complex assembled
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION IN
                                                           composed of SNRPB2, HPRP8BP and CRNKLL.
DISEASE: Patients with systemic lupus erythematosus
antibodies which interact with sn-RNP proteins.
SIMILARITY: BELONGS TO THE U1 A/B" FAMILY.
SIMILARITY: Contains 2 RNA recognition motif (RRM)
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414:865-871(2001).
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etheria; Primates; Catarrhini; Hominidae,
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    jht. It is produced through a collaboration
Bioinformatics and the EMBL outstation -
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01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-APR-1988 (Rel. 07, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pathogenesis-related protein R minor form precursor (PR-R) (PROB12)
(Thaumatin-11ke protein E2).
Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID=4097;
                                 SEQUENCE FROM N.A.

MEDILINE-86230894; PubMed-3713832;

Cornelissen B.J.C., Hooft van Huijsduijn
"A tobacco mosaic virus-induced tobacco
sweet-tasting protein thaumatin.";

Nature 321:531-532(1986).
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Pfam; PF00076; rrm; 2.

SMART; SM00360; RRM; 2.

PROSITE; PS50102; RRM; 2.

PROSITE; PS00030; RRM_RNP_1; 1.

PROSITE; PS00030; RRM_RNP_1; 1.

RIBONUCLEOPROTEIN; Repeat; Systemic lupus erythematosus; 3D-s
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EMBL; AL034428; CAB38777.:
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Plant Mol. Biol. 12:153-155(1989).
-!- SUBCELLULAR LOCATION: VACUOIAI.
-!- MISCELLANEOUS: PR PROTEINS ARE ACID-SOLUBLE, PROTEASE-RESISTANT PROTEINS WHICH ACCUMULATE IN THE INTERCELLULAR SPACES OF MANY PLANTS AS A RESULT OF THE HYPERSENSITIVE REACTION TO A PATHOGEN
-!- MISCELLANEOUS: PR-R EXISTS AS TWO ISOFORMS IN TOBACCO, A MAJOR J
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STRAIN-2603 V/R / Serotype V;

MEDLINE-2222988; pubMed-12200547;

Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S., 
Tettelin H., Masignani V., Cleslewicz M.J., Eisen J.A., Peterson S., 
Tettelin H., Masignani V., Cleslewicz M.E., Maggarit I., Read T.D., 
Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., 
Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., 
DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., 
DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., 
Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., 
Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., 
Tacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., 
Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                                                        "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).

EMBL; AE014266; AAN00510.1; -
TIGR; SAG15466; -
Hypothetical protein; Complete proteome.
SEQUENCE 32 AA; 3831 MW; 2020BF60F8B8D8AD CRC54;
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                                                                                                                                                                                                                                                                                                          Fraser C.M.;
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Similarity 4; Conserv
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Score 26; DB 16;
Pred. No. 1.2e+02;
Mismatches 0;
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Q9KQ98;
01-OCT-2000
                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-EI TOT N1691 / Serotype 01;
MEDLINE-2046833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Seller
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J
Fraser C.M.;
                                                                                             Hypothetical SEQUENCE 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8F552;
Q8F552;
01-MAR-2003
                                                                                                                  TIGR; VC2102;
                                                                                                                            Nature 406:477-483(2000).
EMBL; AE004284; AAF95248.1;
                                                                                                                                                 cholerae.
                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2002) to the EMBL/GenBank EMBL; AE011338; AAN49033.1; -. Hypothetical protein; Complete proteome. SEQUENCE 43 AA; 5278 MW; FAC6704968D
                                                                                                                                                           "DNA sequence of both chromosomes
                                                                                                                                                                                                                                                                                         NCBI_TaxID=666;
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01-MAR-2003 (TrEMBLrel.
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NCBI_TaxID=173;
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45 AA; 5437 MW; FE258F385A7CA5FD CRC64;
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SQUENCE FROM N.A.

STRAIN-ANCC 35092 / DSM 1617 / P2;

STRAIN-ANCC 35092 / DSM 1617 / P2;

MEDLINE-21332296; PubMed-11427726;

She Q. Singh R.K., Confalonieri F., Zivanovic Y., Allard G., She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G., Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A., De Moors A., Erauso G., Fletcher C., Gordon P.M.K., Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N., Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T., Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus ! Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J., Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S. Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.; "The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symbionts ", Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sulfolobus solfataricus
Archaea; Crenarchaeota;
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STRAIN=1330 / Biovar 1;
MEDLINE=22247741; PubMed=12271122;
Paulsen I.T., Seshadri R., Nelson K.E.,
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Brucellaceae;
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NCBI_TaxID=29461;
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                                                     AE006835; AAK42483.1;
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01-MAR-2001 (TrEMBLrel. 16, Las
01-JUN-2002 (TrEMBLrel. 21, Las
Winged helix protein CWH-6 (Fra
Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata; C
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01-NOV-1996
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MEDLINE=96118697; PubMed=7496528;

BOUTSBUX-Eude C., Saint Girons I., Zuerner R.;

BOUTSBUX-Eude C., Saint Girons Leptospira interrogans.";

"IS1500, an IS3-like element from Leptospira interrogans.";

Microbiology 141:2165-2173(1995).

EMBL; U13013; AAA88820.1; -...
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ProDom; PD000425; TF_Fork_head; 1.
SMART; SM00339; FH; 1.
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4; Conserv
                  h 100.0%;
Similarity 100.0%;
4; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 AA;
                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                  60
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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7351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neognathae;
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                                                                                                              MW;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26;
Pred. No.
                                                                                                              B20EDB371F3AD507 CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostom1;
; Galliformes; Phasianidae; Phasianinae;
                                          Score 26; DB 13;
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update)
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  helix proteins.";
nk/DDBJ databases.
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QRLBZI
ID QRLBZI
AC QRLBZI

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Best Local :
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01-JUN-1998
01-JUN-1998
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gw Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hansovan Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artlach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 050765
                                                                                                                                                                                                                                                                                                                    QBLBZ1;
QBLBZ1;
Q1-QCT-2002 (TrEMBLrel. 22, Created)
Q1-QCT-2002 (TrEMBLrel. 22, Last sequence update)
Q1-QCT-2002 (TrEMBLrel. 22, Last annotation update)
Q1-QCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sacteria; Spirochaetes;
NCBI_TaxID-139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-ATCC 35210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid 1p38
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                                            SEQUENCE FROM N.A. Brover V., Troukha Feldmann K.;
                                                                                                                     Genome
[2]
                                                                                                                                                           Haas B.J., Volfovsky N., Town C.D., Troukhan M., Ale
Feldmann K.A., Flavell R.B., White O., Salzberg S.L.
"Full-length messenger RNA sequences greatly improve
annotation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8LBZ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Plasmid; Complete proteome.
SEQUENCE 68 AA; 7927 MW; 03E39BD66E24C09A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000787; TIGR; BBJ10; -.
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EMBL; AE000787; AAC66097.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98065943; PubMed-9403685;
    "Full-Length cDNA from P
Submitted (MAR-2002) to
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith H.O., Venter J.C.; 
"Genomic sequence of a Lyme disease
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
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3 (TrEMBLIEL. 06, 1

2 (TrEMBLIEL. 20, 1

al protein BBJ10.
                                                                      Troukhan M.,
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       Arabidopsis thaliana.";
o the EMBL/GenBank/DDBJ
                                                                        Alexandrov N.,
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Last sequence update)
Last annotation updat
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                                                                             Y.-P.,
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Best Local 9
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01-MAR-2002 (TrEMBLrel. 20, 0
01-MAR-2002 (TrEMBLrel. 20, 1
01-OCT-2002 (TrEMBLrel. 22, 1
Winged helix transcription fi
  George
Sutton
                                                                                                                                                       Q9VFX9 PRELIMINARY; PRT; 70 AA. Q9VFX9; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
    MEDINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F. Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.
                                                                                                                                      CG11686 protein (RH19248p).
CG11686 OR BCDNA:RH19248.
                                                     SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                             Neoptera; Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF343007; AAL73344.1; -.
InterPro; IPR001766; TF_Fork_head.
Pfam; PF00250; Fork_head; 1.
PRINTS; PR00053; FORKHEAD.
PRODOM; PD000425; TF_Fork_head; 1.
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                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8WXT4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AY086916; AAM64480.1;
Hypothetical protein.
SEQUENCE 69 AA; 7446 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens myeloid
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                                                                                                                                                                                                                                                                                                              Local
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  R.A., Lewis S.E., G.G., Wortman J.R.
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                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                         FPFY 24
                                                                                                                                                                                                                                                                                                                                                                       PS00658; FORK_HEAD_2; PS50039; FORK_HEAD_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | FPFY 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FPFY 26
                                                                                                                                                                                                                                                                                                                                           70
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7446 MW;
                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                      70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                           A,
                                                                                                                                                                                                                                                                                                                                          8355 MW;
                                                                                                                                                                                                                                                                                                          100.0%;
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d factor-delta mRNA.";
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                                                                                                                                                                                                                                                                                                 0,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                             Score 26; DB 4;
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                        96487388A0DD80B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; E
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9D7D16D302F6B973 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
 M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     delta
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Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Fragment).
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 Chen
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                                                                                                                                                                                                                                                                                              0;
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         S.N.,
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RA Glodek A. Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A. Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeewam C.,
RA Harris N.L., Houston K.A., Howland T.J., Wei M.-H., Ibeewam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levisky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levisky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Glabs R.A., Myers E.W., Rubin G.M., Venter J.C.,
Theng S.A., Myers E.W., Rubin G.M., Venter J.C.,
Scheng R.A., Myers E.W., Rubin G.M., Venter J.C.,
Schence 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                           Q54321;
01-NOV-1996
01-NOV-1996
01-JUN-1998
                                                                                                                            ORF72
                                                                    Plasmid pRN1.
Archaea; Crenarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patel S., Pl
Celniker S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 SEQUENCE FROM N.A
                                  NCBI_TaxID=43080
                                                        Sulfolobus
                                                                                                         Sulfolobus islandicus.
                                                                                                                                                                                                                   Q54321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase;
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Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
Dourbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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                                                                                                                                                                                                                                                       12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    AE003699; AAF54916.1;
AY070684; AAL48155.1;
se; FBgn0040551; CG11686;
NCE 70 AA; 8200 MW; 5
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                                                                                                                                                                                                                   PRELIMINARY,
                                                                                                                                                                                                                                                                                                            58
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le C., Baxter E.G., Helt G., Nelson
                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                    Thermoprotei; Sulfolobales; Sulfolobaceae;
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01,
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Last annotation updat
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Pred.
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s 0;
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Nelson C.R., Miklos G.L.G.,
                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        databases
                                                                                                                                                                                                                                                                                                                                                                                                              Length 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reese M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ketchum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith
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RESULT
Q9LQ57
ID Q9
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DT 01
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Best Local :
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      Q9LQ57
Q9LQ57;
Q1-QCT-2000
Q1-QCT-2000
                                                                                                                                                                                                                          Waterston R.;
Waterston R.;
Poirect Submission.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U49941; ANB53870.1; -.
WormPep; K10B3.1; CE07364.
Hypothetical protein.
SEQUENCE 73 AA; 8309 MW; 49BE84CA4AE53901 CRC64;
SEQUENCE 73 AA; 8309 MW; DB 5; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          021411 PRELIMINARY;
021411;
01-NOV-1996 (TIEMBLICEL 01, Cr.
01-NOV-1996 (TIEMBLICEL 01, La.
01-MAR-2003 (TIEMBLICEL 23, La.
Hypothetical 8.3 kDa protein.
K10B3.1.
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C. investigating biology. The C. eleganscience 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmid pRN1.";
Plasmid 35:141-144(1996).
EMBL; U36383; AAC44108.1;
                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence of C. elegans cosmid K10B3.";
submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sattung S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96271189;
Keeling P.J., Kler
Zillig W., Doolitt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE-96271189; PubMed-8700967;
Keeling P.J., Kitenk H.P., Singh R.K., Feeley O.,
Zillig W., Doolittle W.F., Sensen C.W.;
"Complete nucleotide sequence of the Sulfolobus :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-REN1H1;
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                                                                                                                                                                    FPFY 4
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     (TrEMBLrel. 15, (TrEMBLrel. 15,
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llarity 100.0%;
Conservative (
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                                                      PRELIMINARY;
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Last annotation update)
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Pred. No. 2.5
0; Mismatches
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                                                      PRT;
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Pred.
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   sequence update)
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                                                    76
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                                                                                                                                                                                               DB 5; I
2.5e+02;
les 0;
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RESULT
Q8JX72
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Conn L., Conway A., Gonzalez A., Hansen N., Howing B.,

Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsi

Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Son

Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Fl

Theologis A., Ecker J.;

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases

R EMBL, AC09317, AAF79751.1;

R EMBL, AC09317; AAF79751.1;

R PROSITE; PS00133; CARBOXYPEPT_ZN_2; 1

SEQUENCE 76 AA; 8899 MW; FD0CD669597E90BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                     STRAIN-SENV-D;
Tanaka Y., Pfeiffer R., Yeo A.E., Mizokami M., Edlin B.R.,
O'Brien T.R., Alter H.J., Shih J.W.;
"PCR-probe capture hybridization assay and statistical mixture
modeling for SEN virus prevalence estimation.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB075270; BAB97340.1;
InterPro; IPR004219; TTVirus_Unk.
                                                                                                                                                                                                                                                                                                        Q8JX72;
01-OCT-2002
01-OCT-2002
01-MAR-2003
Pfam; PF02956; TT_ORF1;
NON_TER 1 1
NON_TER 76 76
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                 NCBI_TaxID=136966;
[1]
                                                                                                                                                                                                                                                                    SEN virus.
                                                                                                                                                                                                                                                                                       ORF1
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Chao Q., Brooks S., Buehler E., Dunn P., Khan S., Kim Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S., I Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. T30E16.14.
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ilarity 100.0%;
Conservative (
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Last sequence Last anno
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Bei B., Chin C., Chiou J., Choi E.,
z.A., Hansen N., Howing B., Koo T., Lam
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Sakano H., Schwartz J., Southwick A.,
berg M., Yu G., Davis R., Federspiel N
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Pred. No.
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Search completed: August 20, 2003, 12:40:30 Job time: 10.6774 secs	Qy 1 FPFY 4 1 Db 49 FPFY 52	SQ SEQUENCE 76 AA; 8656 MW; C62AF6E245301A13 CRC64; Query Match 100.0%; Score 26; DB 12; Length 76; Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0;
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                Score
     444
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48
1 NGWYPW 6
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Match
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Gapop 10.0 , Gapext 0.5
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ABG03291

AAB26455

AAB20924

AAG65229

ABG59477

ABB44094

ABB26986

AAM65117

AAM77824
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                                                Novel human diagno
Drosophila melanog
Drosophila odorant
Mandrill immunodef
Human liver peptide
Peptide #11600 enc
Protein #8985 enco
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     Human brain expres
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Arabidopsis the Arabidopsis th	AAG41264 AAG41263 AAG41262 ABB06171 ABG53484 ABB38629 ABB23722 AAM59252 AAM19313	. 21 23 22 22 22 22 22 22 22	467 5744 12 38 38 38 38 38	777777888	37.5 37.5 37.5 37 37 37 37 37 37 37 37 37	444443336 5422109
<i>:</i>	ABU56123 ABU57118 ABU10697 AABU7589 AAG47999 AAG53566 AAG53566 AAG53565 AAG53564 ABB90965	24 24 21 21 21 23	146 146 146 337 343 452 452 557	79. 79. 79. 79. 79. 22.	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	334
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	AAM21726 AAM38042 ABG46855 AAG48003 AAG07472 AAU47631 ABP78660 AAY99453 AAU29211	222222222222222222222222222222222222222	39 39 39 39 83 83 1117 146			115

ALIGNMENTS

RESULT 1 ABG03291

ABG03291 standard; Protein; 562 AA.

13-FEB-2002 (first entry)

ABG03291;

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Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                          Novel human diagnostic protein #3282.
               WPI; 2001-639362/73.
N-PSDB; AAS67478.
                                                                       31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                30-MAR-2001; 2001WO-US08631.
                                                                                                                  11-OCT-2001
                                                                                                                                 WO200175067-A2.
                                                                                                                                                  Homo sapiens.
                                        Drmanac RT, Liu C,
                                                        (HYSE-) HYSEQ INC.
                                        Tang
                                         YT;
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New isolated polynucleotide and encoded polypeptides, useful in

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RESULT 2
AAB26455
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Note: The sequence data for this patent did not appear in the printed content of the formation of the formation of the formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 5
                 Disclosure;
                                             Novel nucleic acid encoding an insect odorant receptor, modulator compounds that are useful in controlling pest
                                                                                                    N-PSDB; AAA94853
                                                                                                                                                                                                                         25-FEB-1999;
                                                                                                                                                                                                                                                       25-FEB-2000; 2000WO-US04995.
                                                                                                                     WPI; 2000-572081/53
                                                                                                                                                                                      (UYCO ) UNIV
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                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 GWYPW 371
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                 Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                    COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            relates to isolated polynucleotide (I) and II) sequences. (I) is useful as hybridisation probes.
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                 86;
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                                                                                                                                                                                                                                                                                                                                                                                           fruit
              176pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                      DOR83; odour recognition; pest control
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85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 562;
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                                               population
                                                         for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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AAB20924
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receptors. These proteins function as olfactory receptors, and are thought to be members of the G protein-coupled receptor (GPCR) superfamily, which is characterised by the presence of 7 transmembrane helices. Nucleic acids encoding the Drosophila odorant receptors may be used to generate expression constructs, host cells containing such constructs, and transgenic insects. Cells which express the odorant receptor genes may be used in methods to identify agents which modulate expression of these genes, and in methods to identify receptor binding partners. The Drosophila odorant receptor nucleic acids may also be used to identify corresponding genes in other insects, such as those which damage crops or transmit disease. The odorant receptor proteins may be used to identify agents which modulate their activity, to identify binding partners, as antigens to raise antibodies,
                                                                                                                                                                                                                            Sequences AAB20901-B20949
                                                                                                                                                                                                                                                               Claim 12;
                                                                                                                                                                                                                                                                                         New nucleic acid encoding a Drosophila olfactory receptor, useful for identifying modulating agents {	extstyle \cdot}
                                                                                                                                                                                                                                                                                                                                                                                                 Carlson JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200043410-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Odorant receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the previously identified Drosophila melanogaster odorant receptor DOR83. The odorant genes and proteins, such as those provided by the invention, are useful as they aid in the study of the olfactory organ in mammals, as well as aiding the understanding of the link between odour recognition and behaviour in insects. They also enable the identification of compounds capable of activating and inhibiting the receptors, allow the control of pest populations via the use of alarm odour ligands and via the use of ligands which interfere with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-2000; 2000WO-US01823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila odorant receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB20924 standard; Protein; 414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insect behaviour modification;
biosensor; odour detection; odo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nteraction between odorant ligands and receptors associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-coupled
                                                                                                                                                                                                                                                                                                                                                2000-543246/49
DB; AAA72259.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 5; Conserv
                                                                                                                                                                                                                                                           Page 184-185; 303pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Kim J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; olfactory receptor;
                                                                                                                                                                                                                                                                                                                                                                                                 Clyne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.3%;
                                                                                                                                                                                                                             represent Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPCR superfamily; transgenic insect; on; pest control; pollinator attraction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      odour
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Pred. No.
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and in methods to modify insect behaviour. The proteins may be also be used in methods of behaviour modification. Such methods may be used to study or modify insect behaviour in response to odorants such as pheromones. Modification of insect behaviour has a wide range of applications, such as in pest control (e.g., by disrupting the feeding or mating behaviours of pest species), or for enhancing plant pollination (by attracting pollinator species). Odorant receptor proteins and/or nucleotides may also be used to identify appetite suppressants, to trap odours of a specific type, as biosensors for the detection of explosives, drugs, perfumes or pollutants, and in apiculture to modify the behaviour of bees, for example, to increase the production of royal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simian immunodeficiency virus; SIV;
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                                                                                                                                                                                                                                                                                                                                                                                                                      NO200003889-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                Simian immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibody detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG65229 standard; Protein; 853
                                                                                                       Sequence
                                                                                                                              The present invention relates to a new mandrill immunodeficiency virus SIM27, which can be used to detect antibodies directed against the virus. The present sequence is the ENV protein described in the exemplification of the invention.
                                                                                                                                                                                              Example 3; Page 27; 47pp; Norwegian.
                                                                                                                                                                                                                         New mandrill immunodeficiency virus SIM27 useful for antibodies directed against the virus - \,
                                                                                                                                                                                                                                                               WPI; 2001-201061/20
                                                                                                                                                                                                                                                                                        Guertler LG,
                                                                                                                                                                                                                                                                                                                  (DADE-) DADE
                                                                                                                                                                                                                                                                                                                                            03-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mandrill immunodeficiency virus SIM27 ENV protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG65229;
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 416 NVWYPW 421
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5; Conserv
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5; Conserv
                        NGWYPW 6
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                                                  Conservative
                                                                                                                                                                                                                                                                                                                  BEHRING MARBURG GMBH.
                                                                                                                                                                                                                                                                                                                                                                      2000NO-0003889
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83.3%;
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Pred. No. 1.3e+02;
                                                    Score 39; DB
Pred. No. 3.9e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV;
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                                                     DB 22; I
3.9e+02;
hes 1;
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                                                                            Length 853;
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                                                      Indels
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RESULT 5
ABG59477
ID B797
ID B797
ABG59477
XX
XX
ABG59477
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XX
Huma
XX
Huma
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Huma
XX
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XX
Home
XX
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RESULT 6
ABB44094
ID ABB4
XX
AC ABB4
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperilipoproteinaemia, hyperilipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                       Query Match
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID No 38125; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488898/53.
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                         ABB44094;
                                                                                ABB44094 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                          1 NGWYPW 6
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2000US-0207456.
2000US-068408.
2000US-06323686.
2000US-0234687.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             AA,
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Pred. No.
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Mismatches
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                                                              Human; gene expression; he cardiovascular disease; he congenital heart disease.
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
  09-AUG-2001
                       WO200157274-A2
                                          Homo sapiens.
                                                                                                         Protein #8985
                                                                                                                                                                                                                                                                                                                                                        The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.
                                                                                                                             23-JAN-2002
                                                                                                                                                  ABB26986;
                                                                                                                                                                     ABB26986 standard;
                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                  The sequence data
                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome-derived single exon nucleic acid probes useful
zing gene expression in human fetal liver -
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                                                                                                                                                                                                                                             1 NGWYPW 6
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                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                      he sequence data for this patent did not form part of the specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULAR DYNAMICS
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                                                                                                                                                                                                                          SGWHPW 15
                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 36729; 639pp + sequence listing; English
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0234687.
                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                    encoded by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoded
                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                            79.2%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expression; single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                        hypertension;
                                                                                 heart; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INC.
                                                                                                                                                                     39
                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                          Score 38;
Pred. No.
                                                                                                   for measuring heart cell gene
                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     foetal liver single exon probe
                                                                        cardiac
                                                                                                                                                                                                                                                                         DB
25;
                                                                                vascular system,
                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                   Length 39
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                               0;
                                                                                                     expression
                                                                                                                                                                                                                                                               Gaps
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0;

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Matches
                                          Query Match
Best Local
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                     The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, all diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.

Note: The sequence data for this patent did not form part of the printed at fits whose, introductions but was obtained in electronic format directly from WIPO at the publicability of the printed at fits whose into intending the form sequence.
                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                Single exon nucleic acid hearts -
                                                                                                                                                                                                                                                                   The present invention relates to single exon
                                                                                                                                                                                                                                                                                                   Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                        Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-)
                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                         2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                        SG,
1 NGWYPW 6
                           4;
                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                SEQ ID No 28756; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                     39
                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
; 2000US-0236263.
                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001WO-US00666
                                       79.28;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                        Chen
                                                                                                                                                                                                                                                                                                                                            probes
                                                                                                                                                                                                                                                                                                                                                                                                      ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                   INC
                         Score 38; DB
Pred. No. 25;
2; Mismatches
                           2;
                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR
                                                                                                                                                                                                                                                                                                                                         for analyzing gene expression
                                    DB
25;
                                                     22;
                           0,
                                                     Length
                         Indels
                                                     39
                        0;
                                                                                                                                                                                                                                                                                                                                           in
                        Gaps
                                                                                                                                                                                                                                                                                                                                           human
                                                                                                                                                                                                                                     (see
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RESULT 8
AAM65117
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04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                         09-AUG-2001.
                                                                                                                             epilepsy; cancer
                                                                                                                                    Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                               Human brain expressed single exon probe encoded protein SEQ ID NO: 37222
                                                       30-JAN-2001;
                                                                                          WO200157275-A2
                                                                                                            Homo sapiens.
                                                                                                                                                                                    05-NOV-2001
                                                                                                                                                                                                      AAM65117;
                                                                                                                                                                                                                        AAM65117
                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                   SGWHPW 15
2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                       2001WO-US00667.
                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                        Protein;
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Best Local
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                                                                                                                                   04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the important
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           brains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-)
                                                                      Penn
                                                                                                                    21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                  30-JAN-2001;
                                                                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                                                      WO200157276-A2
                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                         microarray;
                                                                                                                                                                                                                                                                   Human; bone
                                                                                                                                                                                                                                                                                    Human bone marrow
                                                                                                                                                                                                                                                                                                      06-NOV-2001
                                                                                                                                                                                                                                                                                                                                        AAM77824 standard; Protein;
                                                                                        (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-483446/52
                       genome-derived single exon nucleic acid probes zing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  esent invention provides a number of single exon nucleic an which are derived from genomic sequences expressed in the They can be used to measure gene expression in brain cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                 NGWYPW 6
                                                                                        MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                       SGWHPW 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                      Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO: 37222; 650pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                               39
                                                                                                                  2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                  marrow expressed exon; gene expression analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                          cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0236359
2000GB-0024263
                                                                                                                                                                                  2001WO-US00668
                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                           2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ă,
       ID NO:
                                                                      Ŗ,
                                                                                                                                                                                                                                                                                   expressed probe encoded protein
                                                                                                                                                                                                                                                         leukaemia; lymphoma; myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                  79.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                      Chen W,
       38130; 658pp + Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes
                                                                                                                                                                                                                                                                                                                                          39
                                                                                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank
                                                                       Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                  NO ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 39
                                                                                                                                                                                                                                                                                    SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                  useful
       English
                                                                                                                                                                                                                                                                                     NO:
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                                                                                                                                                                                                                                                                   probe;
                                                                                                                                                                                                                                                                                     38130
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RESULT 10
AAM21726
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В
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                       specification, at ftp.winn'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human probes which may enable used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                      by one such probe. The SENPs are derived from human HeLa cells. The can be used to produce a single exon microarray, which can be used measuring human gene expression in a sample derived from human cerv epithelial cells. By measuring gene expression, the probes are ther useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                             The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs
                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; human; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide #8160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM21726
                                                              cervical cancer
                                                                                                                                                                               Claim 27; SEQ ID No 26552; 487pp;
Sequence
                                                                                                                                                                                                                                                                                                 (MOLE-)
                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                         SG,
                                      The sequence data fication, but was o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 SGWHPW
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                                                                                                                                                                                                                                                                                                  MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                         Hanzel
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39
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                               2001WO-US00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoded by probe
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                                                                                                                                                                                                                                                                         DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
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                                                                                                                                                                                                                                                                         Chen
                                    a for this patent did not form part of the printed obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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Pred.
                                                                                                                                                                                                                                                                          Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.
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25;
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                                                                            from human cervical probes are therefore cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>.</u>
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Query Match

79.2%;

Score

38;

DB 22;

Length

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RESULT 12
ABG46855
ID ABG46
XX
AC ABG46
XX
DT 19-AU
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                                                                                                                                                                               RESULT 11
AAM38042
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                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                    The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
      19-AUG-2002
                          ABG46855;
                                            ABG46855 standard; Peptide; 39
                                                                                                                                                                                                                                                                    Claim 27; SEQ ID No 38311; 654pp; English.
                                                                                                                                                                                                                                                                                        analyzing
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful
                                                                                                                                                                                                  numan genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; microarray; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #12079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM38042;
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                                                                                                                                                                                                                                                                                                                                         SG,
                                                                                               10 SGWHPW 15
                                                                                                                   1 NGWYPW 6
                                                                                                                                       L Similarity
4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 SGWHPW 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NGWYPW 6
                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                        gene expression
                                                                                                                                                                               39
                                                                                                                                       Conservative
     (first entry)
                                                                                                                                                                                                                                                                                                                                                                               2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0180312.
2000US-0207456.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; placenta; antenatal diagnosis;
                                                                                                                                               79.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%;
                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bу
                                                                                                                                                                                                                                                                                        in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probe for measuring
                                                                                                                                    Score 38; DB Pred. No. 25; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                        human placenta
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                                                                                                                                                                                                                                                                                                                                         Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
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                                                                                                                                                                                                                                                                                                                                        DR;
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                                                                                                                                                         22;
                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  placental gene expression
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                                                                                                                                                         Length 39;
                                                                                                                                      Indels
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                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                 for
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                                                                                                                                     Gaps
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                                                                                                                                    0
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Human
                                                                peptide encoded by genome-derived single
                                                                exon
                                                                probe
                                                                SEQ ID 36520
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Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disfamilial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; hyaline membrane disease. cancer; COPD; ILD;
interstitial lung disease;

Homo sapiens.

WO200186003-A2

15-NOV-2001

04-FEB-2000; 30-JAN-2001; 2001WO-US00665

03-AUG-2000; 26-MAY-2000; 30-JUN-2000; ; 2000US-180312P. 2000US-207456P. ; 2000US-0608408. ; 2000US-0632366. ; 2000US-0632365. ; 2000US-23458PP. ; 2000US-236359P. ; 2000US-0024263.

21-SEP-2000; 27-SEP-2000;

(MOLE-)

MOLECULAR DYNAMICS INC

Penn Hanzel DK, Chen W, Rank DR;

WPI; 2002-114183/15

measure gene expression in human lung samples Spatially-addressable set of single exon nucleic acid probes, used ç

Claim 27; ID No 634pp; English.

cc nucleic acid expressed in the human lung; measuring gene expression in a contacting the derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung cmRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising comprising conditions and (b) detecting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, can be above mentioned microarray; assigning exons to a single exon probe comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (b) measuring the expression of each of the exon in several confiction of the exon probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the confiction of the exons that the exons the expression of the exon pattern of the expression of the exons in the tissues and/or cell types indicates that the confiction of the exons that the expression of the expression of the exons that the expression of the expression of the exons that the expression of the e the exons should be assigned to a single gene; a peptide comprising on of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibers. Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derive from human lung comprising single exon nucleic acid probes having on 12614 nucleic acid sequences mentioned in the specification, or the 1287 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a librosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, derived one of one

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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KW SAPH
KW UV91
KW WO21
XX Infl
KW derm
XX PD 01-
XX PD 01-
XX PD 01-
XX PD 01-
XX PF 20-
XX PF 
                                                                                       Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic CC polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central cc nervous system, however it is particularly involved in the inflammatory clesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a cc. sample with a binding agent that binds to the proteins of the invention cand determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies compression and activity of P. acnes production of antibodies compression and activity of P. acnes polypeptides and cc. therefore treat P. acnes infections. These antibodies can be used as called the compression and activity of P. acnes polypeptides and cc. therefore treat P. acnes infections. The antibodies may also be used as called the compression and activity of P. acnes polypeptides and cc. diagnostic agents for determining P. acnes presence, for example, by called the compression of the printed compression and activity of production of the printed compression and activity of production of the printed compression and activity of production of the printed compression and compression and activity of production of the printed compression and activity of production of the printed compression and compression and activity of production of the printed compression and compression and activity of production of the printed compression and compression and activity of production of the printed compression and c
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L'maisonneuve J, Zhang Y,
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    GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
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NS-09-134-078-62
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NS-08-161-9558-118
NS-08-461-9558-118
NS-08-370-476-118
NS-08-370-476-118
NS-08-160-524A-30
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2742, Appl
27442, Appl
118, Appl
117, Appl
23, Appl
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RESULT 2 US-09-625-972-25 Sequence 25, Application US/09625972 Patent NO. 6566513 GENERAL INFORMATION: APPLICANT: HAUSER, Lutz Gerhard APPLICANT: DONGMO DELOKO, Yvette Beatrice APPLICANT: EXEMO, Leopold APPLICANT: EXEMO, Leopold APPLICANT: KAPTUE, Lazare ITILE OF INVENTION: (MANDRILLUS LEUCOPHABUS) FILE REFERENCE: 067595/0106 CURRENT APPLICATION NUMBER: US/09/625,972 CURRENT FILING DATE: 2000-07-29 PRIOR APPLICATION NUMBER: DE 199 36 003.0 PRIOR FILING DATE: 1999-08-03 NUMBER OF SEQ ID NOS: 57 SOFTWARE: PatentIN version 3.0	Query Match Query Match Best Local Similarity 100.0%; Pred. No. 6. Matches 5; Conservative 0; Mismatches Qy 2 GWYPW 6 Db 56 GWYPW 60	RESULT 1 US-09-252-991A-16759 Sequence 16759, Application US/09252991A Sequence 16759, Application US/09252991A Sequence 16759, Application US/09252991A Sequence 16759, Application US/09252991A SEQUENCE INFORMATION: ALENGINOSA FOR DIAGNOSTICS TITLE OF INVENTION: ALENGINOSA FOR DIAGNOSTICS FILE REFERENCE: 107196.136 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 16759 LENGIN FILING DATE: 1998-07-27 SEQ ID NO 16759 LENGIN FILING DATE: 1998-07-27 ORGANISM: Pseudomonas aeruginosa US-09-252-991A-16759	28 34 70.8 92 4 US-09-663-600A-211 29 34 70.8 184 4 US-09-252-991A-26087 30 34 70.8 218 3 US-08-985-526-1 31 34 70.8 239 5 PCT-US93-01652-1 32 34 70.8 239 5 PCT-US93-01652-1 33 34 70.8 312 3 US-09-252-991A-9648 34 70.8 312 3 US-09-267-177-21 35 34 70.8 314 4 US-09-267-177-21 36 34 70.8 315 3 US-09-736-915-2 37 34 70.8 335 3 US-08-736-915-2 38 34 70.8 433 4 US-09-252-991A-26691 39 34 70.8 433 4 US-09-252-991A-25248 39 34 70.8 441 3 US-09-252-991A-25248 40 34 70.8 575 4 US-09-252-991A-25248 41 34 70.8 900 1 US-08-220-113-5 43 34 70.8 980 1 US-08-220-113-5 44 34 70.8 980 1 US-08-413-118-5 44 34 70.8 980 3 US-08-413-118-5 45 34 70.8 1170 1 US-08-313-288B-20
ce GROUP OF IMMUNODEFICIENCY VIRUSES OF DRILL (AEUS) AND THEIR USE	DB 4; Length 115; 6.1; ees 0; Indels 0; Gaps 0;	O ACID SEQUENCES RELATING TO PSEUDOMONAS STICS AND THERAPEUTICS	0A-211 Sequence 211, App 1A-26087 Sequence 26087, A 2-5731 Sequence 5731, Ap 6-1 152-1 Sequence 1, App11 152-1 Sequence 1, App11 Sequence 21, App1 5-1 Sequence 21, App1 5-1 Sequence 21, App1 11A-26691 Sequence 2, App1 11A-23248 Sequence 25248, A 11A-23248 Sequence 25248, A 11A-20649 Sequence 3, App11 11A-20649 Sequence 3, App11 11A-19257 Sequence 5, App11 8-5 Sequence 5, App11 Sequence 20, App1

PatentIn version 3.0

85.7%;

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; NAME/KEY: UNSURE ; LOCATION: (202) ; LOCATION: (202) ; OTHER INFORMATION: Identity of amino acid at the above locations US-09-252-991A-20604
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US-09-625-972-25
   Query Match
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LENGTH: 555
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LENGTH: 236
TYPE: PRT
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APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS FILE REFERENCE: 107196.136
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PRIOR TILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                       ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                 TYPE: PRT
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 DB 4;
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                                                                                                                                                                                                                                                                                                                                       AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 236;
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                                                   are unknown.
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                                                                                                       GENERAL INFORMATION:
                                                                                                                Sequence 35, Approx No. 6503881
                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                 Query Match
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                                                                         APPLICANT:
                              APPLICANT:
                                                           APPLICANT:
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                APPLICANT:
                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206) 682-603
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Taylor, F
APPLICANT: Erfle, Do
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: NO. 6180604tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                   Local Similarity 100. ses 4; Conservative
                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/915,314 FILING DATE: 20-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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    INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                      amino acid
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Fraser, Janet R.
West, Michael H.P.
McNicol, Patricia J.
VENTION: COMPOSITIONS
                                                        Taylor, Robert
Erfle, Douglas
                                                                                       Krieger, Timothy J.
                                                                                                                                    Application US/09030619B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
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West, Michael H.P.
Krieger, Timothy J.
Taylor, Robert
Erfle, Douglas
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                                                                                                                                                                                                                                                                                                                                                                                     13 amino acids
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100.0%;
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Pred. No
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 AND METHODS FOR TREATING
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ches 0;
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SEQ ID NO 35
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Indolicidin Analogue US-09-030-619-35
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Best Local Similarity 100.
Conservative
Query Match
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TITLE OF INVENTION:
FILE REFERENCE: 660
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CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: NO. 6538106tenburg Ph.D., Carol
REGISTRATION UNMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quence 34, Application US/09667486 tent No. 6538106 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PAtentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fraser,
                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/915,314 FILING DATE: 20-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/667,486 FILING DATE: 22-Sep-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
                                                                            STRANDEDNESS:
TOPOLOGY: 11nd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                              LENGTH:
                                                       DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taylor, Robert
Erfle, Douglas
COMPOSITIONS AND METHODS FOR TREATING
NVENTION: COMPOSITIONS USING ANALOGUES OF INDOLICIDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krieger, Timothy J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EE: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                               13 amino acids
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100.0%; Pred. No.
Live 0; Mismatc
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                                                                                           <Unknown>
 Score 36;
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 DB 4; Length 13;
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US-08-279-058B-10; Sequence 10, Appli; Patent No. 5668004
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US-09-355-166-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5668004
GENERAL INFORMATION:
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Best Local (
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CURRENT FILING DATE: 1999-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes FILE REFERENCE: GC511-PCT
                                                                      TELEFAX: (203)268-1951 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 19
TYPE: PRT
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                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                          SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acid
                                                                                                REFERENCE/DOCKET NUMBER: CR. TELECOMMUNICATION INFORMATION: TELEPHONE: (203)268-1951
                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
MOLECULE TYPE:
                                                                                                                                             NAME: George M. Yahwak
REGISTRATION NUMBER: 2
                                                                                                                                                                                                    APPLICATION NUMBER: US/08/279,058B FILING DATE:
                                                                                                                                                                                                                                                OPERATING SYSTEM:
SOFTWARE: Microsc
                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                              STREET:
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               ropology:
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25 Skytop Drive
                                             334 amino acids
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                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Michael E. O'Donnell
VENTION: DNA POLYMERASE III
                                                                                                                                                                                                                                              Microsoft Word 4.0
                                                                                    (203)268-1951
                                                                                                                                                                                                                                                                            Macintosh
                linear
                                                                                                                                                                                                                                                                                           Floppy disk
peptide
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                                                                                                                                             26,824
                                                                                                                                 CRF D-1056CIP
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Pred. No.
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RESULT 12
US-09-134-078-62
; Sequence 62, Application US/09134078
; Patent No. 6368844
; GENERAL INFORMATION:
    APPLICANT: Bylina, Edward J.
    APPLICANT: Bylina, Edward J.

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                                                                                                                                                                                                                                                                     ; ORGANISM: Chlamydia pneumoniae US-09-198-452A-1132
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US-09-198-452A-1132
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US-08-828-323-10
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US-08-828-323-10
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                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SEQ ID NO 1132
LENGTH: 679
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Griffals, R.
APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, frac
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis,
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: DNA POLYMERASE III HOLOENZYME FILE REFERENCE: 19603/L0214 CURRENT APPLICATION NUMBER: US/08/828,323A CURRENT FILING DATE: 1997-03-28 NUMBER OF SEQ ID NOS: 60 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1132, Application US/09198452A
Patent No. 6559294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: O'Donnell, Michael
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                      Query Match
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Best Local :
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                                                                                                                                                                                                                        Local
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                                                                                                                                            28 WYPW 31
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100.0%; Pr
 Edward J.
GLYCOSIDASE ENZYMES
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100.0%; Pred. No.
tive 0; Mismatc
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Pred. No.
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Pred. No.
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; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-27442
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US-09-252-991A-27442
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; FRAGMENT TYPE:
US-09-134-078-62
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
FILE REFERENCE: 107196.136
                                                                                                                            SEQ ID NO 27442
LENGTH: 705
               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27442, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                 PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
RAPPLICATION NUMBER: 08/949,026
FILING DATE: 10-CCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                              TYPE: PRT
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OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/024002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 4365 Exe
CITY: San Diego
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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)GY: linear
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               Score 36; I
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Pred. No.
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SOFTWARE: FastSEQ for W1
SEQ ID NO 4
LENGTH: 212
TYPE: PRT
ORGANISM: homo sapiens
US-08-860-255A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Smith, Ward
APPLICANT: Shao, Baoguang
TITLE OF INVENTION: Method of Inhibiting Catl
FILE REFERENCE: P50574-X1
CURRENT FILING DATE: 1997-06-26
CURRENT APPLICATION NUMBER: 00/008,108
PRIOR FILING DATE: 1995-10-30
PRIOR FILING DATE: 1995-11-22
PRIOR APPLICATION NUMBER: 60/008,992
PRIOR APPLICATION NUMBER: 60/0013,748
PRIOR FILING DATE: 1995-12-21
PRIOR APPLICATION NUMBER: 60/013,748
PRIOR FILING DATE: 1996-03-20
PRIOR APPLICATION NUMBER: 60/013,747
PRIOR APPLICATION NUMBER: 60/017,455
PRIOR APPLICATION NUMBER: 60/017,892
PRIOR APPLICATION NUMBER: 60/020,478
PRIOR FILING DATE: 1996-05-17
PRIOR APPLICATION NUMBER: 60/020,478
PRIOR FILING DATE: 1996-05-17
PRIOR APPLICATION NUMBER: 60/022,047
PRIOR FILING DATE: 1996-07-22
DPTOR APPLICATION NUMBER: 60/022,047
PRIOR FILING DATE: 1996-07-22
DPTOR APPLICATION NUMBER: 60/023,494
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
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                             APPLICANT: Mottez, Estelle
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods
TITLE OF INVENTION: Determinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT:
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ADDRESS:
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1996-08-07
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Pred. No. 1.4e+02;
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Query Match
Best Local Similarity
Tatches 4; Conserve
Job time
 Search completed: August 20, 2003, 12:44:22 Job time : 5.15663 secs
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acid
                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: POTTET, Jane E. R.
REGISTRATION NUMBER: 33;
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                   LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS-MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                    1 NGWYPW 6
                                                                    3 SGWVPW 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Dunner
1300 I Street, N.W., Suite 700
                                                                                                                                      Conservative
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Pred. No. 1
                                                                                                                                      Mismatches
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                                                                                                                                                    DB 2;
1.8e+02;
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Result
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
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1: //ggn2_6/ptodata/I/pubpaa/U
2: //ggn2_6/ptodata/I/pubpaa/U
3: //ggn2_6/ptodata/I/pubpaa/U
4: //ggn2_6/ptodata/I/pubpaa/U
5: //ggn2_6/ptodata/I/pubpaa/U
6: //ggn2_6/ptodata/I/pubpaa/U
6: //ggn2_6/ptodata/I/pubpaa/U
8: //ggn2_6/ptodata/I/pubpaa/U
9: //ggn2_6/ptodata/I/pubpaa/U
10: //ggn2_6/ptodata/I/pubpaa/U
11: //ggn2_6/ptodata/I/pubpaa/U
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11: //ggn2_6/ptodata/I/pubpaa/U
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12: //ggn2_6/ptodata/I/pubpaa/U
13: //ggn2_6/ptodata/I/pubpaa/U
14: //ggn2_6/ptodata/I/pubpaa/U
15: //ggn2_6/ptodata/I/pubpaa/U
16: //ggn2_6/ptodata/I/pubpaa/U
17: //ggn2_6/ptodata/I/pubpaa/U
18: //ggn2_6/ptodata/I/pubpaa/U
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1 NGWYPW 6
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 summaries
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'/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
'/cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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'/cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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12 US-10-015-387A-390
12 US-10-006-130A-390
12 US-10-199-672-376
12 US-10-199-672-376
12 US-10-194-457-376
14 US-10-194-457-376
15 US-10-174-596-376
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17 US-10-174-598-376
18 US-10-174-5737-376
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US-10-156-761-7581
US-10-183-708-92
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Sequence 32, Appl
Sequence 92, Appl
Sequence 42284, A
Sequence 390, App
Sequence 390, App
Sequence 390, App
Sequence 376, App
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0-174-576-37	-10-173-705-37	-10-173-697-37	3-695-37	-10-176-991-37	-10-184-658-37	-10-176-993-37	-10-176-992-37	-10-176-987-37	-10-176-985-37	-10-176-750-37	-10-176-747-37	-10-176-492-37	0-176-488-37	-10-175-743-37	-10-175-740-37	-10-175-739-37	-10-174-588-37	-10-174-582-37	-10-174-579-37	-10-174-572-37	-10-173-700-37	-10-180-557-37	-10-180-552-37	-10-176-913-37	0-176-757-37	-10-176-482-37	-175-752-37	-10-175	3-706-37
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ALIGNMENTS

RESULT 1 US-09-300-425B-32

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; OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B; OTHER INFORMATION: antibody clone US-09-300-425B-32
B
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SEQ ID NO 32
LENGTH: 6
TYPE: PRT .
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                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NERI, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: VIII, Francesca
APPLICANT: BIRCHLER, Manfred
APPLICANT: BIRCHLER, Manfred
APPLICANT: BIRCHLER, MANFRED
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
TITLE OF INVENTION: ANGIOGENESIS
FILE REFERENCE: SCH-1733P1
CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28
CURRENT FILING DATE: 1999-04-28
CURRENT FILING DATE: 1999-04-28
                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
                                                                                                       Local
                      1 NGWYPW 6
                                                                                  6; Conserv
                                                                                                                                                                                                                                                                                                                                                   PatentIn Ver. 2.1
                                                                                    Conservative
                                                                                                       100.0%; Score 48; DB 11; 100.0%; Pred. No. 4.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                      09/075,338
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RESULT

US-10-156-761-7581

INFORMATION:

, Application US/10156761

US20030119018A1

OMURA, SATOSHI IKEDA, HARUO

APPLICANT:

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RESULT 4
US-09-864-761-42284
Sequence 42284, Application US/09864761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Drosophila Melanogaster US-10-183-708-92
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US-10-156-761-7581
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: AXEL, RICHARD
TITLE OF INVENTION: GENES ENCODING INSECT ODORANT RECEPTORS AND USES THEREOF
FILE REFERENCE: 0575/58715-AA-PCT-US/JPW/ADM/BJA
CURRENT APPLICATION NUMBER: US/10/183,708
CURRENT FILING DATE: 2002-06-25
CURRENT FILING DATE: 70 00 002-3 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/932,227
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: PCT/US00/04995
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 09/257,706
PRIOR FILING DATE: 1999-02-25
NUMBER: 1999-02-25
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ENGTH: 318
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HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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83.3%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40;
Pred. No.
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53;
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US-09-864-761-42284
                       Query Match
Best Local
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                           OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.0THER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.4 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1 OTHER INFORMATION: EXPRESSED IN BOULT LIVER, SIGNAL = 0.0THER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.0THER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/236,359
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                                                                                                                                                        OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: MAP TO AC018720.2
                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 2000-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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Hanzel, David K.
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79.2%; ilarity 66.7%; Conservative
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CURRENT FILING DATE: 2001-09-04
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TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C1
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OR FILING DATE: 1998-09-01
OR APPLICATION NUMBER: 60/098723
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OR APPLICATION NUMBER: 60/098749
OR FILING DATE: 1998-09-01
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DR FILING DATE: 1998-09-09
DR APPLICATION NUMBER: 60/09598
DR FILING DATE: 1998-09-09
DR APPLICATION NUMBER: 60/099602
DR FILING DATE: 1998-09-09
           DR FILING DATE: 1998-09-10

PR APPLICATION NUMBER: 60/099808

PR FILING DATE: 1998-09-10

PR APPLICATION NUMBER: 60/099812

PR FILING DATE: 1998-09-10

PR APPLICATION NUMBER: 60/099815

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Gao, Wei-Qiang
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Williams, P. Mickey
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    Nicholas F
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Kenneth J.
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RESULT 6
US-10-015-387A-390
; Sequence 390, Application US/10015387A
; Publication No. US20030135034A1
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Best Local Similarity
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OR FILING DATE: 1998-10-07

DR APPLICATION NUMBER: 60/103315

DR FILING DATE: 1998-10-07

DR APPLICATION NUMBER: 60/10328

DR FILING DATE: 1998-10-07

DR APPLICATION NUMBER: 60/103395

DR FILING DATE: 1998-10-07

DR APPLICATION NUMBER: 60/103396

DR FILING DATE: 1998-10-07

DR APPLICATION NUMBER: 60/103396

DR FILING DATE: 1998-10-07
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OR FILING DATE: 1998-10-07
OR PRICE TO THE TO 
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OR FILING DATE: 1998-10-01
OR APPLICATION NUMBER: 60/102965
OR FILING DATE: 1998-10-02
OR APPLICATION NUMBER: 60/103258
OR FILING DATE: 1998-10-06
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APPLICATION NUMBER: 60/105266
FILING DATE: 1998-10-22
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FILING DATE: 1998-10-21
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FILING DATE: 1998-09-30
APPLICATION NUMBER: 60/102684
FILING DATE: 1998-10-01
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APPLICATION NUMBER: 60/102570
FILING DATE: 1998-09-30
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FILING DATE: 1998-10-08
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83.3%;
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Pred. No. 1.4e+02;
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Conservative

Mismatches

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Gaps

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Prior Application removed -
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 390
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
US-10-006-130A-390
Query Match
Best Local Similarity
---hes 5; Conserve
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Best Local S
Matches 5
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NUMBER OF SEQ ID NOS: 477
SEQ ID NO 390
LENCTH: 146
TYPE: PRT
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                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/006,130A CURRENT FILING DATE: 2002-03-19
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C54
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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Gao, Wei-Qiang
Goddard, Audrey
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                                                                                                                                                                                                                                                        Paoni, Nicholas F.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth J.
                                                                                                                                                                                                                                                                                                                                          Gao, Wei-Qiang
Goddard, Audrey
                                                                                                                                                                                                                                                                     Pan, James
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Desnoyers, Luc
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                                                                                                                                                                                                                                                                                                                                                                         Sherman
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                           79.2%;
83.3%;
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                           Score 38;
Pred. No.
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Pred. No. 1.4e+02;
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                              1.4e+02;
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                                         Length 146;
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RESULT 8
US-10-199-672-376
; Sequence 376, A
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                                                       US-10-006-172A-390
Sequence 390, Application US/10006172A
Diblication No. US20030153000A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P
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Best Local S
Matches 5
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SEQ ID NO 376
LENGTH: 146
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APPLICANT:
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PRIOR FILLING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
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APPLICANT:
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 APPLICANT:
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FILING DATE: 1997-10-28
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FILING DATE: 1997-10-28
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FILING DATE: 1997-10-28
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FILING DATE: 1997-10-24
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5; Conserv
          Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan 1.
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Watanabe, Colin K.
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Ferrara,
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Pred. No. 1.4e
0; Mismatches
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1.4e+02;
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CURRENT APPLICATION NUMBER: US/10/006,172A CURRENT FILING DATE: 2002-03-19 PRIOR APPLICATION NUMBER: 60/098716 PRIOR FILING DATE: 1998-09-01 PRIOR APPLICATION NUMBER: 60/098723 PRIOR FILING DATE: 1998-09-01 PRIOR FILING DATE: 1998-09-01
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APPLICATION NUMBER: 60/
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Goddard, Audrey
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Hillan, Kenneth J.
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Grimaldi, Christopher
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     INVENTION: SEC
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Chen, Jian
                              Smith, Victoria
Watanabe, Colin F
Wood, William I.
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SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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APPLICATION NUMBER: 60/101279 FILING DATE: 1998-09-22 APPLICATION NUMBER: 60/101071 FILING DATE: 1998-09-18

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APPLICATION NUMBER: 60/102330
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APPLICATION NUMBER: 60/102240 FILING DATE: 1998-09-29 APPLICATION NUMBER: 60/102307

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APPLICATION NUMBER: 60/102207
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FILING DATE: 1998-09-24
APPLICATION NUMBER: 60/101743
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APPLICATION NUMBER: 60/101479 FILING DATE: 1998-09-23

APPLICATION NUMBER: 60/101738

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APPLICATION NUMBER: 60/101476

FILING DATE: 1998-10-01 APPLICATION NUMBER: 60/102687 FILING DATE: 1998-10-01

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APPLICATION NUMBER: 60/102965 FILING DATE: 1998-10-02

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OR APPLICATION NUMBER: 60/101014
OR FILLING DATE: 1998-09-18
OR APPLICATION NUMBER: 60/101068
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US-10-187-749-376
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SEQ ID NO 376
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                            PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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CURRENT FILING DATE: 2002-07-01
                                                                                                                                                PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
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CURRENT FILING DATE: 2002-07-11
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APPLICATION NUMBER: 60/063486
FILING DATE: 1997-10-21
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FILING DATE: 1997-09-18
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APPLICATION NUMBER: 60/063120 FILING DATE: 1997-10-24
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US-10-052-586-376
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NUMBER OF SEQ ID N
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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PRIOR FILING DATE: 1997-10-28
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TYPE: PRT
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PRIOR FILING DATE: 1997-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: P3430R1C1
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FILING DATE: 1997-10-28
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FILING DATE: 1997-10-21
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                            APPLICATION NUMBER: 60/
PTI ING DATE: 1997-10-31
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                                                                                                       FILING DATE: 1997-10-28
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MBER: 60/064103
997-10-31
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Pred. No. 1.4e+02;
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DR APPLICATION NUMBER: 60/065311
DR FILLING DATE: 1997-11-13
DR APPLICATION NUMBER: 60/066120
DR FILLING DATE: 1997-11-21
DR APPLICATION NUMBER: 60/066466
DR FILLING DATE: 1997-11-24

APPLICATION NUMBER: 60/066772 FILING DATE: 1997-11-24

OR APPLICATION NUMBER: 60/69335
OR FILING DATE: 1997-12-11
OR APPLICATION NUMBER: 60/069425
OR FILING DATE: 1997-12-12
OR APPLICATION NUMBER: 60/069870
OR FILING DATE: 1997-12-17
OR APPLICATION NUMBER: 60/68017
OR APPLICATION NUMBER: 60/07450
OR FILING DATE: 1997-12-18
OR APPLICATION NUMBER: 60/077450
OR FILING DATE: 1998-03-10
OR APPLICATION NUMBER: 60/077632

DR FILING DATE: 1998-03-20
DR APPLICATION NUMBER: 60/079664
DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/079786
DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/080107
DR APPLICATION NUMBER: 60/080107
DR FILING DATE: 1998-03-31

APPLICATE: 1998-04-00
FILING DATE: 1998-04-00
APPLICATION NUMBER: 60/0
DATE: 1998-04-09

60/081195

FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/081049 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/080333

APPLICATION NUMBER: 60/080327 APPLICATION NUMBER: 60/080194 FILING DATE: 1998-03-31

APPLICATION NUMBER: 60/081070

FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081838
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082568
FILING DATE: 1998-04-21

APPLICATION NUMBER: 60/082569 FILING DATE: 1998-04-21

APPLICATION NUMBER: 60/082704 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082797

OR FILING DATE: 1998-03-11

OR APPLICATION NUMBER: 60/077649

OR FILING DATE: 1998-03-11

OR APPLICATION NUMBER: 60/078886

OR FILING DATE: 1998-03-20

OR APPLICATION NUMBER: 60/078939

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1998-06-12 NUMBER: 60/089 1998-06-16	1998-06-1 NUMBER: 60) F (NUMBER 1998-	1998-06-11		7 2 2	1998-06-10 NUMBER: 60/088826	NUMBER: 60/088825	NUMBER: 60/088824	1998-06-10	998-06-10	.998-06-10 MBER: 60/08874	NUMBER: 60/088738	NUMBER: 60/088722	NUMBER: 60/088655	NUMBER: 60/088326 : 1998-06-04	.998-06-05	998-06-05	: 1998-06-05 NUMBER: 60/088212	MBER: 60	NUMBER: 60/088167	NUMBER: 60/088033 : 1998-06-04	998-06-04	1998-06-04	: 1998-06-04 NUMBER: 60/088028	NUMBER: 60/088025	NUMBER: 60/087827	NUMBER: 60/087759	L998-06-02	1998-05-28	1998-05-28	IMBER: 60/08	JMBER: 60	NUMBER: 60	1: 1998-05-18	1998-05-15	1998-05-1 NUMBER: 60	NUMBER: 60	NUMBER: 60	1998-05-15	05-15	ER:

PRIOR APPLICATION NUMBER: 60/0 PRIOR FILING DATE: 1998-05-06 PRIOR APPLICATION NUMBER: 60/0

NUMBER: 60/084639 1998-05-07

R FILING DATE: 1998-05 R APPLICATION NUMBER: R FILING DATE: 1998-05 R APPLICATION NUMBER:

1998-05-07

60/084643 60/084640 PRIOR

APPLICATION NUMBER: 60/083559
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/084366
FILING DATE: 1998-05-05
APPLICATION NUMBER: 60/084414

APPLICATION NUMBER: 60/083499 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083496 FILING DATE: 1998-04-29

APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/083495
FILING DATE: 1998-04-29

FILING DATE: 1998-04-22

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RESULT 14
US-10-176-758-376
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-590-376
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Coddard, Audrey
APPLICANT: Goddwski, Paul
APPLICANT: Godowski, Paul
APPLICANT: Gurney, Austin I
APPLICANT: Ban, James
APPLICANT: Watanabe, Colin
APPLICANT: Watanabe, Colin
APPLICANT: Watanabe, Colin
APPLICANT: Watanabe, Colin
APPLICANT: Zhang, Zemin
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PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
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CURRENT FILING DATE: 2002-06-18
Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 376
                                                                                                                                                                                                      Sequence 376, Application US/10176758 Publication No. US20030008353A1
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Best Local Similarity 83.3%;
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APPLICANT:
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Godowski, Paul J.
Gurney, Austin L.
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                                                  Pan, James
Smith, Victoria
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Godowski, Paul J.
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83.3%;
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Pred. No. 1.4e+02;
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Search completed: August 20, 2003, 13:16:47 Job time: 7.50602 secs
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Best Local Similarity
"atches 5; Conserv
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CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or NUMBER OF SEQ ID NOS: 612
SEQ ID NO 376
LENGTH: 146
TYPE: PRT
ORGANISM: Homo Sapien
US-10-175-737-376
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US-10-175-737-376
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US-10-176-758-376
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul :
APPLICANT: Gurney, Austin I
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 376
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Best Local S
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/176,758 CURRENT FILING DATE: 2002-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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TYPE: PRT
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                                                                  48 NGWYIW 53
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                             Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                                                                                                         Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/10175737 o. US20030013153A1
                                                                                                                                   Conservative
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83.3%;
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                                                                                                                                                 Score 38; DB 15;
Pred. No. 1.4e+02;
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0; Mismatches 1
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                                                                                                                                                                 Length 146;
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Perfect score:
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Listing first 45 summaries
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Maximum DB
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length: 2000000000
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48
1 NGWYPW 6
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Gapop 10.0 , Gapext 0.5
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1: /cgn2_6/ptodata/1/paa/I
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 US-09-075-338C-32
US-09-300-425B-32
                                                                                                                SUMMARIES
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                                                      Description
Sequence 32, Appl
Sequence 32, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-075-338C-32
                                                                                                                                               SOFTWARE: P
SEQ ID NO 32
LENGTH: 6
TYPE: PRT
                                                                                                                                                                                                                                                                                               Sequence 32, Application US/09075338C
GENERAL INFORMATION:
APPLICANT: NERI, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfred
TITLE DETERMINENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY
Query Match
Best Local Similarity
                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/075,338C CURRENT FILING DATE: 1998-05-11 NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                     FILE REFERENCE: SCH-1733
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ALIGNMENTS

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; ORGANISM: Artificial Sequence; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B; OTHER INFORMATION: antibody clone
US-09-075-338C-32
                                                                                                                                                                                                                           PatentIn Ver. 2.1
100.0%;
Score 48; DB 14;
Pred. No. 5.2e+06;
                     Length 6;
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Matches

6,

Conservative

0;

Mismatches

0;

Indels

0;

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SEQ ID NO 32
LENGTH: 6
Query Match
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                                                                                                                                                                                                                         PRIOR EPILING DATE: 1999-04-28
PRIOR EPILING DATE: 1998-05-11
NUMBER OF SPO
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APPLICANT: VITI, FRANCESCA
APPLICANT: VITI, FRANCESCA
APPLICANT: BIRCHLER, Manfred
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
TITLE OF INVENTION: ACCOMPAINING THEM AND THERAPBUTIC METHOD FOR TREATMENT OF
TITLE OF INVENTION: ACCOMPAINING THEM AND THERAPBUTIC METHOD FOR TREATMENT OF
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                                                                                                                                                                                                                                                                               FILE REFERENCE: SCH-1733P2
CUTRENT APPLICATION NUMBER: US/09/512,082
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 09/300,425
PRIOR FILING DATE: 1999-04-28
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PRIOR FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 34
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CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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TYPE: PRT
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                                                                     OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                          ORGANISM: Artificial Sequence FEATURE:
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nes 6; Conserv
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VITI, Francesca
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                                                                     Description of Artificial Sequence: anti-ED-B antibody clone
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100.0%; Pred. No. 5.2e+06;
tive 0; Mismatches 0;
             100.0%;
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             Score 48;
             DB
             19;
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Query Match
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US-09-791-537-78362
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                                                                                                                              US-10-156-761-7581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      us-10-156-761-7581
                                                                                                                                                              ; SEQ ID NO 7581
; LENGTH: 318
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 78362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7581, Application US/10156761
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                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                          APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DARKEY, JOSEPH TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Josep
                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 15109
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TYPE: PRT
                                                                                                                                             ORGANISM: Streptomyces avermitilis
106 SCWYPW 111
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                              1 NGWYPW 6
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HORIKAWA, HIROSHI
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                                                            Conservative
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                                                            Score 43; DB 27;
Pred. No. 4.2e+02;
1; Mismatches 0
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; Mismatches 0;
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RESULT 6

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GENERAL INFORMATION:
APPLICANT: MATE J. Rubenfield et al.
APPLICANT: MATE J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/10/419,128
CURRENT FILING DATE: 2003-04-21
CURRENT FILING DATE: 2003-04-21
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Best Local :
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LENGTH: 115
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Best Local 9
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 261895
TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/09/252,991
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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APPLICANT: La Rosa Thomas J
                                                                                                               APPLICANT: La Rosa, Thomas
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
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5; Conserv
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                                                                               Kovalic, David K. Zhon value
                                                                       Zhou, Yihua
Barbazuk, Brad
             Boukharov, Andrey A.
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                                                   Yongwei
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100.0%;
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Pred. No.
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1.5e+02;
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US-10-424-599-191909
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SEQ ID NO 33650
LENGTH: 562
TYPE: PRT
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TITLE OF INVENTION: Face Nucleic Acid Molecules and Other Molecules Associated Wit
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 144814
LENGTH: 179
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Best Local Similarity
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                                                                    NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 191909
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                                                                                                    APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES FILE REFERENCE: 21272-049 CURRENT APPLICATION NUMBER: PCT/US01/08631 CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/649,167 PRIOR FILING DATE: 2000-08-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: PAT_MRT4530_45594C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Oryza sativa
ORGANISM: Glycine max FEATURE:
                                  LENGTH: 203
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity es 5; Conserv
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Kovalic David K
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0; Mismatches
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3.6e+02;
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9.3e+
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                                                ; ORGANISM: Anopheles gambiae PCT-US02-28315-76
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Query Match
Best Local Similarity
                                                                                SOFTWARE: PatentIn version 3.0 SEQ ID NO 76 . LENGTH: 393 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 76, Applica GENERAL INFORMATION:
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Best Local
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LENGTH: 219
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GENERAL INFORMATION
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PRIOR FILING DATE: 2001-09-04
NUMBER OF SEQ ID NOS: 97
                                                                                                                                                                                            CURRENT APPLICATION NUMBER: PCT/US02/28315
CURRENT FILING DATE: 2002-09-04
                                                                                                                                                                                                                            APPLICANT: KÍOŚS, Briań
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF INSECT Or83B ODORANT RECEPTOR
TITLE OF INVENTION: GENES AND USES THEREOF
FILE REFERENCE: 10657-005-228
                                                                                                                                                                                                                                                                                             APPLICANT:
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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CURRENT FILING DATE: 2003-0
NUMBER OF SEQ ID NOS: 285684
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Glycine max
FEATURE:
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LOCATION: (1)..(
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Kloss, Brian
                                                                                                                                                                                                                                                                                                           Ong, Jane
                                                                                                                                                                                                                                                                                                                          Lee,
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Pred. No.
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7.9e+02;
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           Length 393;
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RESULT 15
US-10-183-708-92
; Sequence 92, Application US/10183708
; GENERAL INFORMATION:
; APPLICANT: VOSSHALL, LESLIE
; APPLICANT: AMREIN, HUBERT
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                                                                                                                                                                                                                                                   ; LENGTH: 403
TYPE: PRT
; ORGANISM: Drosophila Melanogaster
US-09-932-227-92
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Best Local Similarity
""" by Conserv.
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 92
                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0 SEQ ID NO 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 92, Applica GENERAL INFORMATION:
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Best Local
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CURRENT ELILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: PCT/US00/04995
PRIOR FILLING DATE: 2000-02-25
NUMBER OF SEO TO
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TITLE OF INVENTION: GENES ENCODING INSECT ODORANT RECEPTORS AND USES THEREOF

FILE REFERENCE: 0575/58715-A-PCT-US/JPW/ADM/BJA

CURRENT APPLICATION NUMBER: US/09/932,227

CURRENT FILING DATE: 2001-08-17
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US00/04995
PRIOR FILING DATE: 2000-02-25
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 108
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APPLICANT: AMREIN, HUBERT
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APPLICANT: AMREIN,
APPLICANT: AXEL, R:
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TYPE: PRT
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                                                                                                                           176 NTWYPW 181
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Minimum DB seq
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compus
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/cgn2_6/ptcdata/1/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptcdata/1/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptcdata/1/paa/US09_NEW_COMB.pep:*
/cgn2_6/ptcdata/1/paa/US09_NEW_COMB.pep:*
/cgn2_6/ptcdata/1/paa/US00_NEW_COMB.pep:*
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US-10-603-114-765A-879
US-10-603-114-76-6025
US-10-10-808-808A-6025
US-10-308-808A-6025
US-10-308-808A-6025
US-10-308-808A-6025
US-10-308-808A-6025
US-10-308-808A-6025
US-10-31-3114-6107
US-10-23-244-3518
US-10-23-244-3518
US-10-23-244-3518
US-10-23-344-3518
US-10-603-114-64629
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US-10-603-114-64629
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PCT-US03-10753-40
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Best Local :
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Sequence 6	Sequence 2	Sequence 3	Sequence 1	Sequence 5	Sequence 1	Sequence 3	Sequence 1	Sequence 1	Sequence 7	Sequence 2	Sequence 1	Sequence 1	Sequence 1	Sequence 1				
6716, Ap	29, Appl	39, Appl	137, Ap	771, Ap	100, App	138, Ap	1772, Ap	5399, Ap	1545, Ap	, Appli	18, Appl	17, Appl	7981, Ap	24, Appl	166, App	•	10, Appl	1442, AP

ALIGNMENTS

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Sequence 37, Application PC/TUS0310753

GENERAL INFORMATION:
APPLICANT: Shockey, Jay M.
APPLICANT: Shockey, John A.
APPLICANT: Browse, John A.
TITLE OF INVENTION: Plant Acyl-CoA Synthetases
FILE REFERENCE: DOM-07655

CURRENT APPLICATION NUMBER: PCT/US03/10753

CURRENT APPLICATION NUMBER: 10/119,136

PRIOR APPLICATION NUMBER: 10/119,136

PRIOR APPLICATION NUMBER: 10/410,031

PRIOR APPLICATION NUMBER: 10/410,031

PRIOR APPLICATION NUMBER: 10/410,031

PRIOR FILING DATE: 2003-04-09

PRIOR APPLICATION NUMBER: 10/410,031

PRIOR FILING DATE: 2003-04-09

NUMBER OF SEVEN
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CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: 10/19,136
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 10/410,031
PRIOR PILING DATE: 2003-04-09
NUMBER OF SEQ ID NOS: 187
SOFTMARE: Patentin version 3.2
SEQ ID NO 40
LENGTH: 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Arabidopsis thaliana PCT-US03-10753-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 40, Application PC/TUS0310753
GENERAL INFORMATION:
APPLICANT: Shockey, Jay M.
APPLICANT: Schnurr, Judy
APPLICANT: Browse, John A.
TITLE OF INVENTION: Plant Acyl-CoA Synthetases
FILE REFERENCE: DOW-07655
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 NGWTYPW 242
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6; Conserv
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85.7%;
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Pred. No. 1e+02;
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CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 878
LENGTH: 258
TYPE: PRT
RGANISM: Homo sapiens
US-10-408-765A-878
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US-10-408-765A-2774
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Best Local Similarity
"~+~hes 6; Conserva
Query Match
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APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradfor
APPLICANT: Taylor, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2774
LENGTH: 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 37
LENGTH: 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILLE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
RUMBER OF SEQ ID NOS: 3077
                                                                                                                                                                                                               APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
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85.7%;
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Pred. No. 1.2e+02;
             Score 36;
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Pred. No. 1.1e+02;
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RESULT 7
PCT-US03-07174-20
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1572
; LENGTH: 258
; TYPE: PRT
; ORGANLSM: Homo sapiens
US-10-408-765a-1572
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LENGTH: 330
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: GARY BRETON
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 199-04-09
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/603,114
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US/09/543,681
PRIOR FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRATITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WAIDOCK, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/408,765A CURRENT FILING DATE: 2003-04-04
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APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ghosh, Soumitra APPLICANT: Fahy, Eoin D.
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Conservative (
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                                                                                                                                                     75.0%; Score 36; 100.0%; Pred. No.
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hes 0;
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APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules And
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53373)A
CURRENT APPLICATION NUMBER: US/10/612,783
CURRENT FILING DATE: 2003-07-02
                                                                                                                                                                                                                                                       US-10-612-783-4924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_6952C.1.pep US-10-612-783-6923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Anopheles gambiae PCT-US03-07174-20
                                                                                                                                                                                                                     Sequence 4924, Applic GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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Best Local Similarity
Matches 4; Conserv
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TYPE: PRT
ORGANISM: Oryza sativa
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                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(5373)A CURRENT APPLICATION NUMBER: US/10/612/783 CURRENT FILING DATE: 2003-07-02 NUMBER OF SEQ ID NOS: 7098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: N9267
CURRENT APPLICATION NUMBER: PCT/US03/07174
CURRENT FILING DATE: 2003-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                         417 WYPW 420
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ilarity 100.0%;
Conservative (
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Pred. No.
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US-10-286-897-2453
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SEQ ID NO 2453
LENGTH: 634
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Best Local
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Matches 4
            APPLICANT: Hyseq Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784FLPCT
CURRENT APPLICATION NUMBER: US/10/258,898A
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR FILING DATE: 2000-01-21
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PRIOR APPLICATION NUMBER: US09/552,317
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PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US/09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
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LOCATION: (1)...(481)
OTHER INFORMATION: unsure at all xaa locations
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US-10-258-898A-2453
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APPLICANT: BAUGHN, Mariah R.

TITLE OF INVENTION: AMINOACYL TRNA SYNTHETASES
FILE REFERENCE: PI-0323 PCT
CURRENT APPLICATION NUMBER: US/10/450,727
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: 60/255,963
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 2
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US-10-408-765A-2458
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; OTHER INFORMATION: Incyte
US-10-450-727-1
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SEQ ID NO 2453
LENGTH: 634
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Best Local (
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PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US09/693,036
PRIOR FILING DATE: 2000-10-19
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PRIOR FILING DATE: 2000-11-29
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APPLICANT: LEE, Ernestine A.
APPLICANT: BAUGHN, Mariah R.
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                                            APPLICANT:
                                                      APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
APPLICANT:
               APPLICANT
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Gibson, Bradford W. Taylor, Steven W. Glenn, Gary M.
                                            Zhang, Bing
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RESULT 15 US-10-258-898A-6025

Sequence 6025, Application US/10258898A
GENERAL INFORMATION:
APPLICANT: Hyseq Inc
APPLICANT: Hyseq Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784FLPCT

CURRENT APPLICATION NUMBER: US/10/258,898A

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, SEQ ID NO 2458
LENGTH: 1063
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2458
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; Sequence 6025, A
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Best Local
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SOFTWARE: pt_FL_genes_b
SEQ ID NO 6025
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NUMBER OF SEQ ID NOS: 3077
SOFTMARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
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PRIOR FILING DATE: 2000-09-14
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332 WYPW 335
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Pred. No.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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48
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ALIGNMENTS

RESULT 1 H64236 C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: H64236
A;Status: preliminary; nucleic acid sequence not shown; translation not shown hypothetical protein MG333 - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 19-May-2000
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 19-May-2000
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 19-May-2000
C;Accession: H64236
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleison, Fibrumann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A. δÃ C; Superfamily: acyl carrier protein phosphodiesterase A;Cross-references: GB:U39715; GB:L43967; NID:g1046026; PID:g1046036; TIGR:MG333 A;Experimental source: strain G-37 A; Molecule type: DNA A; Residues: 1-126 <TIGR> 멍 A; Genetic code: SGC3 Query Match Best Local Similarity Genetics: Matches 68 2 GWYPW 6 5 GWYPW 72 Conservative 87.5%; Score 42; Pred. No. 0 Mismatches , e <u>ب</u> 0 Length 126 Clayton, R.A.; Fleischmann, R. D.M.; Phillips, C.A.; Merrick, Indels 0 Gaps 0

hypothetical protein HI1366 - Mycoplasma pneumoniae (strain ATCC 29342) N;Alternate names: hypothetical protein PO1_orf197

C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb_1997 #sequence_revision 25-Apr-1997 #text_change 17-Mar-2000

B.C.; Herrmann,

G;Date: 4/1200 APR G; Plagens, H.; Pirkl, E.; Li, B.C.; Her G;Accession: S73688 R; Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Her Rydicleic Acids Res. 24, 4420-4449, 1996.

A;Title: Complete sequence analysis of the genome of the bacterium M; A; Reference number: S73327; MUID:97105885; PMID:8948633 A;Accession: S73688 A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-197 <HIM>
A;Residues: 1-197 <HIM>
A;Cross-references: EMBL:AE000034; GB:U00089; NID:g1674031; PIDN:AAE A;Cross-references: EMBL:AE000034; GB:U00089; NID:g1674031; PIDN:AAE Mycoplasma pneumon

NID:g1674031; PIDN:AAB96010.1; to the EMBL Data Library, Novem

PID:g167 mber 1996

not shown

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A; Genetic code: SGC3 C; Superfamily: acyl carrier protein phosphodiesterase

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hypothetical protein [imported] - Brevibacterium linens C;SpecLes: Brevibacterium linens C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text C;Accession: T51117
                                                                                                     RESULT 5
T51117
                                                                                                                                                                                                                                                                                                                                                               hypothetical protein B2126_C2_219 - Mycobacterium C;Species: Mycobacterium leprae C;Jate: 19-Mar-1997 #sequence_revision 25-Apr-1997 C;Accession: S72858 R;Smith, D.R.; Robison, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
S72858
R;Krubasik, P.; Sandmann,
Mol. Gen. Genet. 263, 423
A;Title: A carotenogenic
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A;Title: The complete genome sequence of the murine respiratory A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: H90550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein MYPU_3120 [imported] - Mycoplasma pulmonis (strain UAB C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δõ
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                                                                                                                                                                                                                                                                                                               A; Accession:
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Pred. No.
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red. No. 23;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium leprae
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        Brevibacterium linens with novel lycopene
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RESULT 7
T22377
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S55490
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A;Residues: 1-456 <KRU>
A;Cross-references: EMBL:AF139916; PIDN:AAF65580.1
A;Cross-references: EMBL:AF139916; ATCC9175
                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-708 <WIL>
                                                                                                                                                                                                                           A; Reference number: A; Accession: T22377
                                                                                                                                                                                                                                           A; Reference number: 219556
                                                                                                                                                                                                                                                                                    C;Species: Caenorhabditis
C;Date: 15-Oct-1999 #seque
C;Caccession: T22377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein SPAC5H10.12c - fission yeast (Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 31-Jan-2000 C;Accession: T38976; S55490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: 225303; MUID:20279196; PMID:10821176
A;Accession: T51117
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                         A; Introns:
                                                                                                    A; Map position:
                                                                                                                                                     A; Experimental
                                                                                                                                                                                                  A;Molecule
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A; Residues: 1-371 <CO2>
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                                                                                                                                                                A; Cross-references: EMBL: 280789;
                                                                                                                                                                                                                                                                                                                                    hypothetical protein F48C11.2 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:Z49811; NID:g854599; PIDN:CAA89962.1; PID:g854611; A;Experimental source: strain 972h-; cosmid c5H10
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5; Conserv
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NGWYPW 6
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                                                                                                                                                                                                                                                                                                       #sequence_revision
                                                                                                                                                BL:280789; PIDN:CAB02551.1; clone F48C11
                                          81.2%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barrell, B.G.;
brary, May 1995
                            0;
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                           Score 39; DB 2;
Pred. No. 1.3e+02;
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Pred.
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Pred. No.
                                                                                                                                                                                                                                                            October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                       362/1;
                                                                                                                                                                                                                                                                                                       15-Oct-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70;
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60;
                                                                                       395/1;
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                                                                                                                                                                  GSPDB:GN00028; CESP:F48C11.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                       Length 708;
                                                                                       529/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M.A.; Walsh, S.V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371
                                                                                       547/2;
                                                                                                                                                                                                                                                                                                       18-Feb-2000
                            0;
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                                                                                         576/2;
                            Gaps
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696 NGWKPW 701

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RESULT 10
E90257
                                                                     hypothetical protein SSO1052 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C;Accession: E90257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RiTheologis, A: Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dew ansen, N.F.; Hughes, B.; Huzar, L.

Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T.

A; Althors: Salzberg, S.L.; Schwartz, J.R.; Senter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; PMID:11130712
       R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.;
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A;Cross-references: EMBL:AL021730; PIDN:CAA16831.1; GSPDB:GN00067; SPDB:SPBC4C3.09
A:Experimental source: strain 972h-; cosmid c4C3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: Z21910
A;Accession: T40488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;WOOd, V.; Rajandream, M.A.; Barrell, B.G.; submitted to the EMBL Data Library, February
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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C; Superfamily: pectinesterase
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A; Residues: 1-223 <STO>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: T23J18.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A86141; A; Accession: A86249
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                        313 GWFPW 317
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4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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80.0%;
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Pred. No.
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Pred. No. 61;
1; Mismatches
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1e+02;
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1998
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   Y.; Allard, G.; Awayez, M.J.; Cha
Peng, X.; Thi-Ngoc, H.P.; Redder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 223;
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                                 Chan
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C; Function:
A; Description:
                                                                     A;Gene: celH
                                                                                                       C; Genetics:
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R;Stover, C.K.; Pham, X.Q.; Erwin, A adman, S.; Yuan, Y.; Brody, L.L.; Col.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of A;Reference number: A82950; MUID:204: A;Accession: B83121
                                                                                                                             A; Molecule type: DNA
A; Residues: 1-540 <570>
A; Cross references: GB:AE004836; GB:AE004091; NID:g9950405; PIDN:AAG07585.1;
A; Experimental source: strain PAO1
C; Cenetics:
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                                                                                                                  A; Gene: PA4198
                                                                                                                                                                                                                                                                                                                            probable AMP-binding enzyme PA4198 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                              RESULT
B83121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-764 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der submitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: E90257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: Sulfolobus solfataricus
                                                                        Best
                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                      ; Accession:
                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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235 NGWCYPW 241
                                                                                                                                                                                                                                                                                                                                                                                                                                     74
                            1 NGW-YPW 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GWYPW 6
                                                       Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                       B83121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     GWFPW 78
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A99139
                                                                                                                                                                                                                              sequence of Pseudomonas aeruginosa
                                                                     78.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.
80.
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8
9
                                                      Score 37.5; Depred. No. 1.7e
0; Mismatches
                                                       0
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Pred. No.
                                                                                                                                                                                                                                                                                    Coulter, S.N.; Folger, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
1.9e+02;
0;
                                                                    DB 2;
1.7e+02;
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                                                                                 Length 540;
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A;Cross-references: GB:M31903; NID:g144773; PIDN:AAA23225.1; PID:g144774 A;Note: the authors translated the codon CAG for residue 863 as His C;Comment: Cellulase H is involved in the hydrolysis of cellulose and ar C;Comment: Cellulase H hydrolyzes carboxymethylcellulose, p-nitrophenyl-
                                                                                                                                                                           A;Reference number: JH0157; MUID:90323606; PMID:2197182 A;Accession: JH0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
JH0157
                                                                                                                                                                                                                                                                                                                              N;Alternate names: endo-1,4-beta-glucanase;
C;Species: Clostridium thermocellum
C;Date: 31-Dec-1991 #sequence_revision 31-be
C;Accession: JH0157
                                                                                                                           A; Molecule type: DNA
A; Residues: 1-900 < YAG>
                                                                                                                                                                                                                                             Gene 89, 61-67, 1990
A; Title: Nucleotide
                                                                                                                                                                                                                                                                                                   R;Yaguee, E.; Beguin, P.; Aubert, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                          cellulase (EC 3.2.1.4) H precursor - Clostridium thermocellum
                                                                                                                                                                                                                                                                                                                                                31-Dec-1991 #text_change
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      ellulose and arranged in cel p-nitrophenyl-beta-D-cellob
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1,4-beta-D-glucosidic linkages

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A;Pathway: cellulose degradation
C;Superfamily: Clostridium cellulase repeat homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-44/pomain: signal sequence #status predicted <SIG>
F;45-900/Product: cellulase H #status predicted <CEL>
F;309-324/Region: proline/serine/threonine-rich
F;631-654/Region: proline/serine/threonine-rich
F;633-856/Domain: Clostridium cellulase repeat homology <CCR1>
F;872-895/Domain: Clostridium cellulase repeat homology <CCR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
S43104
                                                                                                                                                                                                                                                                                                                                                                            R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, May 1999
A;Reference number: Z21609
A;Accession: T36541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
T36541
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submitted to the EMBL Data Library, March 199
A;Description: Cloning and expression of the
A;Reference number: $43104
A;Accession: $43104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           outer membrane protein class 5c - Neisseria meningitidis (fragment)
C;Species: Neisseria meningitidis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-250 <GUI>
RESULT 15
                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-262 <MUR>
A; Cross-references: EMBL: ALO49754; PIDN: CAB42038.1; GSPDB: GN00070; SCOEDB: SCH10.29c
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                                                                                                                                                                                                                                           A; Gene:
                                                                                                                                                                                                                                                                                A; Experimental source: strain A3(2)
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                                                                                   141 GWHPW 145
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                                                                                                                          2 GWYPW 6
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Pred. No. 2.7e+02;
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Pred. No. 1e+02;
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A;Title: Cloning and expression in Escherichia coli of opc, the gene A;Reference number: A44611; MUID:92261288; PMID:1813777 A;Accession: A44611
                                                                                                                                                                                                                                                                                                                                                                                                             outer membrane protein class 5C precursor - Neisseria meningitidis (strain 23476)
C;Species: Neisseria meningitidis
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                            R;Olyhoek, A.J.M.; Sarkari, J.; Bopp, M.; Morelli, Microb. Pathog. 11, 249-257, 1991
                                                                                                   δÃ
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Search completed: August 20, Job time: 5.19277 secs
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                                                                                                                                                                                                                              C; Genetics:
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A; Cross-references: GB:M80195
                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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Best Local Similarity
                                                                      170 NGWYINPW 177
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      score greater than or equal to the score or the result אפער and is derived by analysis of the total score distribution.
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HOLB_YERPE
HNLS_SORBI
O69B_DROME
CBP2_WHEAT
CBP2_HORVU
RIK3_MOUSE
YP65_CAEEL
SYV_FUGRU
SYV2_HUMAN
V341_BPMD2
HB20_PAUTR
YNFH_ECOLI
INF7_ECOLI
I
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CP21_HORVU
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Compugen Ltd
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PNUC_SALTY	AAC2_MYCFO	RBB9 RAT	RBB9 MOUSE	RBB9_HUMAN	AAC2_MYCTU	Y069_TREPA	REV_VILVK	REV_VILV	SC16_YEAST
			_		_		-	_	P48415 saccharomyc
	34 70.8 239 1 PNUC_ECOLI P31215 34 70.8 239 1 PNUC_SALTY P24520	34 70.8 195 1 AAC2_WYCFO Q49157 34 70.8 239 1 PNUC_ECOLI P31215 934 70.8 239 1 PNUC_SALTY P24550	34 70.8 186 1 RBB9_RAT 088350 34 70.8 195 1 RAC2_MYCFO Q49157 34 70.8 239 1 PNUC_SALTY P24520	34 70.8 186 1 RBB9_MOUSE 088851 34 70.8 186 1 RBB9_RAT 088350 34 70.8 195 1 AAC2_MYCFO Q49157 34 70.8 239 1 PNUC_SALTY P24550	34 70.8 186 1 RBB9_HUMAN 075884 34 70.8 186 1 RBB9_MOUSE 088851 34 70.8 186 1 RBB9_MAT 088350 34 70.8 195 1 RAC2_MYCFO Q49157 34 70.8 239 1 PNUC_ECOLI P31215 34 70.8 239 1 PNUC_ECOLI P31215	34 70.8 181 1 AAC2_MYCTU P95219 34 70.8 186 1 RBB9_HUMAN 075884 34 70.8 186 1 RBB9_HOUSE 08851 34 70.8 186 1 RBB9_RAT 088350 34 70.8 195 1 AAC2_MYCFO Q49157 34 70.8 239 1 PNUC_ECOLI P31215 34 70.8 239 1 PNUC_ECOLI P31215	34 70.8 176 1 Y069_TREPA 083108 34 70.8 181 1 AAC2_MYCTU P95219 34 70.8 186 1 RBB9_HOUSE 088851 34 70.8 186 1 RBB9_KAT 088350 34 70.8 186 1 RBB9_KAT 088350 34 70.8 195 1 AAC2_MYCFO Q49157 34 70.8 239 1 PNUC_SALTY P24520	34 70.8 167 1 REV_VILVK 70.8 176 1 YOS_TREPA 083108 34 70.8 181 1 AAC2_WICTU P95219 34 70.8 186 1 RBB9_HUMAN 075884 34 70.8 186 1 RBB9_MOUSE 088830 34 70.8 186 1 RBB9_MOUSE 088830 34 70.8 186 1 RBB9_RAT 088350 34 70.8 195 1 AAC2_WICFO Q49157 34 70.8 239 1 PNUC_ECOLI P31215 34 70.8 239 1 PNUC_ECOLI P31215	P21280 P35957 O81108 P95219 O75884 O88550 O88550 Q49157 P31515

RESULT ACPD_M

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Bairoch A.;

Unpublished observations (FEB-1997).

-I- FUNCTION: Converts holo-ACP to apo-ACP by hydrolytic cleavage of the phosphopantetheine prosthetic group from ACP (By similarity).

-I- CATALYTIC ACTIVITY: Holo-[acyl-carrier protein] + H(2)0 = 4'-
phosphopanetheine + apo-[acyl-carrier protein].

-I- SIMILARITY: Belongs to the acpD family.

-I- CAUTION: THIS IS A CONCEPTUAL TRANSLATION, A FRAMESHIFT WAS
INTRODUCED IN POSITION 74 TO MAXIMIZE THE SIMILARITY WITH OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SETRAIN-ATCC 33530 / G-37;

MEDLINE-96026346; PubMed-7569993;

MEDLINE-96026346; PubMed-7569993;

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fritchmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Nguyen D.T., Dougherty B.A., Bott K.F., Hu P.-C., Lucler T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).
                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-47 FROM N.A.

STRAIL-ATCC 33530 / G-37;

MEDLINE-94075230; PubMed-8253680;

Peterson S.N., Hu P.-C., Bott K.F., Hutchison
"A survey of the Mycoplasma genitalium genome
sequencing.";
J. Bacteriol. 175:7918-7930(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACPD_MYCGE STANDARD; PRT; 196 AA. P47575; Q49357; 01-FEB-1996.(Rel. 33, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Putative acyl carrier protein phosphodiesterase (EC phosphodiesterase).
                                                                                                                                                                                                                                                                                                                                                                                                                                       CONCEPTUAL TRANSLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2097;
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Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.A. III;
by using random
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EMBL;

U39714; U02249;

-; NOT_ANNOTATED_CDS. AAD12538.1; ALT_INIT.

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RESULT 2

ACPD_MYCPN
ID ACCPD_MA
AC P75305
DT 01-NOV
DT 
RESULT 3
ACPD_MYCPU
ID ACPD_MYCPU
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Best 1
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HAMAP; MF_01216; -; 1.

InterPro; IPR003680; NADHdh_2.

Pfam; PF02525; Flavodoxin_2; 1.

Pfam; PF02525; Flavodoxin_2; 1.

Hypothetical protein; Hydrolase; Complete proteome.

Hypothetical protein; Hydrolase; MNYQ (IN REF. 3).

CONFLICT 44 A7 NELP -> MNYQ (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997
01-NOV-1997
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMD the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content institute of Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content institutions as long as its content institutions are not provided. Usage by and particular transfer of the statement is not removed. Usage by and particular transfer of the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: Converts holo-ACP to apo-ACP by hydrolytic cleavage of the phosphopantetheine prosthetic group from ACP (By similarity).
-i- CATALYTIC ACTIVITY: Holo-[acyl-carrier protein] + H(2)0 = 4'-phosphopantetheine + apo-[acyl-carrier protein].
-i- SIMILARITY: Belongs to the acpD family.
                                                                                                                                                                                                                                                                                                                Pfam; PF02525; Flavodoxin_2; 1.
Hypothetical protein; Hydrolase;
SEQUENCE 197 AA; 21550 MW; B
                                                                                                                                                                                                                                                                                                                                                                                 PIR; S73688; S73688.
HAMAP; MF_01216; -; 1.
InterPro; IPR003680; NADHdh_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete sequence analysis of the genome of the pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma pneumoniae. Bacteria; Firmicutes;
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(Rel. 35,
(Rel. 41,
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       STANDARD;
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Last annotation update)
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Pred. No.
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Pred. No
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5.6;
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RESULT 4

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O69A_D

O69A_D

P82985

AC P82985

DT 16-OCT

DT 16-OCT

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OC NEOPT

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RN [1]

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STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.
Amanatides P.G., Scherer S.E., Kichards S., Ashburner M., Henderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001).
-!- FUNCTION: Converts holo-ACP to apo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe
Moszer I., Dybvig K., Wroblewski H., Vian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N. STRAIN=UAB CTIP;
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28-FEB-2003 (Rel. 41,
28-FEB-2003 (Rel. 41,
Putative acyl carrier
                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda;
Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                   P82985;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical SEQUENCE 19
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MypuList; MYPU_3120;
HAMAP; MF_01216; -;
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                                                                                                                                                                                                     Putative odorant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rterPro; ipr003680; NADHdh_2.
pfam; pF02525; Flavodoxin_2; 1
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                                                                             SEQUENCE FROM N.A.
                                                                                                          NCBI_TaxID=7227;
                                                                                                                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                                                             069A_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL445564; CAC13485.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Converts holo-ACP to apo-ACP by hydrolytic cleavage of the phosphopantetheine prosthetic group from ACP (By similarity). CATALYTIC ACTIVITY: Holo-[acyl-carrier protein] + H(2)O = 4'-phosphopantetheine + apo-[acyl-carrier protein]. SIMILARITY: Belongs to the acpD family.
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198 AA; 2;
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100.0%;
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Last annotation update)
protein phosphodiesterase
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annotation updat
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Drosophila.
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. No.
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Viari A.,
                                                                                                                                                                                                                                                                                  393
                                                                                                                                                                                                                      update)
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5.6;
                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                          Insecta; Pterygota;
era; Muscomorpha;
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E.P.C.,
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AN Harmoon K.C., Kogers Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayaktaroglu L., Beasley E.M., RA Beaslow K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.M., Burkis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dum P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dum P., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart M.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., RA Lasko P., Lei Y., McIntosh T.C., McLeod M.P., McPherson D., Nelson D.L., RA McIntosh T.C., McLeod M.P., McPherson D. M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Shue B.C., Wendster R.D.C., Scheeler F., Shen H., RA Shue B.C., Wendster D.C., Scheeler F., Shen H., RA Shue B.C., Wendster D.C., Scheeler F., Shen H., RA Shue B.C., Wendster D.C., Scheeler F., Shen H., RA Shue B.C., Wendster D.C., Scheeler F., Shen H., Ra Shue B.C., Shon F., Nelson D., Weinstock G.M., Weissenbach J., RA Wang Z.-, Fernal B., Weinstock G.M., Weissenbach J., Ra Zhung K., Ra Kang R., Ra Kang R., Ra Kang R.
                               TRANSMEM
DOMAIN
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Brandon R.
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FlyBase; FBgn0041622; Or69a.
InterPro; IPR004117; 7tm_6.
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RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamiln N., Harris D., Hidalgo J., Hodgson G.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
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RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Waller S., Sunders S., Stevens K.,
RA Richard S., Waller S., Squares S., Stevens K.,
RA Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadleu E., Dreano S., Gloux S., Lehaure V., Mottler S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Goffeau A., Cadleu E., Dreano S., Gloux S., Lehaure V., Mottler S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Goffeau A., Cadleu E., Dreano S., Gloux S., Lehaure V., Mottler S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Goffeau A., Cadleu E., Dreano S., Gloux S., Lehaure V., Mottler S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
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RA Golfeau A., Cadleu E., Dreano S
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the European Bioinformatics Institute. Then
use by non-profit institutions as long a
modified and this statement is not removed.
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Hypothetical protein C5H10.12c in chromosome
SPAC5H10.12C.
                                                       EMBL; Z49811; CAA89962.1; PIR; T38976; S55490.
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R.,
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                                                                                                                 s requires a license agreement (S an email to license@isb-sib.ch).
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Bacteria;
   Clostridium thermocca-
nacteria; Firmicutes;
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P83218;
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                                                                GUNH_CLOTM STANDARD;
p16218;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                         Endoglucanase H
(Cellulase H).
                                                                                                                                                                                                                                                                                                                                                                                                                              Markovic O., Cederlund E., Griffiths W.J., Lipka T., Joernvall H.;

"Characterization of carrot pectin methylesterase.";

Cell. Mol. Life Sci. 59:513-518(2002).

-I-FUNCTION: Catalyzes the deesterification of methyl-esterified D-
galactosiduronic acid units in pectic compounds. It participates
in modulating cell wall during fruit ripening, cell wall extension
during pollen germination, and in defense mechanisms against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21960069; PubMed-11964128;
Markovic O., Cederlund E., Griffiths W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Daucus carota (Carrot).

Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnollophyta; eudicotyledons; core
Asteridae; campanulids; Apiales; Apiaceae; Daucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Pectinesterase (EC 3.1.1.11) (Pectin methylesterase)
                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4039;
                                                                                                                                                                                                                                                                                                      MOD_RES
                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                              łydrolase;
                                                                                                                                                                                                                                                                               SITE
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                                                                                                                                                                                                                                                                                                                                                                                                           pathogens.
CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307
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Pro; IPR000070; Pectinesterase.
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PS00503; PECTINESTERASE_2; 1.
e; Aspartyl esterase; Cell wall;
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                     thermocellum.
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66.7%;
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3 POTENTIAL.
          Clostridia;
                                                                                                                                                                                                                                                                                                                                                                                                Pectin + N H(2)O = N m
TO THE PECTINESTERASE
                                                      t sequence upd
t annotation u
(EC 3.2.1.4)
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Pred.
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Pred.
                                                                                                                                                                                                                                                                               PYRROLIDONE CARBOXYLIC BY SIMILARITY. BY SIMILARITY.
                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 890BAD4A0E66379B CRC64;
                                                                                                                                                                                                                                                                    359675FF36FD7625 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                        Mismatches
            Clostridiales;
                                                                                                                                                                                                                                             38;
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                                                                                                                                                                                                                                   No.
                                                                             update)
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                                                                                                                 900
                                                                    update)
                                                                                                                                                                                                                              DB
35;
                                                       (EGH) (Endo-1,4-beta-glucanase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Embryophyta;
                                                                                                                 A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
                                                                                                                                                                                                                                                                                                                             Pyrrolidone carboxylic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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ASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                             Length 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 371;
            Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                       ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PE).
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                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                        0;
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RESULT 8
BPT1_YEAST

DAGA

BPT1_YEAST P14772; 01-APR-1990 01-NOV-1997 15-SEP-2003

(Rel. 14, Created)
(Rel. 35, Last sequence up)
(Rel. 42, Last annotation

update)

STANDARD;

PRT;

1559

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                  δÃ
                                                    Query Match
Best Local
                                           Matches
                                                                                                                                                                                                                                                                                InterPro; IPR005087; C
InterPro; IPR002105; I
InterPro; IPR002048; E
InterPro; IPR001547; C
                                                                                  DOMAIN
REPEAT
REPEAT
SEQUENCE
                                                                                                                             ACT_SITE
                                                                                                                                                                        CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yaguee E., Beguin P., Aubert J.-P.;
"Nucleotide sequence and deletion analys
gene celh of Clostridium thermocellum.";
Gene 89:61-67(1990).

-I- FUNCTION: THIS ENZYME CATALYZES THE
                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                       PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=NCIB 10682; MEDLINE=90323606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium.
NCBI_TaxID=1515;
                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <del>-</del>
                                                                                                                                                                DOMAIN
                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                         Cellulose
                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                 EMBL; M31903; AAA23225.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULASE A (FAMILY 5 OF GLYCOSYL HYDROLASES).
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLUCOSIDIC LINKAGES
                                                                                                                                                                                                                                                                                                                             JH0157; JH0157.
; P07985; 1CEC.
 133
                                                                                                                                                                                                                                                    PF00404;
                     H
                                        6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION AS THE BINDING LIGAND FOR THE SL COMPONENT.
                                                                                                                                                                                                                   PS00448; CLOS_CELLULOSOME_RPT; PS00659; GLYCOSYL_HYDROL_F5; 1
 NGDWYPW 139
                     NG-WYPW
                                                                                                                                                                                                                                         PS00018; EF_HAND; UNKNOWN_1.
                                                                                                                                                                                                         degradation;
                                                                                               45
631
655
460
565
833
833
                                                                                      900
                                           Conservative
                                                                                      AA;
                                                                                                                                                                                                                                                   Dockerin_1;
                                                                                                                                                                                                                                                               cellulase;
                     6
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P., Aubert J.-P.;
                                                                                               900
630
900
900
955
895
895
895
                                                                                      102415
                                                     78.1%;
85.7%;
                                                                                                                                                                                                                                                                               EF-hand.
Glyco_hydro_5.
                                                                                                                                                                                                                                                                                                       Dockerin_1.
                                                                                                                                                                                                         Hydrolase; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IN CELLULOSE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             deletion analysis
                                                                                      Œ,
                                                                                                                     ENDOGLUCANASE H.
CATALYTIC (BY SIMILARITY).
CROCTHER-RICH (LINKER).
PROCTHER-RICH (LINKER).
CELLULOSE-BINDING (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
2 X 24 AA APPROXIMATE REPEATS.
                                           0;
                                                      Pred.
                                                                Score
                                            Mismatches
                                                                                      973AFB1954FC246B CRC64;
                                                               37.5;
                                                       No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LICHENIN
                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.
                                                      1e+02;
                                                                                                                                                                                                                               <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENDOHYDROLYSIS OF 1,4-BETA-ICHENIN AND CEREAL BETA-D-
                                                                DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the cellulase-encoding
                                            0,
                                                                                                                                                                                                          Repeat;
                                                                Length
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO CELLULASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
                                                                                                                                                                                                         Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                              a collaboration
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no
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RX MEDLINE-97313267; PubMed-9169871;

RA Johnston M., Hillter L., Riles L., Albermann K., Andre B., Ansorge W.,

RA Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,

RA Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,

RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,

RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,

RA Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,

RA Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,

RA Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,

RA Vierendeels P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,

RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,

RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hohelsel J.D.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";

IN Nature 387:87-90(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #EUNCTION.

MEDLINE=20253522; PubMed=10790694;

MEDLINE=20253522; PubMed=10790694;

Petrovic S., Pascolo L., Gallo R., Cupelli F., Ostrow J

Goffeau A., Tiribelli C., Bruschi C.V.;

Goffeau A., Tiribelli C., Bruschi C.V.;

"The products of YCF1 and YLL015w (BPT1) cooperate for

"The products of YCF1 and YLL015w (BPT1) cooperate for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miosga T., Zimmermann F.K.;
"Sequence analysis of the CEN12 region of Saccharomyces cerevisiae
a 43.7 kb fragment of chromosome XII including an open reading fram
homologous to the human cystic fibrosis transmembrane conductance
regulator protein CFTR.";
Yeast 12:693-708(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-245 FROM N.A.

MEDILINE-89306677; PubMed-2545538;

Boy-Marcotte E., Damak F., Camonis J., Garreau H., Jacquet M.;

"The C-terminal part of a gene partially homologous to CDC 25 suppresses the cdc35-5 mutation in Saccharomyces cerevisiae.";

Gene 77:21-30(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purnelle B., Goffeau A.:

Purnelle B., Goffeau A.:

"The sequence of 32kb on the left arm of yeast chromosome XII reveals six known genes, a new member of the seripauperins family and a new ars transporter homologous to the human multidrug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                     dependent vacuolar transport of unconjugated Saccharomyces cerevisiae."; Yeast 16:561-571(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bile pigment transporter 1.

BPT1 OR YLL015W OR L1313.

Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Cooperates for the ATP-dependent vacuolar transport
                                                                                                                                                                                                                                                                                                                                                                                     bilirubin
                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13:183-188(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cupelli F., Ostrow J.D
C.V.;
                                                                                                      There are no rest
                                         http://www.isb-sib
                                                                                                                                                    he EMBL outstation restrictions on in
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in
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RESULT 9
Y017_METJA
ID Y017_METJA
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                                                                                                            Query Match
Best Local S
Matches 5
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EMBL; X91488; CAA62776.1;
EMBL; M26647; AAA16564.1;
PIR; S64757; S64757
HSSP; P13569; 1NBD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0000329; GO; GO:0015127; GO; GO:0015086; GO; GO:0015723; GO; GO:0015723;
                                                                                                            CARBOHYD
SEQUENCE
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DOMAIN
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DOMAIN
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SMART; SM00382; AAS, 2.
SROSITE: PS00211; ABC_TRANSPORTER_1;
PROSITE; PS50893; ABC_TRANSPORTER_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00664; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
ProDom; PD000006; ABC_transporter;
SMART; SM00382; AAA; 2.
                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0015691; P:cadmium ion transport; IDA. InterPro; IPR003593; AAA_ATPase. InterPro; IPR001410; ABC_TM_transpt. InterPro; IPR003439; ABC_transporter.
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                                           213
                                                                          Similarity
5; Conserv
                                           NGWYP 217
                                                          NGWYP 5
                                                                                                            1053
1096
1117
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1118
1139
1210
1231
1236
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1257
1257
1336
                                                                                                                  Conservative
  STANDARD;
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                                                                                  100.0%;
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LUMENAL (BY
                                                                          Score 37; DB Pred. No. 2e+ 0; Mismatches
                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transport; IGI
                                                                                                                                                                                                                                                                                                    LUMENAL (BY SIMILARITY).
7 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY)
8 (BY SIMILARITY)
                                                                                                                            ATP
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13 (BY SIMILARITY)
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9 (BY SIMILARITY)
CYTOPLASMIC (BY S
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5 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
6 (BY SIMILARITY).
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CYTOPLASMIC (BY SIMILARITY).
4 (BY SIMILARITY).
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CYTOPLASMIC (BY SIMILARITY).
2 (BY SIMILARITY).
LUMENAL (BY SIMILARITY).
                                                                                                                                    CYTOPLASMIC (BY SIMILARITY) ATP (POTENTIAL).
                                                                                                                                                                   LUMENAL (BY SIMILARITY).
15 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
16 (BY SIMILARITY).
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11 (BY SIMILARITY)
                                                                                                            LUMENAL (BY SIMILARITY).

17 (BY SIMILARITY).
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  PRT;
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2e+02;
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RESULT 10
YE66_MCTJA6
ID 60-MCTJA6
AC 05886
DT 01-N(
DT 01-N(
DT 28-F)
DE HYPO
GN MJ14
OS Meth
OC Arch
OX NCB:
RN [1]
RP SEQ
RC STR
RX MEC
RA SU
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01-NOV-1997
01-NOV-1997
28-FEB-2003
                                                                                                                                                                                                                  Q58861;
01-NOV-1997
01-NOV-1997
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschil.";
Science 273:1058-1073(1996).
   STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLIND-96337999; PubMed-8688887;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
                                                                                                                                                                                                                                                                                          _METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanococcus jannaschii.
Archaea; Euryarchaeota; M
Methanocaldococcaceae; Me
                                                                                                                       Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
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                                                                                             SEQUENCE FROM N.A.
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MEDLINE=96337999; F
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                                                                                                                                                                                                                                                                             YE66_METJA
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Hypothetical protein; Complete
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                                                                                                                                                                                                                                                                             STANDARD;
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41,
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41,
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PubMed=8688087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25506 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            75.0%;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                               0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteome.
0F135E2C748F933D CRC64;
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.on update)
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RESULT 11
R18B_MOUSE
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Best Local
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         Arzawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Fleischmann W., Gaasterland T., Mikaido I., Pesole G., Quackenbush Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio Sakai K., Okido T., Furuno M., Aono H., Baddarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q99N84; Q9CRK0; Q9DCR8;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
28s ribosomal protein S18b, mitochondrial precursor
(Mrps18b) (MRP-S18-2).
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                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
STRAIN=C57BL/6J; TISSUE=Embryonic stem
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-21413863; PubMed-11402041;
Suzuki T., Terasaki M., Takemoto-H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Mammalia;
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PIR; A64483; A64483.
                                                                                                                                                                                 Kawai J.,
                                                                                                                                                                                                                                                           Identification J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
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ILARITY: STRONG, TO M.JANNASCHII MJ0017 AND MJ0139.1.
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                                                                                                                                                                                                                                                                                                                                                                                                 ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001584;
                                                                                                                                                                                                                                                           analysis of the mammalian tion of protein components hem. 276:33181-33195(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Rodentia;
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25626 MW;
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Pred. No.
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3C6D5A76051F17EB CRC64;
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                                                                                                                                                                                 Yoshino M.,
                                                                                                                                                                                                                                                                          mitochondrial in the 28 S sn
 Hume D.A.,
Mazzarelli
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RA Strausberg R.L., Feilgold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT "Generation and initial analysis of more than 15,000 full-length

RT "Generation and initial analysis of more than 15,000 full-length

RT "Generation and initial analysis of more than 15,000 full-length

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  Query Match
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Sasaki H.,
Suzuki H.,
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[3]
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Hayashizaki Y.;
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                                                                                                                                                                                     Pfam; PF01084;
PROSITE; PS0005
                                                                                                                                                                                                                             EMBL; AB049954; BAB41007.1; -.
EMBL; AK002554; -; NOT_ANNOTATED_CDS.
EMBL; AK010256; -; NOT_ANNOTATED_CDS.
EMBL; AK010256; -; NOT_ANNOTATED_CDS.
EMBL; BC021752; AAH21752.1; -.
MGD; MGI:1914223; MIPS18b.
GO; GO:0005763; C:mitochondrial small ribosomal subunit;
GO; GO:000575; F:structural constituent of ribosome; ISS
GO; GO:0003735; F:structural constituent of ribosome; ISS
GO; GO:0006412; P:protein biosynthesis; ISS.
InterPro; IPR001648; Ribosomal_S18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note-No experimental confirmation available; SIMILARITY: BELONGS TO THE S18P FAMILY OF RIBOSOMAL CAUTION: Ref. 2 sequence differs from that shown due
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frameshift in position 19.
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PS00057; RIBOSOMAL_S18;
                                                                                                                                                                    protein;
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K., Wang K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ringwald M., Rodriquez I., Sakamoto N.;
Schoenbach C., Seya T., Shibata Y., Storch K.-F
K., Wang K.H., Weitz C., Whittaker C., Wilming
shida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                           28702
  75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence-VSP_005723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 splicing;
  .08
                                             X
X
                                                                              MITOCHONDRION
28S RIBOSOMAL
Missing (in is
Score
                                       Missing (in isoform 2).
/FTId-VSP_005723.
2284983FD5848791 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Named
                                                                                                                                                                                       FALSE_NEG
                                                                                                                                                                    Transit
  36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isoforms=2;
  BB
                                                                                                                                                                    peptide;
                                                                                                    (BY SIMILARITY). PROTEIN S18B.
                                                                                                                                                                                                                                                                        ribosome; ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA collection.";
Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEINS.
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                                                                                                                                                                                                                                                                                                ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
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R18B_HUMAN
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                                                                                                                                                                                                                                            RX MEDLINE-2238257; PubMed=12477932;
RX MEDLINE-2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Radas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley N.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.",
"The Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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G9Y676; Q9BS27;

28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
28 ribosomal protein S18b, mitochondarial precursor
(Mrps18b) (MRP-S18-2) (PTD017 protein) (HSPC183).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDITINE-20499367; PubMed-11042152;
Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G., Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G., Zhang J.-T., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-T., Chen S.-J., Chen S.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Pituitary
Zhang Q.H., Guan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID-9606;
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Homo sapiens (Human).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fu G.,
                                                     J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 previously undefined genes stem/progenitor cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
MEDILINE-21276436; PubMed-11279123;

KOC E.C., Burkhart W., Blackburn K., Moseley A., Spremulli I.

"Phe.small subunit of the mammalian mitochondrial ribosome:
identification of the full complement of ribosomal proteins
J. Biol. Chem. 276:19363-19374(2001).

-1- SUBBUNT: Component of the mitochondrial ribosome small s

(288) which comprises a 12S rRNA and about 30 distinct p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Heart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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no M., Chen J.H.,
TD017 gene.";
d (OCT-1998) to th
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H., Hu R.;
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     subunit
proteins
                                                                                                                                             L.L.;
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RESULT 13
CP21_HORVU
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Best Local S
Matches 4
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TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _HORVU
-1- SUBUNIT: CARBOXYPEPTIDASE II IS A DIMER, WHERE EACH MONOMER IS COMPOSED OF TWO CHAINS LINKED BY A DISULFIDE BOND (BY SIMILARI)
-1- DEVELOPMENTAL STAGE: EXPRESSED IN THE GERMINATING EMERYO. LOW LEVELS IN THE DEVELOPING ALEURONE AND EMBRYO. ALSO FOUND IN THE ROOTS AND SHOOTS OF THE GROWING SEEDLING.
-1- PTM: THE LINKER PEPTIDE IS ENDOPROTEOLYTICALLY EXCISED DURING ENZYME MATURATION (BY SIMILARITY).
                                                                                                                                                                                                                                                         "The expression of serine carboxypeptidases during germination of the barley grain.";
Proc. Natl. Acad. Sci. U.S.A. 91:8209-8213(1994).
-!- CATALYTIC ACTIVITY: Preferential release of a or lysine residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-cv. Alexis; TISSUE-Grain;
MEDLINE-94336715; PubMed-7520177;
Dal Degan F., Rocher A., Cameron-Mills V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare (Barley). Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serine carboxypeptidase II-1 precursor (EC 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P55747;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005763; C:mitochondrial small ribosomal subunit; NAS. GO; GO:0005763; F:structural constituent of ribosome; NAS. GO; GO:0006412; F:structural constituent of ribosome; NAS. GO; GO:0006412; F:protein blosynthesis; NAS. InterPro; IPR001648; Ribosomal_S18: InterPro; IPR001648; Ribosomal_S18; InterPro; IPR00164; Ribosomal_S18; InterPro; IPR00164; Ribosomal_S18; InterPro; IPR00167; RIBOSOMAL_S18; FALSE_NEG. RIBOSOMAL_S18; FALSE_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CP21_HORVU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 WYPW 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258
196
29395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae; Pooideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MITOCHONDRION (BY SIMILARITY).
28S RIBOSOMAL PROTEIN S18B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B4C83E5593796C5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> S (IN REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    von Wettstein D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.4.16.6) (CP-MII.1)
                                                                                                                                                                                                                                                                                                                                                                                      during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                       C-terminal arginine
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                                                                                                                            (BY SIMILARITY).
EMBRYO. LOW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                     Q8K9J2;
28-FEB-2003
28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                         MEDLINE=22084549; PubMed=12089438; Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Erikss Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson "50 million years of genomic stasis in endosymbiotic bac Science 296:2376-2379(2002).

-i- FUNCTION: DNA polymerase III is a complex. multichai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00450; serine_carbpept; 1.
PRINTS; PR00724; CRBOXYPTASEC.
ProDom; PD001189; Serine_carbpept; 1.
PROSITE; PS00131; CARBOXYPEPT_SER_HIS;
PROSITE; PS00560; CARBOXYPEPT_SER_HIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                  +
                                                                                                                                                                                                                                                                                                                 Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                       DNA polymerase III,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X78876; CAB58992.1; HSSP; P08819; IWHT.
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            NCBI_TaxID=98794;
                                                                                                                                                                                                                                                                                                        Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                              HOLB OR BUSG342.
                                                                                                                                                                                                                                                                                                                                                                                                                       HOLB_BUCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S10.005;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                     epsilon and theta chains) that associates with a tau subunit. Core dimerizes to form the POLIII' complex. PolIII' associates with the gamma complex (composed of gamma, delta, delta', psi chi chains) and with the beta chain to form the complete DNA polymerase III complex (By similarity).
                                                                                                                                   FUNCTION: DNA polymerase III is a complex, multichain enzyme responsible for most of the replicative synthesis in bacteria. This DNA polymerase also exhibits 3' to 5' exonuclease activity (By similarity).

CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
                                                                                                              + \{DNA\}(N).

+ \{DNA\}(N).

Core SUBUNIT: DNA polymerase III contains a core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 WYPW 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001563;
                                                                                                                                                                                                                                                                                                                                                         (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation updat
ase III, delta' subunit (EC 2.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carboxypeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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163
41
239
291
109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149
162
324
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37408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
; 70F081D6B9723A60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LINKER PEPTIDE (BY SIMILARITY).
SERINE CARBOXYPEPTIDASE II-1, CHAIN B.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SERINE CARBOXYPEPTIDASE II-1,
                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    core 36; DB 1;
Pred. No. 71;
Mismatches
                                                                                                                                                                                                                                                                                                                                                       n update)
EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                       328
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                                                                                                                                                                                                                                                                                                                                                                                                                       AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zymogen; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 324;
                                                                                                              (composed of alpha
                                                                                                                                                                                                                 , Eriksson A.-S.,
dersson S.G.E.;
otic bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yano M., Horiuchi T.;

A 718-kb DNA sequence of the Corresponding to the 12.7-28.0 DNA Res. 3:137-155(1996).
                                                                                 MEDLINE-97061202; PubMed-8905232;
Oshima T., Aiba H., Baba T., Fujita K., Haya Ikemoto K., Inada T., Itoh T., Kajihara M., Kimura S., Kitagawa M., Makino K., Masuda S., Mori H., Motomura K., Nakamura Y., Nashimoto Sampei G., Seki Y., Tagami H., Takemoto K., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                  Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; Pubmed-9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "DNA polymerase III accessory proteins. delta and delta'.";
J. Biol. Chem. 262.....
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       III holoenzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOLB_ECOLI
P28631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carter J.R., Franden M.A., Aebersold R.H., McHenry C.S.; "Identification, isolation, and characterization of the structural gene encoding the delta' subunit of Escherichia coli DNA polymeras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93285995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
Enterobacteriaceae; Esche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase; DNA-directed DNA polymerase; DNA replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriol.
                                                                                                                                                                                                                                                                                                   complete genome sequence of 
ice 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AE014110; AAM67896.1; -.
                                                                                                                                                                                                                                                                                                                                              Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d and this statement is not removed. s requires a license agreement (See an email to license@isb-sib.ch).
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4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=8509334;
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Last annotation update
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                                    Escherichia coli K-12 genome
) min region on the linkage m
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Pred. No.
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                                                                                                                                                                                                                                                                                                                  Escherichia coli K-12.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Donnell M.;
teins. I. hola
                                                                                              a K., Hayashi K., Honjo A.,
ihara M., Kanal K., Kashimoto K.,
Masuda S., Miki T., Mizobuchi K.,
Nashimoto H., Nishio Y., Saito N.,
emoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (
편
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C 2.7.7.7).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
72;
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Guenther B., Onrust R., Sali A., O'Donnell M., Kuriyan J., "Crystal structure of the delta' subunit of the clamp-loader of E. coli DNA polymerase III.", Cell 91:335-345(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: DNA polymerase III contains a core (composed of alpha, epsilon and theta chains) that associates with a tau subunit. This core dimerizes to form the POLIII', complex, PolIII', associates with the gamma complex (composed of gamma, delta, delta', psi and chi chains) and with the beta chain to form the complete DNA polymerase III complex. The final composition of the complex is: (alpha, epsilon, theta)[2]-tau[2]-(gamma, delta, delta', psi, chi)[2]-
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the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch). This between SWISS-PROT entry is copyright. It is produced through meen the Swiss Institute of Bioinformatics and the Exteropean Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content (See http://www.isb-sib. Usage δq restrictions EMBL Ω for collaboration -L outstation -. G outstation /announce, ö

EMBL; L04577; AAA23708.1; -.
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Transferase; DNA-directed DNA polymerase; DNA replication; EcoGene; EG11500; InterPro; IPR0046; 3D-structure; 166 Complete holB proteome. -> G (IN REF.

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Q97734 sulfolobus
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Q8h223 populus x c
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Q8txq5 methanopyru
Q94c39 arabidopsis
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Nature 414:450-453(2001).
EMBL; AL590445; CAD26573.1;
InterPro; IPR003151; FAT.
Pfam; PF02259; FAR; 1.
                                                                                                                                                                                                                                                                   "Phylogeny of the genus Flavivirus.";
J. Virol. 72:73-83(1998).
EMBL; AF013413; AAC58801.1;
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Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P.
Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
Weissenbach J., Vivares C.P.;
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Kuno G., Chang G.J., Tsuchiya K.R
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rel. 22, Last
n ECU05_0540.
                   83.3%;
                                                                                                                                                                                                                                                                                                                                   Tsuchiya K.R.,
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Last annotation updat
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                   Score 40; DB 12;
Pred. No. 1.1e+02;
                                                                                 DC667CC97761AB5D CRC64;
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                                                                                                                                                                                                                                                                                                                                   Karabatsos
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                                      Length 345;
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Codson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hastin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Hastin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Laing Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rahnert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
"The genome sequence of Drosophila melanogaster.";
RT "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
Abril J.F., Agbayani A., An H.J., Andrews-Ffannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Beckva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Benos P. V., Berman B.P., Brokstein P., Brottier P.,
Brottier P., Chandra
                   Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Gonzalez M., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
                                                                                                                                        Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Bu
Carlson J.W., Center A., Champe M., Davenport L.B., Diet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8IQJ1;
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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01-MAR-2003
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Paragas
ong S., I
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Scherer S.E., Li P.W., Hoskins R.A.,
is S.E., Richards S., Ashburner M., H
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  Park S.,
man G.S.,
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  Patel S.,
Puri V.,
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1., Galle R.F.,
Henderson S.N.,
                                          K.A., Nunoo
                                                                                                                                            Dietz
                                                                                                                                                                                                     Holt R.A.,
                                                                                                                                          .C., Rogers Y., Busam D.A., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                     Yao Q.A., Ye J.,
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                                                                                                                                                                                                                                                                                                                                Smith H.O.
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Vallet D., Sharp

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RESULT 6
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Best Local S
Matches
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Best Local
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 50.2 kDa protein (Fragment).
Brevibacterium linens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Brevibacteriaceae; Brevibacterium.
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-DSM 20426;
MEDLINE-20279196; PubMed-10821176;
Krubasik P., Sandmann G.;
"A carotenogenic gene cluster from
lycopene cyclase genes involved in
carotenoids.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.
Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
"Annotation of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     Mol. Gen. Genet. 263:423-432(2000)
EMBL; AF139916; AAF65580.1; -.
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Adams M.D., Celniker
Submitted (MAR-2000)
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                            Hypothetical protein NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1703;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2002)
EMBL; AE003539; AAN1
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5; Conserv
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                                                                                                                   NGWYSW
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                                                                                                                                                                                                                                                                                                    456 AA;
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                                                                                                                                                                                                            Conservative
  PRELIMINARY;
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83.3%;
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e EMBL/GenBank/DDBJ
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Pred. No.
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Pred. No.
PRT;
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the synthesis of aromatic
  919
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. 1.4e+02;
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J databases
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Best Loc
Matches
       investigating biology.";
Science 282:2012-2018(1998).
EMBL; 280789; CAB02551.1; -.
WormPep; F48C11.2; CE10750.
InterPro; IPR001304; Lectin_C; fam; PF00059; lectin_C; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00034; CLECT; 1.
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MEDLINE-99370217;
Reer B.E., Bailes
                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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01-FEB-1997 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Q93744;
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InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprote
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Submitted (FEB-1999) to the
EMBL; AF131870; AAD39758.1;
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01-NOV-1999 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
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J. Virol. 73:7734-7744(1999).
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E., Goeken R., Dapolito
J.P., Gautier-Hion A., V
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01-MAR-2003
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DNA Res. 8:123-140(2001).
EMBL; AP000984; BAB65951.1;
EMBL; AP000984; BAB65951.1;
InterPro; IPR001092; HLH_basic.
PROSITE; PS00038; HLH_j: 1.
Transferase; Hypothetical protein; Complete proteome.
SEQUENCE 767 AA; 83742 MW; 277493A13462EC18 CRC64;
                                                                                                                                                                                                                                                                       Populus x canescens.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Malphyhiales; Salicaceae; Populus.

NCBI_TaxID-80863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Ka Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Ogu Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;
                                                                                  EMBL;
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PubMed=11572479;
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Kato Y.
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Q8PKV7
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RX MEDLINE-20022145; pubMed-12024217;

RX MEDLINE-22022145; pubMed-12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A duaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Alves L.M.C., do Amaral A.M., Bertolini S. C.C., Faranco L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Forto M.I.T.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Martins E.C., Machado M.A., Madeira A.M.B.N., Martinez Rossi N.M.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Moreira L.M., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Pereira H.A., Rossi A., Tamura R.E., Teltseira E.C., Tezza R.I.D.,

RA Polibal J.C., Kitajima J.P.;

**Tomparison of the Bronnes of two Manthompas nathonomy with differing

**Tomparison of the Bronnes of two Manthompas nathonomy with differing
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01-OCT-2002 (
01-OCT-2002 (
01-MAR-2003 (
                               Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria;
Xanthomonadaceae; Xanthomonas.
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PROSITE; PS00178; AA_TRNA_LIGASE_I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Comparison of the genomes of two host specificities.";
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical XAC2050.
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01-MAR-2003
                                                                                                                                         Hypothetical XCC2157.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 417:459-463(2002).
EMBL; AE011840; AAM36912.1;
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3 (TrEMBLrel. 23, Last a
al protein XAC2050.
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(TremBLrel. 22, Last sequence up
(TremBLrel. 23, Last annotation
| protein XCC2157.
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ClB1FB23AA6E930B CRC64;
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ed. No. 68;
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RX MEDLINE-2202145; PubMed-12024217;
RA da Silva A.C.R. Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighteri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Martins E.C., Meddanis J., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira M.C., Oliveira V.R.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
RA Setubal J.C., Kitajima J.P.,;
RA "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
Nature 417.459-463(2002).
DR Interpro; IPRO0112; tRNA-synt_I.
DR RHD; AE01232; AAM41437.1;
DR Interpro; PS00178; AA_TRNA_LIGASE_I;
DR RROSTTE; PS00178; AA_TRNA_LIGASE_I;
DR Hypothetical proteen; Complete proteome.
SO SEQUENCE 171 AA; 18661 MW; B9C10E17FA22051D CRC64;
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Matches 4
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                                                                                       Submitted (OCT-2000) to the EMBL/GenBank/DDBJ database: EMBL; ACO11661; AAF16637.1; - IPR000070; Pectinesterase. Pfam; PF01995; Pectinesterase; 1. PROSITE; PS00503; PECTINESTERASE_2; 1. PROSITE; PS00503; PECTINESTERASE_2; 1. SEQUENCE 223 AA; 25031 MW; 289B968B773078B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      T23J18.24.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Roside eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                              Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S. Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J. Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9LPX8;
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nilarity 80.0%;
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1.5e+02;
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                                                                                                                                  Duesterhoeft A.;
Submitted (FEB-1998) to the EMBL/GenB Submitted (FEB-1998) to the EMBL/GenB EMBL; ALO21730; CAAL6831.1; -
GeneDB_SPombe; SPBC4C3.09; -
InterPro; IPR002495; Glyco_trans_8.
Pfam; PF01501; Glyco_transf_8; 1.
SEQUENCE 376 AA; 44095 MW; 09D82A
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01-JUN-1998 (Tremblr
01-MAR-2003 (Tremblr
SPBC4C3.09 protein.
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Wood V., I
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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"Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium Loti.";

"Nakayama S., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4896;
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EMBL; AP003011; BAB53262.1; -
InterPro; IPR001173; Glyco_trans_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 345 AA; 39450 MW; 131B52D5E56507E1 CRC64;
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MEDLINE=21082930; PubMed=11214968;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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   Score 38; DB 3;
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Search completed: August 20, 2003, 12:40:32 Job time: 13.4605 secs
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OBTXQ5;

O1-JUN-2002 (TrEMBLrel. 21, Cr

O1-JUN-2002 (TrEMBLrel. 21, La

O1-JUN-2002 (TrEMBLrel. 21, La

Predicted transposase.
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NCBI_TaxID=2320;
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Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
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179 GWFPW 183
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Minimum
Maximum
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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length: 2000000000
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1 GGWLPY 6
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd
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ABJ04311
ABG51866
ABB37019
ABB37019
ABB37714
ABB22333
AAM57746
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AAM17988
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Human colon specif
Human liver peptid
Peptide #441 enco
Peptide #4525 enco
Protein #4332 enco
Human brain expres
Human bone marrow
Peptide #4422 enco
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AAM84712	AAM85213	AAU42647	AAU86421	AAU70947		АВВ67506		AAW26704	AAR91939	AAG64143	AAW70516	AAY45012	AAY35514	AAY37433	AAY84911	AAG40277	AAG17603	AAG40278	AAG17604	ABP99342	AAU04849	AAY31800	AAU56988	AAU55735	ABG01626	AAG40279	AAG17605	ABU71020 .	AA000711	ABU11869	AAO11246		79	tπ	AAM30495
Human immune/haema	Human immune/haema	Propionibacterium	Androgen receptor	M. tuberculosis Rv	Cell division cycl	Drosophila melanog	Mouse ischaemic co	Mouse Cyp7b steroi	-		Candida parapsilos	വ	Chlamydia pneumoni	đ	α				Arabidopsis thalia	Orthosomycin biosy	Micromonospora eve	Beak and feather d	Propionibacterium	nibact			Arabidopsis thalia	_	polypepti		Human polypeptide	₽	eptide	#4308	Peptide #4532 enco

ALIGNMENTS

RESULT 1 ABG90939 Human; colon specific nucleic acid; CSNA; colon specific polypeptide; CSP; vaccine; diagnosis; metastasis; colon cancer; cancer; immune response; staging; imaging; colorectal cancer; gene therapy; N-PSDB; ABS67078, ABS67079 Human colon specific polypeptide, #12. 29-NOV-2002 (first entry) ABG90939; ABG90939 standard; Protein; WPI; 2002-657591/70 Piderit A, Macina RA, 13-FEB-2001; 2001US-268291P 12-FEB-2002; 2002WO-US04240. 22-AUG-2002 WO200264744-A2 Homo sapiens. transgenic; engineered colon tissue. (DIAD-) DIADEXUS INC. Sun Y, Liu 51 ₹ ü

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RESULT 2
ABJ04311
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                                                                 Novel colon specific polypeptides and polynucleotides useful for detecting, diagnosing, monitoring, treating, staging and predict cancers in humans having cancer and non-cancerous colon disease
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Claim 11; Page 208; 228pp; English.
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43 GGWLPF 48
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disease;
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ed. No. 13;
Mismatches
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cytostatic; gene therapy
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The present invention provides protein and coding sequences of human colon specific genes and proteins. These can be used in the treatment of colonic diseases, including colon and colorectal cancers. The present

Query Match
Best Local Similarity
Matches 5; Conser

Conservative

87.8%; 83.3%;

Score 36; DB Pred. No. 19; 1; Mismatches

22;

Length 49

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Indels

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RESULT 3
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                     liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                   The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult
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Sequence
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27-SEP-2000;
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03-AUG-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                        genome-derived single exon nucleic acid probes useful sing gene expression in human adult liver -
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2000US-0632366.
2000US-0234687.
2000US-0236359.
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2000US-0207456.
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                                                                                                                                                       The invention relates to a spatially-addressable set of single exon called acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labeled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                               New spatially-addressable set of single exon nucleic acid puseful for measuring gene expression in sample derived from breast, comprises number of single exon nucleic acid probes
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                                                                        Sequence
                                                                                               Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                              present sequence is a peptide encoded probe of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide #4441 encoded by breast cell single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB31790;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SG,
                                                                                                                                                                                                                                                                                                                                                                                                    27; SEQ ID NO 14758; 327pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 GGWLPH 44
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2000US-0207456
2000US-0608408
2000US-0632366
2000US-06323687
2000US-0234687
2000US-0234687
2000US-02346359
2000US-0024263
               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                          87.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
            Score 36; DB
Pred. No. 19;
1; Mismatches
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             1.
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                             рв
19;
                                                                                                                  in electronic format dire
                                         22;
             0;
                                         Length 49
                                                                                                                  format directly
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             0
            Gaps
            0
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RESULT 5
ABB37019
ID ABB37019
ID ABB37019
AC ABB3
XX ABB3
XX ABB3
XX ABB3
XX ABB3
XX Pept
XX Huma
XX WO20
XX O9-A
XX O9-A
XX O9-A
XX O4-F
PR 03-J
PR 03-J
PR 03-J
PR 04-F
PR 0
RESULT 6
ABB22333
ID ABB2
XX
AC ABB2
XX
DT 23-J
XX
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234589.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
                            23-JAN-2002
                                                                                 ABB22333;
                                                                                                                                    ABB22333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID NO 29654; .639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #4525 encoded by human foetal liver single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04 FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB37019;
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                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                           1 GGWLPY 6
                                                                                                                                                                                                                                                                                                                                                                                Similarity
5; Conserv
                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGWLPH
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                         (first entry)
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                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                          87.8%;
83.3%;
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Pred. No. 19;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
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RRESULT 7
AAM571746
ID AAM57
XX AAM57
AC AAM56
XX AAM50
DT 05-N
XX XX
DE Huna
XX Huna
KW Huma
KW micro
KW epil
XX XX
XX -
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                           measuring human gene expression in a sample derived from human heart (see ABA21335-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                     Human; brain expressed exon; gene expression analysis; probe, microarray; Alzheimer's disease; multiple sclerosis; schizopi
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene expression; heart; microarray; vascular system
cardiovascular disease; hypertension; cardiac arrhythmia;
congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157274-A2
          Homo sapiens
                            epilepsy; cancer.
                                                                  Human
                                                                                     05-NOV-2001
                                                                                                       AAM57746;
                                                                                                                          AAM57746 standard;
                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart
                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                        Single exon nucleic acid probes for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488899/53
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SG,
                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                 brain
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                                                                                                                                                                                                            Similarity
5; Conser
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                                                                                                                                                                                          GGWLPY 6
                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID No
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                 expressed single
                                                                                                                                                                                                             Conservative
                                                                                    (first entry)
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                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                           24103; 530pp;
                                                                                                                                                                                                                    87.8%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heart; microarray; vascular system;
                                                                                                                          49
                                                                                                                                                                                                             μ;
                                                                                                                                                                                                                     Score 36;
Pred. No.
                                                                 exon
                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rank DR;
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                                                                                                                                                                                                             Mismatches
                                                                 probe encoded
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                                                                                                                                                                                                                     DB
19;
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                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                       gene expression in human
                                                                 protein
                                                                                                                                                                                                                               Length 49
                                                                                                                                                                                                             Indels
                                      schizophrenia
                                                                 SEQ ID
                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression.
                                                                  NO:
                                                                                                                                                                                                            Gaps
                                                                  29851.
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                                                                                                                                                                                                                                                          RESULT 8
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Best Local :
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          21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single
brains
                                                                                                                                                              microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
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                                                                                                       09-AUG-2001
                                                                                                                                                                                                            06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                        Human; bone
                                                                                                                                                                                                                                AAM70159
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04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the hubrain. They can be used to measure gene expression in brain cell sa
                                                                                                              30-JAN-2001;
                                                                                                                                                                                                                                                                                     Human bone marrow expressed probe encoded protein
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26-MAY-2000;
                                                                                                                                                                              WO200157276-A2
                                                                                                                                                                                                          Homo sapiens.
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27-SEP-2000;
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03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGWLPH
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; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
                                                                                                                                                                                                                                         marrow expressed exon; gene expression analysis; probe;
cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                               2001WO-US00668
                                                                                                                                                                                                                                                                                                                    (first entry)
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2000US-0207456.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44
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                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB Pred. No. 19; 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for analyzing gene expression
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19;
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                                                                                                                                                                                                                                                                                        SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                          NO:
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                                                                                                                                                                                                                                                                                        30465
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2000GB-0024263

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RESULT 9
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Best Local :
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single even minimum.
                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn
                                              Claim
                                                                                                              Penn
                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                               WO200157278-A2
                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                     AAM17988 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single eanalyzing gene expression in
                                                               analyzing
                                                                                                                                (MOLE-)
                                                                                                                                                                                                                            30-JAN-2001;
                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                     cervical cancer.
                                                                                                                                                                                                                                                                                                               Probe;
                                                                                                                                                                                                                                                                                                                                                  12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                     AAM17988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention provides a number of single exon nucleic acid es which are derived from genomic sequences expressed in the human emarrow. They can be used to measure gene expression in bone marrow les, which may enable the improved diagnosis and treatment of cancers as lymphoma, leukaemia and myeloma. The present sequence is a ein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention
                                                                                                                                                                                                                                                                                   sapiens.
                                                                                                              SG,
                                                                                            2001-488901/53
                                              27;
                                                               genome-derived single exon nu
zing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                    39
                                                                                                                                                                                                                                                                                                             human; microarray;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                #4422 encoded
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| GGWLPH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; SEQ ID
                                                                                                                                MOLECULAR DYNAMICS INC.
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                                              SEQ
                                                                                                             Hanzel
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                                                                                                                                                2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                              22814;
                                                                                                                                                                                                                                                                                                                                                 entry)
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                                                                                                             Chen
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                                                                                                                                                                                                                                                                                                                               probe
                                                                                                                                                                                                                                                                                                            gene
                                                                                                             Σ
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                                             487pp;
                                                               exon nucleic acid probes useful n human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon nucleic acid probes useful human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                       49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.
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Pred.
                                                                                                              Rank
                                                                                                                                                                                                                                                                                                             expression;
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                                              English.
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                                                                                                                                                                                                                                                                                                                               measuring
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                                                                                                                                                                                                                                                                                                              cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                              cervical gene expression.
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                                                                                                                                                                                                                                                                                                             epithelial
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RESULT 10
AAM30495
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Query Match
Best Local S
Matches
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Best Local S
Matches
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                      The present invention relates to single exon nucleic acid prosee AAI31315-AAI57546). The present sequence is a peptide ence such probe. The probes are useful for producing a microarray predicting, measuring and displaying gene expression in sampl from human placenta. The probes are useful for antenatal diaghuman genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did no specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         measuring human gene expression in a sample derived epithelial cells. By measuring gene expression, the useful in grading and/or staging of diseases of the
                                                                                                                          Claim
                                                                                                                                                                                                                                04-OCT-2000;
                                                                                                                                                                                                                                                                               04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #4532 encoded by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cervical cancer.
                                     Sequence
                                                                                                                                            analyzing
                                                                                                                                                                                                                                                                                                            30-JAN-2001;
                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                 WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                      genetic
                                                                                                                                                                                                                                                                                                                                                                                                Probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM30495;
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                                                                                                                                                                                                             (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                   sapiens.
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                                                                                                                                                                        2001-488897/53.
                                                                                                                          27;
                                                                                                                                           genome-derived
zing gene expres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 GGWLPH
                                                                                                                                                                                                                                                                                                                                                                                              microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGWLPY 6
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5; Conserv
Similarity
5; Conser
                                                                                                                                                                                                              MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                       disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                          SEQ
                                                                                                                                                                                           Hanzel
                                     49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49
                                                                                                                                                                                                                               2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
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 Conservative
                                                                                                                                                                                                                                                                                                            2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                      A,
                                                                                                                         ID No 30764; 654pp;
                                                                                                                                           erived single expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44
                                                                                                                                                                                           DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                               human;
         87.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.8%;
83.3%;
                                                                                                                                                                                           Chen
                                                                                                                                                                                                                                                                                                                                                                                               placenta;
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                                                                                                                                          exon nucleic acid
n human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49
Score 36; DB Pred. No. 19; 1; Mismatches
                                                                                                                                                                                           Rank
                                                                                                                                                                                                                                                                                                                                                                                                                 for measuring placental gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₿
                                                                                                                          English
                                                                                                                                                                                                                                                                                                                                                                                               antenatal diagnosis;
                                                                                                                                                                                           DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not
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format
                                                                                                                                                     probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                   Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e probes are of cervix, note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49
                                                                 diagnosis
                                                                                             encoded (
                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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0;
                                                                                                                                                                                                                                                                                                                                                                                                                  expression.
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                                                                  derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Gaps
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ABG39797
ID ABG3
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AAM05626
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                                     RESULT 12
                                                                                                                                      Query Match
Best Local
                                                                                                                            Matches
            ABG39797 standard;
                                                                                                                                                                                                         breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                 nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                                                                                                                                                                                                                                                              The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by on such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM05626
                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                       in a
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide #4308 encoded by probe
                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SG,
                                                                                                                                                                                                                                                                                                                                                                                                       human
                                                                                                                                                                                                                                                                                                                                                                                                      single exon nucleic acid probe used to measuring gene expression human breast .
                                                                           39
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                                                                                                                            5
                                                                                                                                      Similarity
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| GGWLPH 44
                                                                        GGWLPH 44
                                                                                                 GGWLPY 6
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                                                                                                                                                                                                                                                                                                                                                                             SEQ ID No 14366; 322pp;
                                                                                                                                                                            49
                                                                                                                            Conservative
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2000US-0632366.
2000US-0234687.
2000US-0236359.
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2000US-0207456.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000GB-0024263.
                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DK,
            Peptide; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                        87.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen
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                                                                                                                                      Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for measuring breast gene expression
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                                                                                                                         0;
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                                                                                                                         Gaps
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CC nucleic acid expressed in the human lung; measuring gene expression in a cc sample derived from human lung, comprising (a) contacting the array with a cc sample derived from human lung, comprising (a) contacting the array with cc a collection of detectably labeled nucleic acids derived from human lung comprising (c) mRNA, and (b) measuring the label detectably bound to each probe of cc (a) algorithmically predicting at least one exon from genomic sequences (c) of the eukaryote; and (b) detecting specific hybridisation of detectably clabeled nucleic acids from eukaryote lung mRNA, to a single exon probe, comprising a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several crissues and/or cell types using hybridisation to a single exon of captures and for cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the capression analysis, and for identifying exons in a gene, particularly cusing human lung derived mRNA and for the study of lung diseases (COPD), interstital lung disease (ILD) familial idiopathic pulmonary disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from human lung comprising single exon nucleic acid probes having 12614 nucleic acid sequences mentioned in the specification, or the complements or the 12387 open reading frames derived from the 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample deriv from human lung comprising single exon nucleic acid probes having o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG39797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spatially-addressable set of single exon nucleic acid probes, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-')
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neurofibromatosis,
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Matches 5
The invention relates to a substantially pure polypeptide comprising an amino acid sequence selected from Rv0284, Rv0285, Rv0455c, Rv0455c, Rv19569, Rv19569, Rv1986, Rv3477, Rv3878, Rv3879c or Mr3106.1 (also disclosed are ORF13A and Rv0284ct), or their immunogenic portion, nucleic acids encoding them and an amino acid sequence analogue having at least 70% sequence identity to the polypeptide and is immunogenic. The protein is useful in preparing a pharmaceutical composition for diagnosing tuberculosis and in preparing a vaccine against tuberculosis caused by virulent mycobacteria. The vaccine or immunogenic, pharmaceutical composition can be used prophlactically in a subject not infected with a virulent mycobacterium, or therapeutically in a subject already infected with a virulent mycobacterium. The protein is useful for preventing, treating and detecting infections caused by species of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Mycobacterium tuberculosis antigens, useful for diagnosing tuberculosis, and as a vaccine for treating or preventing infections caused by species of tuberculosis complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3;
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21-FEB-2001; 2001DK-0000283
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agger
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                                 cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                       The invention the encoded
                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                               Claim 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytckine; cell proliferation; cell differentiation; vaccine; peptide therapy; stem cell growth factor; haematc tissue growth factor; humunomodulatory, cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tuberculosis complex (M. tuberculosis, M. bovis, M. africanum). The nucleic acids may be used for effecting in vivo expression of the antigen, and in diagnostic assays for detecting the presence of pathogenic organisms in a sample. The vaccine is an improvement of the living BCG vaccine presently available, where one or more copies of the genome of the microorganism to allow the microorganism to express secrete the polypeptide. Incorporation of more than one copy of a nucleotide sequence enhances the immune response. The present sequence represents an immunogenic peptide derived from an M. tuberculosis protein of the invention.
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18-MAY-2000; 2000US-0577409
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                                                                                                                                                                                                                                           invention relates to human polynucleotides (AAI79941-AAI93841) and encoded proteins (AAO00010-AAO13910) that exhibit activity elating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-514838/56
DB; AAI91177.
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               leukaemia, nervous system disorders,
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; SECP; secreted protein; micro-array; liver disease; hepatitis; cirrhosis; cell proliferative disease; cancer; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; cardiovascular disorder; hypertension; angina pectoris; allergy; myocardial infarction; immune disorder; inflammatory disorder; hypothyroidism; acquired immunodeficiency syndrome; Cushing's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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27-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein SECP-24,
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13-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   developmental disorder.
The invention relates to an isolated polypeptide comprising any of 30 secreted human proteins (SECP1-SECP30) appearing as ABU11846-ABU11875, caturally occurring amino acid sequence at least 90-98 % identical to
                                                                           preventing diseases or condit expression e.g. cancer, AIDS, hepatitis, cirrhosis
                                                                                          New human secreted proteins (SECP) useful for diagnosing, treating preventing diseases or conditions associated with the aberrant SECF expression e.g. cancer, AIDS, atherosclerosis, epilepsy, allergies.
                                                                                                                                                                                                                                                                                                    19-MAR-2002;
                                                    Claim 1; Page 161; 192pp;
                                                                                                                                                           WPI;
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DB; ABX49971.
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5; Conser
                                                                                                                                                                                 AA, Hafalia AJA, Duggan BM, Warren BA, Emerling BM; ey CM, Arvizu CS, Honchell CD, Nguyen DB, Kallick DA; Au-Young JK, Ramkumar J, Li JX, Thangavelu K, Gietze Baughn MR, Yao MG, Walia NK, Mason PM, Lal PG, Gra Becha SD, Sapperstein SK, Richardson TW, Tran UK; VS, Tang YT, Azimzai Y, Yan L, Xu Y;
                                                                                                                                                                                                                                                                             INCYTE GENOMICS INC
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2001US-287114P.
2001US-286640P.
2001US-290516P.
2001US-292184P.
2002US-347503P.
2002US-358279P.
2002US-366041P.
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                                                      English.
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coligonucleotide or polynucleotide sequence specifically hybridiable with coligonucleotide or polynucleotides of the target polynucleotide. CC at least 30 contiguous nucleotides of the target polynucleotide. CC The polypeptides and polynucleotides are useful in diagnosing, cc treating and preventing diseases or conditions associated with the cc decreased expression or overexpression of SECP, such as liver (e.g. hepatitis, cirrhosis), cell prollferative (e.g. cancer, cc atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, cc infarction), immune/inflammatory (e.g. acquired immunodeficiency cc syndrome (AIDS), allergies) and developmental (e.g. Hypothyroidism, cc syndrome) disorders (many other diseases and conditions cc are given in the specification). These are also useful in assessing the cffects of exogenous compounds on the expression of nucleic acid and cc amino acid sequences of SECP. The SECP or its fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polypeptides, or in altering the expression of the target compounds that specifically bind to or modulate the neasuring protein protein interactions, drug-target interactions, and gene expression profiles. The present sequence is a SECP protein of the creating the protein of the protein of the present sequence is a SECP protein of the creating the protein of the present sequence is a SECP protein of the creating the protein of the present sequence is a SECP protein of the creating the protein of the present sequence is a SECP protein of the creating the protein of the protein protein protein protein sequence is a SECP protein of the creating the protein of the present sequence is a SECP protein of the creating the protein prot
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Вþ Ş 62 1 GGWLPY 6 GNWLPY 67

Query Match Best Local S Matches 5

similarity 5; Conserv

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Score 35; DB Pred. No. 48; 0; Mismatches

Length 80 Indels

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Sequence

Search completed: August Job time: 15.1928 secs 20, 2003, 12:33:48

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Perfect score:
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
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US-09-252-991A-27172
US-09-252-991A-27172
US-09-252-991A-27172
US-09-268-311-3
US-09-18-744-12
US-09-18-744-12
US-09-18-744-12
US-08-314-309A-21
US-08-314-309A-21
US-08-314-309A-21
US-08-318-432-8
US-08-318-432-8
US-08-318-432-2
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US-09-107-532A-5075
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Sequence 8, Appli
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US-08-460-309-12	US-08-152-019A-38	US-08-152-019A-37	US-08-988-856B-25	US-08-752-852A-145	US-09-341-587-3	US-09-326-203A-24	US-09-252-991A-21769	US-09-328-352-5600	US-09-252-991A-18162	US-09-252-991A-27429	US-09-252-991A-23170	US-08-339-582-2	US-08-587-680A-4	US-08-567-375-4	US-08-587-680A-2	US-08-567-375-2	05-08-4/5-891A-2
	Sequence 3	Sequence 3	Sequence 2					Sequence 5	Sequence 1	Sequence 2	Sequence 2	Sequence 2	Sequence 4	Sequence 4	Sequence 2	Sequence 2	Sequence 2
.2, Appl		37, Appl	15, Appl	145, App	3, Appli	24, Appl	~	5600, Ap	18162, 7	27429, 1	23170, /	Appli	, Appl	, Appli	?, Appl:	?, Appl:	2, Appl

ALIGNMENTS

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: MATC J. Rubenfield et al.

APPLICANT: MATC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO F

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS:

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 32682

LENGTH: 497
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US-09-107-532A-5075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Pseudomonas
US-09-252-991A-32682
                                                                                                                                                                                                                              Sequence 5075, Application Us/09107532A
Patent No. 6588275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCCOCCUS
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS
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                                                            STREET: 100 Beaver St
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                      CORPORATION
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OPERATING

SYSTEM: <Unknown>

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                                                                                                                          ; ORGANISM: beak and feather disease virus US-09-267-177-8
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                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09267177 Patent No. 6287856
                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                              Matches
                                                                                         Query Match
                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/267,177
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: 60/077,890
EARLIER FILING DATE: 1998-03-13
                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Vaccines against Circovirus Infections FILE REFERENCE: 21099.0057
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Poet, Steven E.
APPLICANT: Ritchie, Branson W.
APPLICANT: Niagro, Frank D.
APPLICANT: Lukert, Phil D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 5075: SEQUENCE CHARACTERISTICS:
                                                                                                                                                             TYPE: PRT
                                                                                                                                                                             ENGTH: 220
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                                                             Local Similarity
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FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: YES
138 GWLPY 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 GWLPY 30
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                              2 GWLPY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII
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                                                              Conservative
                                                       85.4%; pr
100.0%; pr
0;
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; Pred. No
                                                                          Score 35;
Pred. No.
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                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
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                                                                Gaps
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Sequence 4, Application US/08845161A

Patent No. 5976850

GENERAL INFORMATION:
APPLICANT: Lathe, Richard
APPLICANT: Rose, Kenneth A.
APPLICANT: Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED TOWNSEES OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5976850th Glebe Rd. 8th floor
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; Sequence 932, Application US/09198452A
; Patent No. 6559294
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Thehes 5; Conservi
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LENGTH: 421
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Griffals,
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Patent No. H002022
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn V
SEQ ID NO 8
LENGTH: 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/0 CURRENT FILING DATE: 1998-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/041,075A CURRENT FILING DATE: 1998-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Heidler, APPLICANT: Radding, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1997-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Candida parapsilosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 5; Conserv
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X-11242 Sequence Lst
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steven A
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thes 0;
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2e+02;
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US-09-270-751-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Wilson, Mary J.

REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 604-408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEPAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: 1inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Applicatio Patent No. 6184350 GENERAL INFORMATION:
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Matches 5; Conserva
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9421093.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/270,751

FILING DATE: 17-Apr-2000

CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19-OCT-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 21-APR-1997
                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 6184350th Glebe Rd.
                                                                                                                                                                                                                                                                                                                                                             Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
SEQUENCES CODING THEREFOR AND USED THEREOF
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lathe, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 GWLPY 53
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                                                                                                                                                                                                                                                                CITY: Arlington
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09270751
APPLICATION NUMBER: PCT/GB95/02465 FILING DATE: 18-OCT-1995
                                                                                                                                                                                                                                           COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Rose, Kenneth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.4%; Score 35; 100.0%; Pred. No.
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2.4e+02;
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-270-751-4
                                                                                                                           ; ORGANISM: Murine sp. US-09-168-218B-5
                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/168,218B
CURRENT FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 9607289.7
PRIOR FILING DATE: 1996-04-09
PRIOR PELICATION NUMBER: 9608445.5
PRIOR FILING DATE: 1996-04-24
PRIOR APPLICATION NUMBER: 9704905.0
PRIOR FILING DATE: 1997-03-10
PRIOR FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN Ver. 2.1
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US-09-168-218B-5
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                                                               Best Loc
Matches
                                                                                                                                                                                          SEQ ID NO 5
                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NEUROSTEROIDS FILE REFERENCE: 604-460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                         LENGTH:
                                                          Local Similarity
nes 5; Conserv
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REGISTRATION NUMBER: 32,955
REPERENCE/DOCKET NUMBER: 604-408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: GB 9421093.7 FILING DATE: 19-OCT-1994 ATTORNEY/AGENT INFORMATION:
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49 GWLPY 53
                                                                                                                                                                           507
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                               2 GWLPY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SECKL, JOHNATHAN
BEST, RUTH
YAU, JOYCE L.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 703-816-4100
                                                               Conservative
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                                                                          85.4%; Score 35; DB 4; L
100.0%; Pred. No. 2.4e+02;
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100.0%; Pred. No. 2.4e+02;
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US-09-252-991A-18847 Sequence 18847, Application US/09252991A Patent no. 6551795 GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al.

RESULT 9

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US-09-252-991A-29895; Sequence 29895, App.; Patent No. 6551795
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US-09-252-991A-29895
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SEQ ID NO 29895
LENGTH: 201
                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION: APPLICANT: Marc J.
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Patent No. 6551795
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                   FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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NUMBER OF SEQ ID NO
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
NUMBER OF SEQ ID NOS:
SEQ ID NO 22211
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UMBER: US 60/074,788
1998-02-18
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1998-07-27
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Pred. No.
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SEQ ID NO 27172
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Best Local
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APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                              Sequence 106, Application US/09599360B Patent No. 6548633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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SEQ ID NO 106
LENGTH: 385
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                                                                                                     PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR FILING DATE: 1999-06-25
                                  NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
                                                                    PRIOR APPLICATION NUMBER: 09/469,099 PRIOR FILING DATE: 1999-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/599, 360B CURRENT FILING DATE: 2000-06-21
                                                                                                                                                                                                                         APPLICANT: Bouqueleret, L.

APPLICANT: Jobert, S.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
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NAME/KEY: UNSURE
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VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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100.0%; Pred. No.
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Pred. No.
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hes 0;
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ORGANISM: Homo

Sapiens

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GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Shi, Yanggu
APPLICANT: Roben, Steve M.
FILE OF INVENTION: Interleukin 17 Receptor-Like Protein
FILE REFERENCE: pp398p1
CURRENT APPLICATION NUMBER: US/09/268,311
CURRENT APPLICATION NUMBER: 60/059,133
EARLIER APPLICATION NUMBER: 60/059,133
EARLIER FILING DATE: 1997-09-17
EARLIER APPLICATION NUMBER: 09/154,219
EARLIER FILING DATE: 1998-09-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 426
TYPE: PRT
ORGANISM: Homo sapiens
US-09-268-311-3
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CURRENT FILING DATE: 1999-03-16
EARLIER APPLICATION NUMBER: 60/059,133
EARLIER FILING DATE: 1997-09-17
EARLIER APPLICATION NUMBER: 09/154,219
EARLIER FILING DATE: 1998-09-16
ENUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
SEQ ID NO 2
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US-09-268-311-3
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Best Local Similarity 100.00
"atches 5; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-268-311-2
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; NAME/KEY: SIGNAL
; LOCATION: -184..-1
US-09-599-360B-106
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Ouery Match 82.9%; Score 34; DB 4; Length 426 Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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Patent No. 6482923
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APPLICANT: Ruben, Steve M.
TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
FILE REFERENCE: PF398P1
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100.0%; Pred. No. 2.6e+02;
                                        Length 426;
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Search completed: August 20, 2003, 12:44:23 Job time : $5.15663 \ \text{secs}$.

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Result
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Maximum DB seq
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Perfect score:
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                                                    1110987654
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length: 2000000000
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Match
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90.2
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/pubpaa/US07_NEW_UBL pep:*
/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_NEW_UBL pep:*
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/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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  US-09-864-761-37631

US-10-083-357-859

US-10-083-357-907

US-10-083-357-934

US-09-853-450-32

US-09-853-450-32

US-10-156-761-13728

US-10-278-536-196

US-09-742-580-8

US-09-742-581-8

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US-09-989-919-85
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Sequence 33, Appl
Sequence 85, Appl
Sequence 87, App
Sequence 97, App
Sequence 94, Appl
Sequence 32, Appl
Sequence 13728, A
Sequence 18, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 9541, Ap
Sequence 9541, Ap
Sequence 9541, Ap
Sequence 12623, A
Sequence 41798, A
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ALIGNMENTS	-867 -586-	-10-194-457-	-10-187-749-	-10-199-672-40	US-10-063-735-158		US-09-908-827-12	US-09-747-259-12	US-09-816-744-12	US-09-874-503-12	US-09-778-971-5	US-09-886-404-18	US-09-778-971-7	US-10-183-708-102	US-09-148-545-259.	-09-981-876-	-09-764-864-	-10-219-834-20	-10-225-567A-	-10-183-116-3	-09-995-225-2	-09-995-225-2	-10-219	-09-778-971-	-738-626-	-10-017-161-	-09-148-54		-09-764-868-
	158,	400,	400		15.		3	2	2	5	IJ.	B.	7	10	Sequence 259, App	25	equence 82	20.	674		2	20		ω,	4691,	1600,	e 136, Ap	136, A	Sequence 1233, Ap

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TITLE OF INVENTION: SPECIFIC BINDING MOLECUL
TITLE OF INVENTION: CONTALMING THEM AND THER
TITLE OF INVENTION: ANGIGENESIS
FILE REFERENCE: SCH-1733P1
CURRENT FILING DATE: 199-04-28
CURRENT FILING DATE: 199-04-28
PRIOR APPLICATION UNMBER: 09/075.338
PRIOR FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 33
LENGTH: 6
                                                       Query Match
Best Local Similarity
""" 6; Conserv
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                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B
; OTHER INFORMATION: antibody clone
US-09-300-425B-33
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US-09-300-425B-33
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APPLICANT: MERI, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33, Application US/09300425B Publication No. US20030045681A1
                                                                                                                                                                                                                    LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
                                   1 GGWLPY 6
GGWLPY
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
                                                                                         100.0%;
                                                                         0;
                                                                       Score 41; DB 11;
Pred. No. 4.5e+05;
Mismatches 0;
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RESULT 2

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US-09-989-919-85
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SEQ ID NO 85
LENGTH: 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: Acomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILLING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                              OR APPLICATION NUMBER: PCT/US01/00664
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00669
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00665
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00668
OR APPLICATION NUMBER: PCT/US01/00668
OR APPLICATION NUMBER: PCT/US01/00668
OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 09/632,366 FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                             FILING DATE:
                                                            APPLICATION NUMBER: PCT/US01/00663
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43 GGWLPF 48
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NUMBER: PCT/US01/00662
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RESULT 5
US-10-083-357-907
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                                                                                                                                                                                                   ; TYPE: PRT ; ORGANISM: Saccharomyces cerevisiae US-10-083-357-859
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SEQ ID NO 859
LENGTH: 55
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Publication No. US20 GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                               FILE REFERENCE: 032796-090
CURRENT APPLICATION NUMBER: US/10/083,357
CURRENT FILING DATE: 2002-02-27
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NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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5; Conserv
                                                                                                                      2 GWLPY 6
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              Application US/10083357
o. US20030054370A1
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D IN ADULT LIVER, SIGNAL
D IN FETAL LIVER, SIGNAL
D IN HETAL LIVER, SIGNAL = 19
D IN HELA, SIGNAL = 21
D IN PLACENTA, SIGNAL = 18
D IN BT474, SIGNAL = 18
D IN BT474, SIGNAL = 16
D IN BARROW, SIGNAL
D IN BORE MARROW, SIGNAL
NHIT: AM468873.1, EVALUE
                                                                                                                                                  0;
                                                                                                                                                               Score 35;
Pred. No.
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Pred. No.
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55;
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APPLICANT: Qiandong TITLE OF INVENTION:

Zeng et al. Systemic Discovery of

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Sequence 934, Application US/10083357
Publication No. US20030054370A1
GENERAL INFORMATION:
APPLICANT: Qiandong Zeng et al.
TITLE OF INVENTION: Systemic Discovery of New Genes
FILE REFERENCE: 032796-090
CURRENT APPLICATION NUMBER: US/10/083,357
CURRENT FILING DATE: 2002-02-27
NUMBER OF SEQ ID NOS: 1346
SEQ ID NO 934
LENGTH: 61
TYPE: PRT
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US-10-083-357-934
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APPLICANT: Pelaz, Soraya
APPLICANT: Ditta, Gary
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 32
LENGTH: 237
TYPEE. REF
                                     Query Match
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      Best Local Similarity 100 Matches 5; Conservative
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CURRENT APPLICATION NUMBER: US/10/083,357
CURRENT FILING DATE: 2002-02-27
NUMBER OF SEQ ID NOS: 1346
SEQ ID NO 907
                                                                                                   ORGANISM: Arabidopsis thaliana FEATURE:
                                                                              OTHER INFORMATION: SEPALLATA3 (SEP3)
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TYPE: PRT
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100.0%; Pr
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100.0%; Pred. No. 93
tive 0; Mismatches
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0; Mismatches
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Pred. No.
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93;
                 DB 10;
2.7e+02;
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              FEATURE:
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CURRENT APPLICATION NUMBER: US/10/278,536
CURRENT FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 196
LENGTH: 251
TYPE: PRT
; OTHER INFORMATION: G145
US-10-278-536-196
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13728
LENGTH: 246
TYPE: PRT
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JF 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                           APPLICANT: Broun, Pierre
TITLE OF INVENTION: STRESS-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-011
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
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                                                        ORGANISM: Arabidopsis thaliana
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les 5; Conserv
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Yu, Guo-Liang
Keddie, James
Ratcliffe, Oliver
Pilgrim, Marsha
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HORIKAWA, HIROSHI
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Jiang, Cai-Zhong
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100.0%; Pred. No.
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. 2.8e+02;
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Gaps

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CURRENT APPLICATION UMMBER: US/09/742,582
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/041,075
PRIOR FILING DATE: 1998-03-10
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 505
RESULT 12
US-Q9-742-581-8
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US-09-742-580-8
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Best Local :
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SEQ ID NO 8
LENGTH: 505
TYPE: PRT
ORGANISM: Candida parapsilosis
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TITLE OF INVENTION: IPC SYNTHASE GENES FROM FUNGI
FILE REFERENCE: X-11242 Sequence Lst
Patent No. US20010012615A1
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Best Local Similarity
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APPLICANT: Radding, Jeffrey A
TITLE OF INVENTION: IPC SYNTHASE GENES FROM FUNGI
FILE REFERENCE: X-11242 Sequence Lst
CURRENT APPLICATION NUMBER: US/09/742,580
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/041,075
PRIOR APPLICATION NUMBER: 09/041,075
PRIOR FILING DATE: 1998-03-10
NUMBER OF SEQ ID NOS: 24
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100.0%; Pred. No. 4.9e+02;
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100.0%; Pred. No.
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2.8e+02;
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RESULT 14
US-10-156-761-12623
US-10-156-761-12623, Application US/10156761
; Sequence 12623, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: IKEDA, JUN
; APPLICANT: ISSIEAWA, JUN
; APPLICANT: ISSIEAWA, JUN
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                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Streptomyces avermitilis us\hbox{-}10\hbox{-}156\hbox{-}761\hbox{-}9541
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                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 5
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SEQ ID NO 9541
LENGTH: 505
TYPE: PRT
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SEQ ID NO 8
LENGTH: 505
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Heidler, Steven A
APPLICANT: Radding, Jeffrey A
TITLE OF INVENTION: IPC SYNTHASE GENES FROM FUNGI
FILE REFERENCE: X-11242 Sequence Lst
CURRENT APPLICATION NUMBER: US/09/742,581
CURRENT FILING DATE: 2000-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
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nes 5; Conserv
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                                                    85.4%; Score 35; ilarity 100.0%; Pred. No. Conservative 0; Mismatci
                                                                                                                                                                                                                                                                                                         Mismatches
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4.9e+02;
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IKEDA, HARUO ISHIKAWA, JUN HORIKAWA, HIROSHI

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SEQ ID NO 12623
LENGTH: 520
TYPE: PRT
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR-
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
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09-864-761-41798
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PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: Aeomica-x-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quence 41798, Application US/09864761
tent No. US20020048763A1
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PPLICANT: SAKAKI, YOSHIYUKI
PPLICANT: HATTORI, WASAHIRA
TILE OF INVENTION: NOVEL POLYNUCLEOTIDES
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                                                                                        OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00663
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00662
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00661
OR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                               TOR APPLICATION NUMBER: PCT/US01/00664

COR FILING DATE: 2001-01-30

COR APPLICATION NUMBER: PCT/US01/00669

COR APPLICATION NUMBER: PCT/US01/00665

COR APPLICATION NUMBER: PCT/US01/00665

COR APPLICATION NUMBER: PCT/US01/00666

COR FILING DATE: 2001-01-30

COR FILING DATE: 2001-01-30

COR FILING DATE: 2001-01-30

COR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR APPLICATION NUMBER: GB 24263.6
OR FILING DATE: 2000-10-04
OR APPLICATION NUMBER: US 60/236,359
OR FILING DATE: 2000-09-27
OR APPLICATION NUMBER: PCT/US01/00666
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00667
OR REPLICATION NUMBER: PCT/US01/00667
OR FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30 APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
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Similarity 83.3%;
5; Conservative
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Pred. No.
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Search completed: August Job time : 6.50602 secs

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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 41798
LENGTH: 98
                                                                                                                                                                                                                                                                                    Query Match
Best Local :
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OTHER INFORMATION: E
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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1 GGWLPY 6
|||:|:
36 GGWIPW 41
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                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                         Conservative
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EXPRESSED IN HELA, SIGNAL = 1.9

EXPRESSED IN BRAIN, SIGNAL = 1.4

EXPRESSED IN FETAL LIVER, SIGNAL = 1.6

EXPRESSED IN HEART, SIGNAL = 1.0

EXPRESSED IN HEART, SIGNAL = 1.0

EXPRESSED IN HEART, SIGNAL = 1.10

EXPRESSED IN HEART, SIGNAL = 1.10

EXPRESSED IN HELANDER 1.10

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Pred. No. 1.9e+02;
2; Mismatches 0;
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Sequence 33, Appl Sequence 78364, A Sequence 32682, A Sequence 112199,

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                         Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 1s derived by analysis of the total score distribution.
                                                                              Score
                41
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                                                           Query
Match
           100
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                                                                                                                                                                                                                                                       'cgn2_6/ptodata/1/paa/US081_COMB.pep:*
'cgn2_6/ptodata/1/paa/US081_COMB.pep:*
'cgn2_6/ptodata/1/paa/US081_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US06
                                                                         Length DB
           99
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      US-09-075-338C-33
US-09-300-425B-33
                                                                                                                                       SUMMARIES
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7_COMB.pep:*
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                                                                  Description
    Sequence 33, Appl
Sequence 33, Appl
                                                Sequence 33 Application US/09075338C

GENERAL INFORMATION:
APPLICANT: NERI, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: VITI, Francesca
APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfred
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY
FILE REFERENCE: SCH-1733
CURRENT APPLICATION NUMBER: US/09/075,338C
CURRENT FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B
OTHER INFORMATION: antibody clone
US-09-075-338C-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
US-09-075-338C-33
Query Match
Best Local Similarity
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12 US-09-791-537-78364

10 US-10-437-963-112199

PCT-USO2-04240-67

10 US-10-437-963-112199

PCT-USO2-04240-67

10 US-10-216-583-1397

10 US-10-216-599-171560

US-10-217-999-33023

10 US-10-437-963-104557

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11 US-09-664-761-3763

12 US-09-664-761-3763

12 US-10-182-999-2895

17 US-10-182-999-2895

17 US-10-182-999-2896

18 US-10-203-135-29462

18 US-10-203-135-29462

18 US-10-203-135-30564

18 US-10-203-138-14758

18 US-10-203-138-14758

18 US-10-203-138-14758

18 US-10-203-139-1952

18 US-10-203-139-1952

18 US-10-203-139-1952

18 US-10-203-139-1952

18 US-10-203-139-1952

18 US-10-23-33-726-907

18 US-10-033-37-66033

18 US-10-033-37-6003

18 US-10-1083-357-934

18 US-10-108
Score
Pred.
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N 1.
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Sequence 67, Appl Sequence 1397, App Sequence 1397, App Sequence 1397, App Sequence 171560, Sequence 3764, A Sequence 3764, A Sequence 27814, A Sequence 27814, A Sequence 3764, A Sequence 3764, A Sequence 3764, A Sequence 3764, A Sequence 1436, A Sequence 1436, A Sequence 1478, A Sequence 15851, A Sequence 15852, A Sequence 15854, A Sequence 15852, A Sequence 15852, A Sequence 15858, Sequence 15853, A Sequence 15853, App Sequence 15952, App Sequence 1473, App Sequence 272, App Sequence 273, App Sequence 275, App Sequence 3759, App

DB 14; 5.2e+06;

Length

B 8

Matches

Conservative

0,

Mismatches

0;

Indels

0;

Gaps

0

GGWLPY 6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-300-425B-33
                                      ; OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B; OTHER INFORMATION: antibody clone US-09-512-082-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   닭
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-512-082-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: P
SEQ ID NO 33
LENGTH: 6
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Query Match
                                                                                                                                                                                        SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF FILE REFERENCE: SCH-1733P1
CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28-
                                                                                                                                                                                                                                           TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF TITLE OF INVENTION: ANGLOGENESIS
FILE REFERENCE: SCH-1733P2
CURRENT APPLICATION NUMBER: US/09/512,082
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 09/300,425
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NERI, Dario
APPLICANT: TARLI, LOTENZO
APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 34 SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                         FEATURE:
                                                                                                                                                                  ENGTH: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGWLPY 6
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VITI, Francesca
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      100.0%;
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      Score
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      41;
      DВ
        19;
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  Length
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; ORGANISM: HOMO
US-09-791-537-78364
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US-10-437-963-112199
S-10-437-963-112199
; Sequence 112199, Application US/10437963
; GENERAL INFORMATION:
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Best Local Similarity
"hes 5; Conserva
                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-419-128-32682
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 78364
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 32682, Application US/10419128
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MARC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: MCCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
SEQ ID NO 32682
LENGTH: 497
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Matches
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US/09/252,991
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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CURRENT FILING DATE: 2003-04-21
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                                                                                                                        458 GGWIPY 463
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6; Conserv
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                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                          95.1%;
83.3%;
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                                                                                                                                                                                                                          Score 39; DB 30;
Pred. No. 9.4e+02;
                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                             Length 497;
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                                                                                                                    US-09-989-919-85
                                                                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                       ; PRIOR FILING DATE: 2001
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin vers
; SEQ ID NO 67
; LENGTH: 51
                                                                                                                                                                                                                                                                                                  PCT-US02-04240-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US02-04240-67
                                                                                    Sequence 85, Applica GENERAL INFORMATION:
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Best Local
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SEQ ID NO 112199
LENGTH: 107
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                                                                         APPLICANT: Macina, Roberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5321)B CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/268,291
                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: PCT/US02/04240 CURRENT FILING DATE: 2002-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Compositions and Methods FILE REFERENCE: DEX-0309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sun, Yongming APPLICANT: Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: diaDexus, Inc
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                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                      Local Similarity
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5; Conserv
Pluta, Jason
Ghosh, Malavika
Sun, Yongming
Liu, Chenghua
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Kovalic, David
                                                                                                     Application US/09989919
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Macina, Roberto
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                                                          Recipon, Herve
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83.3%;
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Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                      DB 1;
2.7e+02;
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3.5e+02;
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                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                  Length 51;
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Best Local Similarity
Whethes 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prior application data removed -
NUMBER OF SEQ ID NOS: 1983
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 1397
LENGTH: 150
                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and FILE REFERENCE: DEX-0289
CURRENT APPLICATION NUMBER: US/09/989,919
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,505
PRIOR APPLICATION NUMBER: 60/252,505
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/760,469
CURRENT FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: PT254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 51
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE LOCATION: (39)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                           LOCATION: (127)
OTHER INFORMATION:
                                                                                                                                                                                                     NAME/KEY: SITE
                                                                                                                                                                                                                   LOCATION: (117)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                LOCATION: (115)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE LOCATION: (92)
                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                NAME/KEY: SITE
140 GGWLPF 145
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                          1 GGWLPY 6
                                                        Similarity
5; Conserv
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                                                          Conservative
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                                                                                                                               Xaa equals any of the naturally occurring L-amino
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                                                       Score 37; DB Pred. No. 6.96
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                                                                                  Length 150
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RESULT 10

US-10-216-583-1397 ; Sequence 1397, Application US/10216583 ; GENERAL INFORMATION:

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                                                                                                                                            US-10-216-583-1397
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                                                                       Matches
                                                                                        Query Match
Best Local
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CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/760,469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/220,963 PRIOR FILING DATE: 2000-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PTZ54ClN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/214,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/179,065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/217,496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/217,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-01-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (39)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                    LOCATION: (127)
OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (92)
OTHER_INFORMATION: Xaa equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (148)
                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (115)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OCATION: (110)
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                                                                     Local Similarity
nes 5; Conserv
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APPLICATION NUMBER: 60/
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FILING DATE: 2000-07-14
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                                                                                                                                                             INFORMATION: Xaa
140 GGWLPF 145
                                   1 GGWLPY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATION NUMBER: 60/180,628
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                                                                       Conservative
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83.3%;
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Pred. No.
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                                                                                        6.9e+02;
                                                                                                       DB 28; Length 150;
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RESULT 11
US-10-437-963-104557
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_125934C.1.pep
US-10-424-599-171560
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                         QΥ
                                             Query Match
Best Local Similarity
Thes 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                               Sequence 171560, Application US/10424599 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 104557, App GENERAL INFORMATION:
                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 171560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local 9
                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Soy Nucleic Acid Molecules TITLE OF INVENTION: Plants and Uses Thereof for FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                              CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: La Rosa Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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NAME/KEY: unsure
LOCATION: (1)..(175)
OTHER INFORMATION: unsure at all xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                    LENGTH: 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity es 5; Conserv
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169 GGWLPF 174
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                             1 GGWLPY 6
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                                                                                                                                                                                                                                                                                                                                          Zhou Yihua
                                                                                                                                                                                                                                                                                                                                                    Ja Rosa Thomas J
Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barbazuk, Brad
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Pred. No. 7.9e
1; Mismatches
                                                                          Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                           Molecules and Other Molecules Associated With Thereof for Plant Improvement
                                                                           9.4e+02;
                                                                                          DB 30;
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                                                                                        Length 211;
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RESULT 13 US-10-219-999-33023

equence 33023, Application US/10219999 . ENERAL INFORMATION:

Michael D

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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28
INUMBER OF SEQ ID NOS: 73128
SED ID NO 39507
LENGTH: 382
TYPE: pp...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LIU, JINGONG
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-09-1
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEG ID NOS: 63520
SEQ ID NO 33023
LENGTH: 382
TYPE: PRT
                                                                                                  RESULT 15
US-60-312-544-5701
                                                                                                                                                                                                      Query Match
Best Local Similarity 83.38
""+ ches 5; Conservative
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                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE;
; OTHER INFORMATION: Clone ID: 700238067_FLI.pep
US-10-425-114-39507
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US-10-219-999-33023
                                                                   GENERAL INFORMATION:
                                                                                      Sequence 5701,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.2%;
Best Local Similarity 83.3%;
Matches 5; Conservative
APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, M
APPLICANT: Hinkle, Gre
APPLICANT: Kovalic, Da
                                                                                                                                                                1 GGWLPY 6
||||:
163 GGWLPF 168
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| 163 GGWLPF 168
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Kovalic, David K.
                                                                               Application US/60312544
                                                                                                                                                                                                                                            90.2%;
                                                                                                                                                                                                                                        Score 37; DB 30; Length 382; Pred. No. 1.6e+03;

    Mismatches

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Search completed: August 20, 2003, 13:13:45 Job time: 63.4096 secs
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                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 10730
SEQ ID NO 5701
LENGTH: 382
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: 700238067_FLI US-60-312-544-5701
                                                                                                                                                   Query Match
Best Local
                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                    APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REPERENCE: 38-10(52726)A
CURRENT APPLICATION NUMBER: US/60/312,544
CURRENT FILING DATE: 2001-08-15
                                                                                                                              Local Similarity es 5; Conserv
                                                                163 GGWLPF 168
                                                                                               1 GGWLPY 6
                                                                                                                              Conservative
                                                                                                                                             90.2%;
                                                                                                                                        Score 37; DB 31;
Pred. No. 1.6e+03;
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                                                                                                                                                         Length 382;
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Title: Perfect score: Sequence:

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Scoring table:

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1 GGWLPY 6 US-09-512-082-33

Minimum DB seq length: Maximum DB seq length:

Database

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/paa/U
2: /cgn2_6/ptodata/1/paa/U
3: /cgn2_6/ptodata/1/paa/U
4: /cgn2_6/ptodata/1/paa/U
5: /cgn2_6/ptodata/1/paa/U
6: /cgn2_6/ptodata/1/paa/U
7: /cgn2_6/ptodata/1/paa/U
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/cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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                      US-10-294-433-253
US-10-286-897-1865
US-10-286-897-5437
US-10-286-897-5437
US-10-286-897-5437
US-10-286-898-5437
PCT-US03-19871-10
US-10-408-765A-1125
US-10-408-765A-1127
US-10-401-397A-2
US-10-292-798-1274
PCT-US03-19871-8
PCT-US03-19871-6
US-10-603-114-545
PCT-US03-19871-2
PCT-US03-19871-2
US-10-617-773-12
PCT-US03-19871-4
US-10-603-114-6420
US-10-603-113-26574
US-10-603-113-26574
US-10-603-113-26574
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Compugen Ltd
                 Sequence 253, App Sequence 1865, App Sequence 1867, App Sequence 10, Appli Sequence 1125, App Sequence 1125, App Sequence 1274, Appli Sequence 64, Appli Sequence 5455, Appli Sequence 6420, Appli Sequence 6420, Appli Sequence 555, Appli Sequence 6420, Appli Sequence 555, Appli Sequence 555, Appli Sequence 550, Appli Sequence 550, Appli Sequence 550, Appli Sequence 5574, Appli Sequence 5574, Appli Sequence 7515, Appli Sequence 7515, Appli Sequence 666, Appli Sequence 7515, Appli Sequence 5574, Appli Sequence 5574, Appli Sequence 5574, Appli Sequence 6530, Appli Sequence 6530, Appli Sequence 6530, App Sequence 6530, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID N
SOFTWARE: Custom
SEQ ID NO 253
LENGTH: 131
TYPE: PRT
ORGANISM: Homo se
US-10-294-433-253
RESULT 2
US-10-286-897-1865
; Sequence 1865, Application US/10286897
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PRIOR APPLICATION NUMBER: US/10/294,433
CURRENT FILLING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/989,600
PRIOR FILLING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR FILLING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: 10/115,831
PRIOR FILLING DATE: 2002-04-02
PRIOR PILLING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 09/677,298
PRIOR APPLICATION NUMBER: 09/695,781
PRIOR APPLICATION NUMBER: 09/695,781
PRIOR APPLICATION NUMBER: 10/150,802
PRIOR FILLING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: 09/715,869
PRIOR APPLICATION NUMBER: 09/715,869
PRIOR APPLICATION NUMBER: 10/167,379
PRIOR APPLICATION NUMBER: 10/167,379
PRIOR APPLICATION NUMBER: 10/167,379
PRIOR APPLICATION NUMBER: 10/167,379
PRIOR APPLICATION NUMBER: 09/715,730
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US-10-294-433-253
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Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 10/2
PRIOR FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 2001-22-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 792CIP4
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                                                                                                                                                   1 GGWLP 5
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5; Conserv
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                                                                                                                                                                                                                        Conservative
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100.0%; Pred. No.
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US-10-603-113-15999
US-10-603-114-7525
US-10-603-114-7525
US-10-603-114-764
PCT-US02-18638-26
US-10-612-783-5154
US-10-612-783-5154
US-10-612-783-5154
US-10-612-783-5159
US-10-612-783-5159
US-10-612-783-5159
US-10-613-783-79
PCT-US02-41847A-11
US-10-603-114-6379
PCT-US02-41847A-21
US-10-273-573-9338
US-10-273-573-9338
US-10-369-072-43
US-10-369-072-43
US-10-369-072-43
US-10-369-072-43
US-10-294-433-256
US-10-294-433-688
US-10-294-433-688
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Mismatches
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Sequence 15999, A
Sequence 50, Appl
Sequence 7825, Ap
Sequence 7864, Appl
Sequence 3649, Ap
Sequence 5154, Appl
Sequence 5155, Ap
Sequence 6115, Appl
Sequence 6179, Ap
Sequence 6379, Ap
Sequence 639, Ap
Sequence 41, Appl
Sequence 256, App
Sequence 256, Appl
Sequence 256, Appl
Sequence 688, Appl
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Result No.

Score

Query Match

Length

B

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Gaps

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CURRENT APPLICATION NUMBER: US/10/286,897

TLE OF INVENTION: Novel Nucleic Acid and Polypeptides

ILE REFERENCE:

784FLPCT Inc

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US-10-286-897-1865
                                                                                                                                                ; ORGANISM: Homo sapiens US-10-258-898A-1865
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Best Local Similarity
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SEQ ID NO 1865
LENGTH: 294
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: pt_FL_genes_b
SEQ ID NO 1865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -10-258-898A-1865
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PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US/09/620,312
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PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US/09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR PRIOR PRIOR TO TO THE TOTAL PRIOR TO T
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FILE REFERENCE: 784FLPCT
CURRENT APPLICATION NUMBER: US/10/258,898A
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-04-25
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PRIOR APPLICATION NUMBER: US/09/727,344
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APPLICATION NUMBER: US09/620,312
FILING DATE: 2000-07-19
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                                         82.9%;
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US-10-286-897-5437
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US-10-286-897-5437
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SEQ ID NO 5437
TENGTH: 310
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Best Local Similarity
Matches 5; Conser
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PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US/09/598,042
PRIOR FILING DATE: 2000-06-20
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                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/258,898A CURRENT FILING DATE: 2002-10-29
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                                                                                                                                    PRIOR APPLICATION NUMBER: US09/598,042 PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                 PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/09/488,725
                                                                                                                                                                                                                                                                            FILE REFERENCE: 784FLPCT
                                                                                                                                                                                                                                                                                                            APPLICANT: Hyseq Inc
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TYPE: PRT
                                                                               PRIOR APPLICATION NUMBER: US09/653,450
                                                                                                 PRIOR APPLICATION NUMBER: US09/620,312 PRIOR FILING DATE: 2000-07-19
                                                                                                                                                                                                           PRIOR FILING DATE: 2000-01-2
                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/662,191 FILING DATE: 2000-09-14 APPLICATION NUMBER: US/09/693,036
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                                                CATION NUMBER: US09/662,191
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NUMBER: US09/693,036
2000-10-19
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; ORGANISM: Homo sapiens
US-10-408-765A-1125
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US-10-258-898A-5437
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GENERAL INFORMATION:
APPLICANT: Eli Lilly and Company
TITLE OF INVENTION: Novel Proteins and Their Uses
FILE REFERENCE: X-15815
                                                            APPLICANT: Glenn, Gary P.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660084.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
CURRENT FILING DATE: 2003-04-04
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SEQ ID NO 10
LENGTH: 312
TYPE: PRT
                                                       NUMBER OF SEQ ID NOS: 3077

SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1125
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SOFTWARE: pt_FL_genes_b Versions 1.0
SEQ ID NO 5437
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CURRENT FILING DATE: 2003-07-23
NUMBER OF SEQ ID NOS: 24
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hes 5; Conservative
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Taylor, Steven W.
Glenn, Gary M.
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PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1274
LENGTH: 322
TYPE: PRT
ORGANISM: Homo sapiens
US-10-292-798-1274
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS AND COMPOUNDS FOR PREVENTION AND TREATMENT OF ELEVATED TITLE OF INVENTION: INTRAOCULAR PRESSURE AND RELATED CONDITIONS FILE REFERENCE: 4518/IM674US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Peri, Krishna G. APPLICANT: Moffett, Serge APPLICANT: Abran, Daniel
                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS FILE REFERENCE: 084335/166
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                                                             Conservative
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US-10-603-114-5455
; Sequence 5455, Application US/10603114
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
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SEQ ID NO 8
LENGTH: 328
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local
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                                                TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/10/603,114
CURRENT FILING DATE: 2003-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: PCT/US03/19871
CURRENT FILING DATE: 2003-07-23
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Eli Lilly and Company TITLE OF INVENTION: Novel Proteins and Their Uses FILE REFERENCE: X-15815
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CURRENT FILING DATE: 2003-07-23
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TITLE OF INVENTION: Novel Proteins and Their Uses
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EQ ID NO 6
LENGTH: 371
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                                 PRIOR APPLICATION NUMBER: US/09/543,681
                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MISC_FEATURE LOCATION: (1)..(371) OTHER INFORMATION: LP393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)..(328)
OTHER INFORMATION: LP394
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APPLICATION NUMBER:
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Pred. No. 67;
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PCT-US03-19871-2
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SEQ ID NO 5455
LENGTH: 416
TYPE: PRT
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APPLICANT: Eli Lilly and Company
TITLE OF INVENTION: Novel Proteins and Their Uses
FILE REFERENCE: X-15815
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APPLICANT:
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CURRENT FILING DATE: 2003-07-23
NUMBER OF SEQ ID NOS: 24
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APPLICANT: YADSULA, DANIEL THEREOF TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF FILE REFERENCE: P1881RIC1P4(US)
CURRENT APPLICATION NUMBER: US/10/617,573
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TYPE: PRT
ORGANISM: Homo sapiens
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OTHER INFORMATION: LP391
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                                                                                        VanLookeren, Menno
Vandlen, Richard
Watanabe, Colin
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                                                                        Williams, P.Mickey
                                                                                      Watanabe,
                                                                                                                                  Starovasnik, Melissa.
                                                                                                                                                    Tumas, Daniel
                                                                                                                                                                 Hillan, Kenneth J.
Hymowitz, Sarah
                                                                                                                                                                                                           Gurney, Austin
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Grimaldi, J.Christopher
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Godowski, Paul 1
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Sequence 4, Application PC/TUS0319871

GENERAL INFORMATION:
APPLICANT: Eli Lilly and Company
ITILE OF INVENTION: Novel Proteins and Their Uses
FILE REFERRNCE: X-15815
CURRENT APPLICATION NUMBER: PCT/US03/19871
CURRENT FILING DATE: 2003-07-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 531
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(531)
OTHER INFORMATION: LP392
PCT-US03-19871-4
Search completed: August 20, 2003, 12:45:15 Job time: 2.73494 secs
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; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 12
; LENGTH: 502
; TYPE: PAT
; ORGANIZM: Homo Sapien
US-10-617-573-12
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PCT-US03-19871-4
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Best Local Similarity luv.
Thes 5; Conservative
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PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/138387
PRIOR FILING DATE: 1999-06-09
PRIOR PPLICATION NUMBER: 60/172096
PRIOR RPLICATION NUMBER: 60/172481
PRIOR APPLICATION NUMBER: 60/175481
PRIOR APPLICATION NUMBER: 60/175481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/191007
PRIOR FILING DATE: 2000-03-21
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FILING DATE: 1998-12-23
APPLICATION NUMBER: 60/130232
FILING DATE: 1999-04-21
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137.621 Million cell updates/sec
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ALIGNMENTS

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-167 <TET>
A;Cross references: GB:AI
A;Experimental source: se
C;Genetics:
A;Gene: NMB1733
C;Superfamily: 1
                                                                                                                                                                                                                                                                                                         hypothetical protein NMB1733 [imported] - Neisseria meningitidis (strain MC58 serogro C;Species: Neisseria meningitidis Neisseria Neisse
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A;Moleotettype: L178 <RES>
A;Residues: 1-178 <RES>
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R;Hansen, G.; Larribe, M.; Vaubert, D.; Tempe, J.; Biermann, B.J.; Montoya, A.L.; Proc. Natl. Acad. Sci. U.S.A. 88, 7763-7767, 1991
A;Title: Agrobacterium rhizogenes pRiB196 T-DNA: Mapping and DNA sequence of funct A;Reference number: 139720; MUID:91352070; PMID:1909028
A;Accession: 139722
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139722
ORF12 - Agrobacterium rhizogenes plasmid pRi8196
C;Species: Agrobacterium rhizogenes
C;Species: Agrobacterium rhizogenes
C;Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 08-Oct-1999
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A;Note: encoded within the T-DNA (transferred
t disease
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    meningitidis hypothetical protein NMB1733
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                                                                                                                       GB:AE002098; NID:g7226980; B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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Pred. No.
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                                                                                                                                                            PIDN: AAF42078.1;
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RESULT 4
B83012
                               RESULT
S47151
outer capsid protein VP2 - African hors C; Species: African horse sickness virus
                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000
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                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-235 <S1
                                                                                                                                                                                                                                                                                                                         A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: B83012
                                                                                                                                                                                                                                                                                                                                                                        adman, S.; Yuan, Y.; Brody, .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: B83012
R; Stover, C.K.; Pham, X.Q.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein PA5071 [imported] -C; Species: Pseudomonas aeruginosa
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A; Residues: 1-172 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete DNA sequence of a serogroup A strain of A;Reference number: A81775; MUID:20222556; PMID:10761919 A;Accession: B81828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Parkhill, J.; Achtman, M.; James, Holroyd, S.; Jagels, K.; Leather, Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical integral membrane protein NMA1989 [imported] - Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: B81828
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                                                                                                                                                                                                                                                                                                             A; Status: preliminary
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Best Local Sir
Matches 5;
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Best Local :
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                                                                                                                          1 GGWLPY 6
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5; Conser
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                                                                                                                                                        Conservative
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83.3%;
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83.3%;
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L.L.; Coulter, S.N.; Folger, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB:AL157959; NID:g7380371; PIDN:CAB85209.1; A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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Pred. No.
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Pred. No.
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Pred. No. 7
                   horse
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S.; Moule, S.;
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                   sickness
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7.2;
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                 virus
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Mungall, K.; Quail, M.A.;
                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein NMB1733
                                                                                                                                                                                     Length 235;
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                 (serotype
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Larbig,
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Rajandream
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K.; Lim,
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                                                                                                                     R;Barlow, K.
submitted to the EMBL Data
submitted to the EMBL Data
                                                            A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-637 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: NuoH
C; Superfamily:
                               A; Experimental source:
                                                                                                         A; Reference number: A; Accession: T26593
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                                               A; Cross-references:
                                                                                                                                                                       C; Accession: T26593
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A; Residues: 1-352 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status:
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A; Accession: E90175
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Best Local S
Matches 5
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Best Local S
Matches 5
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5; Conserv
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5; Conserv
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                                   EMBL:AL021474;
be: clone Y32F6A
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A; Variety: serotype 3
C; Date: 23-Nov-1994 *sequence_revision 03-Nov-1995 *text_change C; Accession: $47151
R; Vreede, F.T.; Huismans, H.
submitted to the EMBL Data Library, September 1993
A; Description: The cloning, characterization and expression of t A; Reference number: $47151
A; Accession: $47151
                                                                                                               hypothetical protein Y32F6A.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #te:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Away Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Sulfolobus solfatarious
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change
C;Accession: E90175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Map position: segment 2
C;Superfamily: African horse sickness virus
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A;Residues: 1-1057 <VRE>
A;Cross-references: EMBL:Z26316; NID:g499374; PIDN:CAA81225.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: serotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Description: Sulfolobus solfataricus complete genome
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                                                                                                                                                                                                                                                                                                                                                                                                                     NADH dehydrogenase
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83.3%;
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83.3%;
                                                       Library,
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Pred. No.
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Pred.
from
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                                                       January 1998
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GB/EMBL/DDBJ
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35;
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47;
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                                                                                                                      #text_change
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hi-Ngoc, H.P.; Redder
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PIDN:CAA16307.1;

GSPDB:GN00023;

CESP:Y32F6A.2

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C;Species: human herpesvirus 6
A;Varlety: strain HST
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T43952; T44059
R;Isegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.
J. virol. 73, 8053-8065, 1999
A;Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants
A;Recession: T43952
A;Accession: T43952
A;Status: preliminaru. +----
                         A:Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues; 1-759 < LOO2 A;Cross-references: EMBL:AF157706; PIDN:AAD49682.1 A;Experimental source: strain 229; variant B
                                                                                                                                                                                                                                                                                                      DR1 protein [imported] - human herpesvirus 6 (strain 229)
C;Species: human herpesvirus 6
A;Varlety: strain 229
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C;Accession: T44142; T44239
R;Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett,
J. Virol. 73, 8040-8052, 1999
                                                                                                                                          A:Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-759 <DOM>
A:COSS-references: EMBL:AF157706; PIDN:AAD49614.1
A:Experimental source: strain 229; variant B
A:Genetics: GNI
                                                                                                                                                                                                                                                   A;Title: Human herpesvirus 6B genome sequence: coding content A;Reference number: Z22734; MUID:99412318; PMID:10482553 A;Accession: T44142
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                                                                                                                            A; Accession:
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743952
hypothetical protein DR2 [imported] - human herpesvirus 6
C;Species: human herpesvirus 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-647 < IS2>
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A; Status: prelimina
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A; Introns: 45/3; 275/3;
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A; Residues: 1-647 <ISE>
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nes 5; Conserv
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|||||:
5 GGWLPF 240
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5; Conserv
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83
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Pred. No. 64;
1; Mismatches
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Pred. No.
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64;
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63;
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Mol. Gen. Genet. 229, 41-51, 1991
A;Title: Relationship between tryptophan biosynthesis and A;Reference number: S17702; MUID:91375449; PMID:1896020
A;Accession: S17702
A;Status: preliminary
                                                                                                                                                                                                                                            hypothetical protein 1 - Azospirillum brasilense
C;Speckes: Azospirillum brasilense
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Accession: S17702
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A; Map position: 87/1
A; Introns: 87/1
C; Genetics: <GN2
A; Gene: DR1
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A; Residues: 1-150 <ZIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Sallx gilgiana
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change
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A; Accession: T52331
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A; Introns: 87/1
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5; Conserv
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83.3%;
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Pred. No.
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Pred. No.
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Pred. No. 76;
1; Mismatches
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33;
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MADS box pro
N; Alternate
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A;Genetics:
A;Genetics:
A;Genetics:
A;Geneticon:
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A;Map position:
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A;Introns: 62/2; 90/3; 113/2; 146/3; 160/3; 174/3; 222/2
A;Introns: 62/2; 90/3; 113/2; 146/3; 160/3; 174/3; 222/2
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homol C:Keywords: DNA binding; nucleus; transcription regulation
C;Keywords: DNA binding; nucleus; transcription regulation
C;Keywords: DNA binding domain homology <SRF>
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R;Federspiel, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Cc; Vysotskaia, V.S.; Yu, G.; Ecker, J.; Theologis, A.; Davis, submitted to the EMBL Data Library, February 1998
A;Reference number: Z14197
A;Accession: T00656
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N;Alternate names: protein F316.19
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MADS box protein D - white mustard
WADS-box protein AGL9 homolog
C;Species: Sinapis alba (white mustard)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999
C;Accession: T10467
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T10467
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A;Molecule type: DNA
A;Residues: 1-251 <FED>
                                                                                                                                   probable hydroxylase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
C;Accession: T35032
R;Seeger, S.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Bonhomme, F.; Sommer, H.; Bernier, G.; Jacqmard, A. Plant Mol. Biol. 34, 573-582, 1997
A;Title: Characterization of SaMADS D from Sinapis alba A;Reference number: 217032; MUID:97390682; PMID:9247539
A;Accession: T10467
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T35032
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                                                                 A; Reference number: 221565
A; Accession: T35032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                               submitted to the EMBL Data Library, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues:
A; Residues: 1-263 <SEE>
                          A; Molecule
                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
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                        type: DNA
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A;Cross-references: EMBL:AL079355; PIDN:CAB45588.1; GSPDB:GN00070; SCOEDB:SC4C6.24c A;Experimental source: strain A3(2) C;Genetics:
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A; Gene:
                                                                                                                                                                                                                                                             A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: D70875
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C;Species: Mycobacterium tuberculosis
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T 15-DEC-1998 (Rel. 37, Last sequence update)

T 15-EEP-2003 (Rel. 42, Last annotation update)

E Developmental protein SEPALLATA3 (Agamous-like MADS box SEP3 OR AGL9 OR AT1024260 OR F316.19.

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Hypothetical 16.3 kDa pr
Azospirillum brasilense.
                              Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dew. Dunn P., Ergu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C., Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hutter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam J., Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam J., La
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Zimmer W., Aparicio C., Elmerich C.;
Zimmer W., Aparicio C., Elmerich C.;
Relationship between tryptophan biosynthesis and indole-3-acetic
acid production in Azospirillum: identification and sequencing of
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Langin-Hooper
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rangin-Hooper S., Le
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MEDLINE-21016719; PubMed-11130712;
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                                                                                   Huizar L.,
                                                                                                                          Dewar K.,
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                                                                                                                                                                        S.Y.,
                                       В.,
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EMBL; AF015552; AAB67 EMBL; AC002396; AAC00 EMBL; AK118696; BAC43 PIR; T00656; T00656. HSSP; P11746; IMNM.

AAB67832.1; AAC00586.1; BAC43290.1;

ALT_INIT.

InterPro;
InterPro;

; T03032; -. ; IPR002487; ; IPR002100;

TF_Kbox.
TF_MADSbox

TRANSFAC;

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Lin X., Liu S.X., Liu Lin, Nierman W.C., Usbulle Willischer J., Miranda M., Nguyen M., Nierman W.C., Usbulle V., Milischer J., Miranda M., Nguyen M., Rooney T., Rowley D., Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M. Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W., "Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced SSP consortium (Salk/Stanford/PGEC)."; submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         floral organs.":
Nature 409:525-529(2001).

Nature 409:525-529(2001).

development and floral organogenesis. Functions with SEPALLATA1/AGL2 and SEPALLATA2/AGL4 to ensure proper development of petals, stamens and carpels and to prevent the indeterminate growth of the flower meristem. Interacts with APETALA1, AGAMOUS of APETALA3/PISTILLATA to form complexes, that could be involved in APETALA3/PISTILLATA to form complexes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes
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PubMed=10821278;
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"B and C floral organ
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"Specific interactions between
of the MADS domain family of D
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                                                                                                                                                                                                                                                                                                                                                                genes regulation during floral meristem development. SUBUNIT: Heterodimer with API or AG capable of binding sequences. Binds AP3/PI to form a ternary complex. SUBCELLULAR LOCATION: Nuclear (By similarity). DEVELOPMENTAL STAGE: Expressed early during flower devenithin petals, stamens, and carpels.
                                                                                                                                                                                                                                                                                                                                                    within petals, stamens, and carpels.
MISCELLANEOUS: Triple mutations in the SEP1,
                                                                                                                                                                                                                                                                                                 result in the replacement of the stamens and petals by seporal of the carpels by a new mutant flower with sepaloid organs SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPT
                                                                                                                                                                                                                                                                       SIMILARITY: Contains 1 K-box dimerization domain.
                                                                                                                                                                                                                                                                                         FACTORS
                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
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12:999-1010(1997).
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en the K domains of AG
DNA binding proteins."
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Y functions
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Nierman W.C., Osborne
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EMBL; Y08626; CAA69916.1; -.

PIR; T10467; T10467.

HISSP; P11746; INNM.

TRANSFAC; T03170; -.

InterPro; IPR002487; TF_Kbox.

InterPro; IPR002487; TF_Kbox.

InterPro; IPR002100; TF_MADSbox.

Pfam; PF01486; K-box; 1.

PFLNTS; PR00404; MADSDOMAIN.

PRINTS; PR00404; MADSDOMAIN.

PROSITE; PS00350; MADS_BOX_1; 1.

PROSITE; PS00366; MADS_BOX_2; 1.

PROSITE; PS0066; MADS_BOX_2; 1.
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Best Local
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15-DEC-1998 (Rel. 3
28-FEB-2003 (Rel. 4
Agamous-like MADS k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **Bonhomme F., Sommer H., Bernier G., Jacqmard A.; **Characterization of SaMADS D from Sinapis alba suffunction of the gene: in inflorescence development organogenesis."; **plant wol mark of the same statement organogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWI
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the Euro
                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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AGL9.
Sinapis alba (White mustard) (Brassica hirta).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Sinapis.
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PROSITE; PS50066; MADS_BOX_2; 1.
Plowering; Transcription regulation; Activ
Nuclear protein; DNA-binding; Coiled coil.
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SUBCELLULAR LOCATION: Nuclear (By similarity).
SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 K-box dimerization domain.
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RESULT 5
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EMBL; AF02940
EMBL; AF12709
EMBL; AF17680
Genew; HGNC:
MIM; 603711;
MIM; 231100;
                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WW Z.L., Martin K.O., Javitt N.B., Chiang J.Y.L.;
"Structure and functions of human oxysterol 7alpha-hydroxylase and gene CYP7B1.";
J. Lipid Res. 40:2195-2203(1999).
-!- PATHWAY: Conversion of cholesterol to bile acids; first (repartway: Conversion of cholesterol to bile acids)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Liver, and Spleen;

MEDLINE-99021668; PubMed-9802883;
Setchell K.D.R., Schwarz M., O'Connell N.C., Lund E.G., Davis D.L.,
Lathe R., Thompson H.R., Tyson W.R., Sokol R.J., Russell D.W.;

"Identification of a new inborn error in bile acid synthesis: mutation
of the oxysterol 7-alpha-hydroxylase gene causes severe neonatal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             limiting) step.
-i- SUBCELLULAR LOCATION: Membrane-bound.
-i- TISSUE SPECIFICITY: Brain, testis, ove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-Hippocampus;
MEDLINE-20057832; PubMed-10588945;
Wu Z.L., Martin K.O., Javitt N.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the oxysterol disease.";
J. Clin. Invest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CP7B_HUMAN STANDARD; PRT; 506 AA.
075881; 09UNF5;
15-JUL-1999 (Rel. 38, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cytochrome P450 7B1 (Oxysterol 7-alpha-hydroxylase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND DISEASE.
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                                                                                                                                                                                                                                                                                                                                                                  hepatitis [MIM:231100]. Patients present severe cirrhosis and liver synthetic failure. SIMILARITY: Belongs to the cytochrome P450 famil
                                                                                                                                                                                                                                                                                                                                                                                                                                        kidney, and small intestine.
DISEASE: Defects in CYP7B1 are a
                                                  AF127090;
AF127090;
AF176805;
AF176800;
AF176801;
AF176802;
AF176803;
AF176803;
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                                                  AAC95426.1;
AAD20021.1;
AAK11850.1;
AAK11850.1;
AAK11850.1;
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EDD65155060BFD46 CRC64;
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15-JUL-1999
15-JUL-1999
28-FEB-2003
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METAL
449 449 IRON (HEND CONFILTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0008396; F:oxysterol 7-alpha-hydroxylase activity; TAS GO; GO:0006699; P:bile acid biosynthesis; TAS. InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                  PROSITE; PS00086; CYTOCHROME_P450; FALSE_NEG.
Oxidoreductase; Monooxygenase; Electron transport; Membrar
Microsome; Endoplasmic reticulum; Cholesterol metabolism.
METAL 47 IRON (HEME AXIAL LIGAND) (BY
SEQUENCE 507 AA; 58417 MW; AB3D502F935B7ED6 CRC64;
                                                                                                                  EMBL; U3699; AAA92615.1; -.
MGD; MGI:104978; Cyp7b1.
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; P450; 1.
                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                -
                                                                                                                                                                                                                                                                                                                   "A novel cytochrome P450 expressed primarily in brain.";
J. Biol. Chem. 270:29739-29745(1995).
-i- PATHWAY: Conversion of cholesterol to bile acids; fi
                                                                                                                                                                                                                                                                                                                                                   Stapleton G., Steel M., Richardson Morris R.G., Lathe R.;
                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Brain, and Liver; MEDLINE-96102021; PubMed-8530364;
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytochrome
                                                                                                          PRINTS; PR00385; P450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                             limiting) step.
SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
subcern specificity: Highly expressed in Brain; ALSO express
                                                                                                                                                                                                                                                                         LIVER AND KIDNEY
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        Similarity
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9 (Rel. 38, Last sequence update)
3 (Rel. 41, Last annotation updat
p450 7B1 (Oxysterol 7-alpha-hydr
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Rodentia;
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IRON (HEME AXIAL LIGAND) (BY
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7-alpha-hydroxylase) (EC 1.14.13.-)
                                                                                  Electron transport; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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61;
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                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                           LPH_RAT
                                                                                                                                                                                                                                                                                                                       Coat protein
SEQUENCE 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=86060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses;
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Q02401; Q63712; Q63719; Q02401; Q63712; Q63719; Q02401; Q63712; Q63712; Q63712; Q63712; Q63713; Q63712; Q63712; Q63712; Q63712; Q63712; Q63712; Q63712; Q63712; Q64712; Q64712
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SEQUENCE FROM N.A.
STRAIN-Wistar; TISSUE=Intestine;
MEDLINE=91365258; PubMed=1909681;
Duluc I., Boukamel R., Mantei N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: THE VP2 PROTEIN IS ONE OF THE TWO PROTE WHICH CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID.
MAJOR TARGET OF THE HOST IMMUNOGENIC RESPONSE.
-i- SIMILARITY: BELONGS TO THE REOVIRUSES VP2 FAMILY.
                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00898; Orbi_VP2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001742; Orb1_VP2.
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(Rel. 37, Last sequence up
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Pred. No.
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Sciurognathi;
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thi; Muridae;
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Matches 5
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PRINTS; PRO0131; GLYYDRLASEL.
Probom; PD000650; Glyco_hydro_1; 4.
ProSTTE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
PROSTTE; PS00653; GLYCOSYL_HYDROL_F1_2; 2.
PROSTTE; PS00653; GLYCOSYL_HYDROL_F1_2; 2.
PROSTTE; PS00653; GLYCOSYL_HYDROL_F1_2; 2.
PROSTTE; PS00653; GLYCOSYL_HYDROL_F1_2; 2.
PROSTTE; PS00653; GLYCOSYL_HYDROL_F1_2; 7:
PROSTTE; PS00653; GLYCOSYL_HYDROL_F1_2; 7:
PROSTTE; PS00653; GLYCOSYL_HYDROL_F1_2; 2.
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DOMAIN
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EMBL; X56747; CAA40069.1; -.
EMBL; L04635; AAA41539.1; -.
PIR; JS0610; JS0610.
HSSP; P26205; 1CBG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The rat LPH gene 5' region: comparative structure with the human gene.";
pun Seq. 3:119-121(1992).
-i- FUNCTION: LPH SPLITS LACTOSE IN THE SMALL INTESTINE.
-i- FUNCTION: LPH SPLITS LACTOSE + H(2)0 = D-glucose + D-galactose.
-i- CATALYTIC ACTIVITY: Lactose + H(2)0 = D-glucose + H(2)0 = a sug
                                                                                                                                                                                                                                                                                                                                                                           REPEAT
REPEAT
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MEDLINE-93091244; PubMed-1339333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00232; Glyco_hydro_1; PRINTS; PR00131; GLHYDRLASE1.
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. BRUSH BORDER TISSUE SPECIFICITY: INTESTINE.
DOMAIN: THE SEQUENCE EXHIBITS 4 REGIONS (I-IV) OF INTERNAL
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                                                                                                                             85.48;
                                                                                                                                                                         217266
                                                                                                          100.0%;
                                                                                                                                                                    PROTON DONOR (POTENTIAL):
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (POTENTIAL):
NUCLEOPHILE (BY SIMILARITY).
A -> R (IN REF. 1; AAA41539).
Q -> E (IN REF. 1; AAA41539).
E -> D (IN REF. 1; AAA41539).
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                                                                                                        Score 35;
Pred. No.
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                                                                                   Mismatches
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HAVE EVOLVED BY TWO
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There are no restrictions
ng as its content is in
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SEQUENCE FROM N.A.
STRAIN-Malish 7;
MEDLINE-21442074; PubMed-11557893;
MEDLINE-21442074; PubMed-11557893;
Oqata H., Audic S., Renesto-Audiffren P., Fournier P.-E.,
Oqata M., Roux V., Cossart P., Weissenbach J., Claverie
                  022769;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
MADH-ubiquinone oxidoreductase 24 kDa subun
(EC 1.6.5.3) (EC 1.6.99.3).
AT4G02580 OR T10P11.14.
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METAL
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Pfam; PF01257; complex1_24kD; 1.
ProDom; PD003859; Cmplx1_24kDa; 1.
PROSITE; PS01099; COMPLEX1_24K; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE008611; AAL03019.1; -. PIR; A97760; A97760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
-i- FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and iron-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiaceae; Rickettsieae; Rickettsia.
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
NADH-quinone oxidoreductase chain E (EC 1.6.99.5) (NADH dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUOE_RICCN
Q92ID9;
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19156 MW;
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(Mouse-ear cress).
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IRON-SULFUR (2FE-2S)
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 34;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + ubiquinol.

CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced accep
                                                                                                                                                                                                                                                                                                                                                                     THIS IS A COMPONENT OF THE FLAVOPROTEIN FRACTION.
SUBCELLULAR LOCATION: MATRIX AND CYTOPLASMIC SIDE OF THE
MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
SIMILARITY: BELONGS TO THE COMPLEX I 24 KDa SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COFACTOR: Binds 1 2Fe-2S cluster (Potential).
SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS
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                                                   pean Bioinformatics Institute. The non-profit institutions as long and this statement is not removed
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InterPro; IPR002023; Cmplx1_24kDa.

Pfam; PF01257; Complex1_24kD; 1.

ProDom; PD003859; Cmplx1_24kDa; 1.
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                                                                                                                                                                                                                                   the European Bioinformatics Institute.
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                                                        X57968; CAA41034.1;

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(POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                      191, 193,
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A38489; DNWTU1.

Resp_NADH_dh1 h; 1.

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RESULT 13
NU1M_MARPO
ID NU1M_M
AC P26845
DT 01-AUG
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NU1M_CHOCR
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Matches 5
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SEQUENCE 325 AA;
                                                                                                                                                                                              EMBL; 247547; CAA87617.1; ...
pir; S59101, S59101.
InterPro; IPR001694; Resp_NADH_dhl.
pfam; pF00146; NADHdh; 1.
PROSITE; PS00667; COMPLEX1_ND1_1; 1.
PROSITE; PS00668; COMPLEX1_ND1_2; 1.
NUIM_MARPO STA
P26845;
01-AUG-1992 (Rel.
                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long we modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         J. Mol. Biol. 250:484-495(1995).
-I- CATALYTIC ACTIVITY: NADH + ubiquinone - NAD(+) + ubiquinol
-I- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                             "Complete sequence of the mitochondrial DNA of the Chondrus crispus (Gigartinales). Gene content and gorganization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase chain 1 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NU1M_CHOCR P48898;
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                                                                                                                                                                           Oxidoreductase; SEQUENCE 326 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leblanc C., Boyen
Kloareg B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chondrus crispus (Carragheen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95341681;
Leblanc C., Boyen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Apices;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Rhodophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2769
                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through wen the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
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                                                                                                      1 GGWLP 5
                                                                                                                              Similarity
5; Conserv
                                                                                GGWLP
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                         STANDARD;
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                                                                                                                                                                          NAD; Ubiquinone; Mitochondrion; AA; 36447 MW; 6D33B81B09173EE2
  23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=7616569;
C., Richard O.,
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COMPLEX1_ND1_2;
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100.0%; Pro
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MPLEX1_ND1_2; 1.
Ubiquinone; Mitochondrion;
  Created)
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Pred. No.
                                                                                                                                        Score 34;
Pred. No.
                         PRT;
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                         328
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                                                                                                                                      DB
61;
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61;
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                                                                                                                                                   Length 326
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                                                                                                                                                                           CRC64;
                                                                                                                                                                                     Transmembrane
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                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          genome
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Best Local S
Matches 5
                                                                                                                                                                                                                            P31839;
01-JUL-1993 (Rel. 2
01-JUL-1993 (Rel. 2
15-JUL-1999 (Rel. 3
NADH-ubiquinone oxi
SEQUENCE FROM N.A., AND RNA EDITING.
MEDILINE-91208684; PubMed-1850322;
Wissinger B., Schuster W., Brennicke A.;
"Trans splicing in Oenothera mitochondria: nadl mRNA
exon and trans-splicing group II intron sequences.";
Cell 65:473-482(1991).
Cell 65:473-482(1991).
-i- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) +
-i- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 F
-i- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-7
                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eleurosids II; Myrtales; Onagraceae; Oenothera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M68929; AAC09438.1; -.
PIR; S25993; S25993;
InterPro; IPR001694; Resp_NADH_dh1.
Pfam; PF00146; NADHdh; 1.
PROSITE; PS00667; COMPLEX1_ND1_1; 1
PROSITE; PS00668; COMPLEX1_ND1_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion.
                                                                                                                                                                                                    Oenothera bertiana (Bertero's evening
                                                                                                                                                                                                                   ND1 OR NAD1.
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15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase chain 1 (EC 1.6.5.3).
ND1 OR NAD1.
                                                                                                                                    NCBI_TaxID=3950;
                                                                                                                                                                                                                                                                                                   NU1M_OENBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oxidoreductase; NAD; Ubiquinone; Mitochondrion; SEQUENCE 328 AA; 36518 MW; F0F6F009567264DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta; Marchantiineae; Marchantiidae; Marchantiales; Marchantiineae; Marchantiaceae; Marchantia.
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Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-92114051; PubMed-1731062;
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                                                                                                                                                                                                                                                                                                                                                                    252
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                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 5; Conserv
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llarity 100.0%;
Conservative (
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1. 26, Last sequence update)
1. 38, Last annotation update)
oxidoreductase chain 1 (EC 1.6.5.
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                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                               PRT;
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61;
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eudicots; Rosidae;
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form of plant
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    THE INITIATOR
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RESULT
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                                                                                                                                                                                                    RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Boyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Davies P.,
RA Borkova D., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA George K., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harlis M. K. Hallsh F. Karron G. H. K.P. Z. Kennison T. A. Ketchmin K.A.
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Best Local :
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                 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Muy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hazapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative odorant receptor 88a. OR88A OR CG14360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9VFN2;
16-OCT-2001
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InterPro; IPR001694; Resp_NADH_dh1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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MEDLINE-91352070, PubMed-1009028;

MEDLINE-91352070, PubMed-1009028;

A Hansen G., Larribe M., Vaubert D., Tempe J., Biermann B.J.,

A Montoya A.L., Chilton M.-D., Brevet J.;

"Agrobacterium rhizogenes pRi8196 T-NNA: Mapping and DNA sequence of functions involved in mannopine synthesis and hairy root differentiation.";

Proc. Natl. Acad. Sci. U.S.A. 88:7763-7767(1991).

R Proc. Natl. Acad. Sci. U.S.A. 88:7763-7767(1991).

R InterPro; IPR006064; Glycosidase.

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                                                                                                                                                                                                                                                                                                                                                              STRAIN-22491 / Serogroup A / Serotype 4A;

MEDLIKE-2022556; PubMed-10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

Klee S.R., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd

Jayels R.M., Davis P., Devlin K., Feltwell T., Hamlin N.A.,

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Whitehead S., Spratt B.G., Barrell B.G.;
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                                                                                                                                                                                                                                     Whitehead S., Spratt B.G., B "Complete DNA sequence of a meningitidis Z2491.", Nature 404:502-506(2000). EMBL; AL162757; CAB85209.1;
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01-DEC-2001 (TrEMBLrel.
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PubMed=10710307;
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173631A183372CDE
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Q9HUB2;
Q1-MAR-2001
Q1-MAR-2001
Q1-MAR-2003
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01-MAR-2003
01-MAR-2003
01-MAR-2003
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrer Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Le Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yu Brody L.L., Coulter S.M., Folger K.R., Kas A., Larbig K., Lin Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004920; AAG08456.1;
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TIGRFAMs; TIGR00046; TIGR00046; 2.
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MEDLINE=20437337;
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Pseudomonadaceae; Pseudomo
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                                            virus serotypes,";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY163330; AAN74570.1; -
SEQUENCE 1057 AA; 123656 MW; 43EF1F41E37EE77C CRC64;
                                                                                      SEQUENCE FROM N.A. Potgleter A.C., Cloete M., van Dijk Potgleter A.C., Cloete M., van Dijk "A first full outer capsid protein o' Cloning, sequencing, expression and full-length outer capsid VP2-genes c
                                                                                                                                                         African horsesickness virus Viruses; dsRNA viruses; Reov CBI_TaxID=40050;
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26097 MW; E874C787AAC00DFF CRC64;
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VP2-genes of the nine
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, Last sequence update)
, Last annotation update)
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W.O., Kowalik D.J., Lagrou M.
Yuan Y.,
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X MEDLINE-21332296; PubMed-11427726;

B She Q. Singh R.K. Confalonieri F., Zivanovic Y., Allard G.,

A Awayez M.J. Chan-Weiher C.C.-Y. Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

A Helkamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

A Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

A Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Charlebois R.L., Bensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus p2."

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

REMBL; AED06667; ARA40660.1;

REMBL; AED06667; ARA40660.1;

Refam: PF00166; NADHdh; 1.
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Q8Y326;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein RSC0155.
RSC0155 OR RSO1025.
MEDLINE-21681879; pubMed-11823852;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguler P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
BMBL; AL646057; CAD13683.1; -.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NADH dehydrogenase subunit H (NuoH).
Sulfolobus solfatari
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               MEDIINE=91374590; PubMed=1654446;
Martin M.E., Nicholas J., Thomson B.:
"Identification of a transactivating
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[6]
                                                                                   SEQUENCE FROM
STRAIN-U1102;
                                                                                                                                         MEDLINE-91226542; PubMed-1851252; Thomson B.J., Efstathiou S., Honess R.W.; "Acquisition of the human adeno-associated human herpesvirus type-6."; Nature 351:78-80(1991).
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-U1102;
                                                                                                                                                                                                                                                                                                         MEDLINE-91333007; PubMed-1651403;
Teo I.A., Griffin B.E., Jones M.D.;
"Characterization of the DNA polymerase
J. Virol. 65:4670-4680(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification, characterization, encoding a phosphoprotein of human J. Virol. 65:2884-2894(1991).
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01-NOV-1996
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Human herpesvirus 6 is closely related J. Virol. 64:287-299(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gompels U.A., Nicholas J., Lawrence G., Jones M., Thom Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.; "The DNA sequence of human herpesvirus-6: structure, cand genome evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human herpesvirus 6.
Viruses; dsDNA viruses,
Betaherpesvirinae; Rose
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Pfam; PF02636; DUF185; 1.
Hypothetical protein; Complete
SEQUENCE 397 AA; 42650 MW;
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Efstathiou S., Lawrence G.L., Brown C "Identification of homologues to the family in human herpesvirus 6.", J. Gen. Virol. 73:1661-1671(1992).
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Gen. Virol.
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J. Virol. 65:5381-5390(1991).
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herpesvirus 6.";
virol. 66:3918-3924(1992).
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The right end of the unique
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MEDLINE=94025558;
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                                                          MEDLINE=93389439; PubMed=8397282;
Liu D.X., Gompels U.A., Nicholas J., Lel
"Identification and expression of the hu
H and interaction with an accessory 40K
                                                                                                               SEQUENCE FROM
                                                                                                                                                       MEDLINE-93224882; PubMed-8385692;
Sompels U.A., Carrigan D.R., Carss A.
"Two groups of human herpesvirus 6 id
laboratory strains and variants from
                   STRAIN-U1102
                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                    The right end of the unique region of U1102 contains a candidate immediate comologue of the human cytomegalovirus Gen. Virol. 73:1649-1660(1992).
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n. Virol. 74:495-500(1993).
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Virology
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Greenamoyer C., Dambaugh T.R.
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Dewhurst S., Dollard S.C., Pellett P.E.,
"Identification of a lytic-phase origin
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Nicholas J.;
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                                                      Thompson
Frenkel N
                                                                                                                                                                                                              STRAIN-ULLUZ;
MEDLINE-94202284; PubMed-8151768;
Schiewe U., Neipel F., Schreiner
Schiewe U., Neipel F., Schreiner
                                                                                                                                                                                                                                                                                                                        "Nucleotide sequence analysis of a 38.5-kilobase-pair region genome of human herpesvirus 6 encoding human cytomegalovirus early gene homologs and transactivating functions.";

J. Virol. 68:597-610(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94118404; PubMed=8289364
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J. Virol. 67:7680-7683(1993).
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herpesvirus 6 and relationship to rep
J. Gen. Viról. 76:451-458(1995).
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                                                                                                                                                                    herpesvirus 6 genome.";
J. Virol. 68:2978-2985(1994).
                                                                                                                                                                                        Schiewe U., Neipel F., Schre
"Structure and transcription
herpesvirus 6 genome.";
                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                               MEDLINE=94181269;
                                                                                                                                     SEQUENCE
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    Similarity
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                                                                      J.,
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                                                                                                                                   FROM N.A
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                                                            Rosenthal
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                                                                         1269; PubMed=8134119;
Choudhury S., Kashan
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      DB 12;
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Best Local S
Matches 5
          Isegawa T., Mukai T., Nakano K., Kagaw Sunagawa T., Sashihara J., Zou P., Kos A. Comparison of the complete DNA sequ 6 variant A and B.", Virol. 0:0-0(1999).

EMBL; AB021506; BAA78320.1; -.

EMBL; AB021506; BAA78213.1; -.

InterPro; IPR002965; P_rich_extensn.

InterPro; IPR003360; US22.
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Q9W9G4;
01-NOV-1999 (TrEMBLrel. 1:
01-NOV-1999 (TrEMBLrel. 1:
01-CCT-2002 (TrEMBLrel. 2:
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                                                                                                                                                                                                                                          STRAIN-HST;
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Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DR2R protein.
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PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.
SEQUENCE 637 AA; 72425 MW; 9C31788B8C04E013 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             investigating biology.";
Science 282:2012-2018(1998).
EMBL; ALO21474; CAA16307.1; -.
WormPep; Y32F6A.2; CE16609.
InterPro; IPR000175; Na/ntran_symport.
Pfam; PF00209; SNE; 1.
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Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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01-JUN-1998 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Barlow K.;
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83.3%;
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., Kosuge H., Yamanishi K
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2.3e+02;
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RESULT 12
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Best Local S
Matches 5
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01-MAY-2000
01-OCT-2002
SEQUENCE FROM N.A.
                                          "Human herpesvirus 6B genome with human herpesvirus 6A."; J. Virol. 73:8040-8052(1999)
                                                                                                                                       MEDLINE-99412318; PubMed-10482553; Dominguez G., Dambaugh T.R., Stame
                                                                                                                          Dominguez G.,
Pellett P.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            Betaherpesvirinae;
NCBI_TaxID=32604;
                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                    Human herpesvirus 6B
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Pfam; PF02705; K_trans; 1.
TIGREAMS; TIGRO0794; kup; 1.
SEQUENCE 715 AA; 79662 MW; B708C
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel 20, 01-MAR-2002 (TrEMBLrel 20, 01-MAR-2003 (TrEMBLrel 23,
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PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 647 AA; 69466 MW;
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83.3%;
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Last sequence up
Last annotation
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Pred. No.
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                                                                                                                                                                                         Q8XQH8 PRELIMINARY; PRT;
Q8XQH8;
Q9XQH8;
Q1-MAR-2002 (TrEMBLrel. 20, Create)
Q1-MAR-2002 (TrEMBLrel. 21, Last a)
Q1-JUN-2002 (TrEMBLrel. 21, Last a)
Probable transcription regulator p)
RSP1247 OR RS03191
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Q94DV0;
Q1-DEC-2001
01-DEC-2001
01-DEC-2002
P0454H12:20
P0454H12:20
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Peallett P.E., Dominguez G., Dambaugh T.R., Stamey F.R.,
Inoue N.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF157706; AAD49682.1;
EMBL; AF157706; AAD49682.1;
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR003360; US22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (Rice).

Bukaryota; Viridiplantae; Streptophyta; Er

Spermatophyta; Magnoliophyta; Liliopsida;

Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID=4530;
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PRINTS; PR01217; PRICE
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                                                                                                         plasmid megaplasmid.
Bacteria; Proteobacteria;
Ralstoniaceae; Ralstonia.
                    SEQUENCE FROM N.A. STRAIN=GMI1000;
    MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                       Ralstonia solanacearum (Pseudomonas solanacearum)
                                                                                  NCBI_TaxID=305;
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(TrEMBLrel. 19,
(TrEMBLrel. 22,
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A; 82564 MW;
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                                                                                                                               Betaproteobacteria; Burkholderiales;
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Pred. No. 2.8e+02;
1; Mismatches 0
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Pred. No.
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a; Poales; Poaceae;
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A Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,

Weissenbach J., Boucher C.A.;

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

It Nature 415:497-502(2002).

R EMBL; AL646083; CAD18398.1; -.

R InterPro; IPR000005; HTHARAC.

R FAINTS; PR00155; HTHARAC.

R PRINTS; PR00032; HTHARAC.

R PRINTS; PR00032; HTHARAC.

R PROSITE; PS00141; HTH_ARAC_FAMILY_1; 1.

R PROSITE; PS00141; HTH_ARAC_FAMILY_2; 1.

R PROSITE; PS01041; HTH_ARAC_FAMILY_2; 1.
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Search completed: August 20, Job time : 14.4605 secs
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Best Local S
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Best Local
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Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demang
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
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01-OCT-2002
01-OCT-2002
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                                                                                                                                                                                                                                                                                                             pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                    Q8KN98
                                                                                                                                                                                       aeruginosa.";
J. Bacteriol. 184:3614-3622(2002).
                                                                                                                                                                                                                 MEDLINE=22053227; PubMed=12057956;
Raymond C.K., Sims E.H., Kas A., Spencer D.H., Kutyavin T.V.,
Raymond C.K., Sims E.H., Kas A., Spencer D.H., Kutyavin T.V.,
Ivey R.G., Zhou Y., Kaul R., Clendenning J.B., Olson M.V.;
"Genetic Variation at the O-Antigen Biosynthetic Locus in Pse
                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               NCBI_TaxID=287;
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nes 5; Conserv
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NCE 382 AA;
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                                                                                1 GGWLPY .6
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AA; 43581 MW;
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83.3%;
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Pred. No. 1.7e
1; Mismatches
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Pred. No.
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                                                                                                                                                                 565B3B2F274764D0 CRC64;
                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16;
1.7e+02;
                                                                                                                           DB 2;
2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nac S., Demange N., in W., Schiex T., Levy M.,
                                                                                                                                       Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                 Indels
                                                                                                                                                                                                                         Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Result
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                       Query
Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1107863 seqs, 158726573 residues
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Gapop 10.0 ,
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(*SIDS1/gcgdata/geneseq/geneseqp-emb1/AA198, DAT: *

(*SIDS1/gcgdata/geneseq/geneseqp-emb1/AA198, DAT: *

(*SIDS1/gcgdata/geneseq/geneseqp-emb1/AA199, DAT: *

(*SIDS1/gcgdata/geneseq/geneseqp-emb1/AA200, DAT: *

(*SIDS1/gcgdata/geneseq/geneseqp-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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\(\subset\)SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
\(\subset\)SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
\(\subset\)SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
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108
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                AAY56833
AAY53774
AAE08819
AAB25366
AAG00142
AAB25115
AAB25115
AAB25326
AAB25447
AAB25447
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Apple LRPKm1 LRR s
VL component of an
Human scFV L19 ant
Pinus radiata cell
Human secreted pro
Pinus radiata cell
Eucalyptus grandis
Pinus radiata cell
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888.22	
307 307 312 333 334 705 999 420 420 771 1147 2284 342 342 342 342 342 342 342 342 343 343	
222 222 222 222 222 222 222 222 222 22	<u>.</u>
AAU14225 AAU14225 AAU14227 AAU00443 ABB65742 AAB55519 AAY56824 AAB756824 AAB710593 ABG15146 ABG15146 ABG15146 ABG15146 ABG25770 AAB25382 AAR37818 AAR27817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37819 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR37817 AAR3	ה ניני
An antibody with i Proplonibacterium Human novel protei Human novel protei Human novel protei Maize disease resi Drosophila melanog Pinus radiata cell Apple leucine-rich Human immune/haema Human novel protei Novel human diagno Pinus radiata cell Sequence of varian H. pylori secreted Sequence of fungin Polygalacturonase Pinus radiata cell H. pylori GHPO 113 Herbicidally activ Drosophila melanog Herbicidally activ Drosophila melanog Herbicidally activ Maize disease resi Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis steroid re Propionibacterium Propionibacterium	

ALIGNMENTS

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RESULT 1
AAY56833
                           WPI;
                                         Cervone F,
                                                     (AGRA-) IST AGRARIO DI SAN MICHELE ALL'ADIGE.
                                                                     08-JUN-1998;
                                                                                   08-JUN-1999;
                                                                                                                W09964600-A1
                                                                                                                              Malus domesticus.
                                                                                                                                        LRPKml gene; leucine-rich protein kinase; apple; fungal pathogen;
Venturia inaequalis; transgenic plant; plant defense; scab; LRR.
                                                                                                                                                                Apple LRPKm1 LRR sequence #8
                                                                                                                                                                                11-APR-2000
                                                                                                                                                                                               AAY56833;
                                                                                                                                                                                                            AAY56833 standard;
                                                                                                  16-DEC-1999.
                          2000-147095/13
                                        De Lorenzo
                                                                                                                                                                              (first entry)
                                                                    98IT-RM00367.
                                                                                  99WO-IT00165
                                                                                                                                                                                                            peptide;
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New leucine-rich protein useful to increase plant resistance to fungal pathogens, especially Venturia inaequalis

Disclosure;

Fig

4

45pp;

English.

inventionrelates

from

apple

for

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RRESULT 2
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XX AAXY1
XX AAXY1
XX SCF
XX SCF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resistance to the fungal pathogen Venturia inaequalis. Vectors comprising the polynucleotides can be used to produce transgenic plants (especially apple species; resistant to fungal pathogens, especially V. inaequalis. For example, the gene sequence encoding the protein could be incorporated with the 3S promoter of the CaMV cauliflower mosaic virus to introduce a plant defense mechanism against the pathogen, or the promoter sequence upstream from the gene could be used in chimeric constructs to promote sequences encoding for proteins which inhibit V. inaequalis. V. inaequalis is the most severe and economically important fungal pathogen of apples, causing a disease known as scab. Sequences AAY56826-848 represent apple LRPKml LRR sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenesis; vascular proliferation; diabetic retinopathy;
age-related macular degeneration; tumour; immunoscintigraphic detection;
blood coagulation; blood vessel occlusion; ocular angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY53774;
                                                  The present sequence represents the VI component of a modified human scFv antibody which has specific affinity for a characteristic epitope of the ED-B domain of fibronectin. The affinity of the antibody for this epitope was improved by introducing a number of mutations in the complementarity determining region (CDR) residues located at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            angiogenesis-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scfv; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VL component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY53774 standard;
                            this epitope was improved by increase complementarity determining region complementarity determining site. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09958570-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                     Claim 10;
                                                                                                                                                                                                                                                                           antibodies
                                                                                                                                                                                                                                                                                                       Fibronectin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EIDG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-1998;
28-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-MAY-1999;
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     targeting
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                                                                                                                                                                                                                                                                                                                                                                                                               Tarli L,
     markers
                                                                                                                                                                                                                     Page 38; 59pp;
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                                                                                                                                                                                                                                                                                                    ED-B domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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99US-0300425.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an antibody with improved specificity for fibronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ED-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  es to a LRPKml gene encoding a leucine-rich protein (Malus x domestica) cultivar Florina responsible fo fungal pathogen Venturia inaequalis. Vectors
     of angiogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                  Viti F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain
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                                                                                                                                                                                                                                                                                                    epitope specific antibodies
                                                                                                                                                                                                                        English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                  Birchler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB
Pred. No. 11;
); Mismatches
        improved antibody is used for rapid
for detecting diseases characterized
                                                                                                                                                                                                                                                                                                                                                                                                                  X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fibronectin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          marker;
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                                                                                                                                                                                                                                                                                                            conjugate
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RESULT 3
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Best Local S
Matches
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                                        The invention relates to an antibody with specific affinity for a characteristic epitope of the ED-B domain of fibronectin, where the antibody has improved affinity to ED-B. The invention also relates to conjugates comprising antibodies with a suitable photoactive molecule useful in the detection and/or coagulation of blood vessels. An antibody with improved affinity to the ED-B domain is useful for diagnosis and therapy of tumours and diseases characterised by vascular proliferation, cancer, rheumatoid arthritis, neo-vasculature associated ocular comprises and psoriasis. Treatment of anglogenesis related pathologies comprises the injection of conjugates comprising antibody and a molecule capable of inducing blood coagulation and blood vessel occlusion. The present sequence is single-chain variable antibody fragment (scFV) L19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                     An antibody, with specific affinity for ED-B domain of fibronectin for the treat by vascular proliferation –
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                                                                                                                                                                                                                                                                                                                                                                                          Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-541701/60
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                                                                                                                                                                                                                                                                                                                                                                                       Page 36; 73pp; English.
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variable light

chain (VL) region related

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F
                                                                                                                                  and protein sequences isolated from eucalyptus (Eucalyptus yranuls).

C and protein sequences

C are involved in cell signalling. The polynucleotide and protein

CC sequences can be used to modify the response of plant cells to external

CC signals e.g. environmental changes or pathogens during the growth and

CC differentiation, elongation and survival, resistance to disease and

CC nutrient metabolism. Examples of modifications which can be produced are

CC altered fruit ripening and senescence of leaves and flowers e.g. to

CC delay senescence and prolong the life of cut flowers or enhance

CC senescence of reproductive organs to engineer sterile plants. Other

CC organs providing fruit and vegetables which have a longer shelf life

CC organs providing fruit and vegetables which have a longer shelf life

CC between harvest and consumption, or to decrease branching frequency in

CC organs provided and timber furniture and veneers.
Query Match
Best Local Similarity
5 6; Conserve
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                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide and protein sequences isolated from eucalyptus (Eucalyptus grandis) or pine (Pinus radiata also known as Monterey pine). The protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified r to external signals - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification; plant cell signalling; modulation; transgenic plant; pathogen; growth; environmental change; development; cell proliferation; differentiation; elongation; survival; disease resistance; nutrient metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strabala TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JAN-1999;
01-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pinus radiata cell signalling involved protein SEQ ID NO:685
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                100.
milarity 100.
Conservative
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Pred. No.
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RESULT 6
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AAG00142
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                                                                                                                                                                                Query Match
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                                                                                                                                                                     Matches
                                                                                                                                                                                                                                      The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' CTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                          AAB25115;
                                                 AAB25115 standard;
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedure
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; SEQ ID 4223; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-500381/45.
N-PSDB; AAC00148.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-1999;
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                                                                                                                                                                  6; Conserv
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                                                                                                                                                                                                                     144 AA;
                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
                                                  Protein;
                                                                                                                                                                            100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID
                                                  153
                                                                                                                                                                 0;
                                                                                                                                                                               Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO:
                                                 B
                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Giordano
                                                                                                                                                                            62;
                                                                                                                                                                                           DB
                                                                                                                                                                                        21;
                                                                                                                                                                 0
                                                                                                                                                                                        Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  mapping procedures
                                                                                                                                                              0
                                                                                                                                                              Gaps
                                                                                                                                                             0
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27-NOV-2000

(first entry)

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RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cc and protein sequences isolated from eucalyptus (Eucalyptus grandis) or cc pine (Pinus radiata also known as Monterey pine). The protein sequences cc are involved in cell signalling. The polynucleotide and protein cc sequences can be used to modify the response of plant cells to external cc signals e.g. environmental changes or pathogens during the growth and cc differentiation, elongation and survival, resistance to disease and cc differentiation, elongation and survival, resistance to disease and cc altered fruit ripening and senescence of leaves and flowers e.g. to cc delay senescence and prolong the life of cut flowers or enhance cc enescence of reproductive organs to engineer sterile plants. Other corgans providing fruit and vegetables which have a longer shelf life cc between harvest and consumption, or to decrease branching frequency in cc forest tree species giving long stretches of valuable knot-free clear cc wood which can be used in solid timber furniture and veneers.
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eucalyptus grandis; Pir plant cell signalling; environmental change; delongation; survival; delongation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated polynucleotide encoding a polypeptide involved in celsignaling used for generating transgenic plants with modified to external signals \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JAN-1999;
01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200042171-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENESIS RES & DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA79263 to AAA79736 and AAB25100 to AAB25570 represent
                  Eucalyptus grandis; Pinus radiata;
plant cell signalling; modulation;
environmental change;
                                                                                        Eucalyptus
                                                                                                                                    27-NOV-2000
                                                                                                                                                                                 AAB25326;
                                                                                                                                                                                                                           AAB25326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-476052/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              radiata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    radiata
                                                                                                                                                                                                                                                                                                                                        126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Page 82-83; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    1 TGRIPP 6
                                                                                                                                                                                                                                                                                                                                                                                                                            6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                        TGRIPP 131
                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153
                                                                                        grandis cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-US00724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cel1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nieuwenhuizen NJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0228986
99US-0162866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 signalling involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pinus radiata; Monterey pine; plant; modification;
ng; modulation; transgenic plant; pathogen; growth;
ne; development; cell proliferation; differentiation;
il; disease resistance; nutrient metabolism.
                                                                                                                                                                                                                           Protein;
                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.
; modulation;
development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                 red. No. 66;
Mismatches
Monterey pine; plant; modification; transgenic plant; pathogen; growth; cell proliferation; differentiation
                                                                                          involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                               SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO:83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modification;
                                                                                               ID NO:645
                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     responses
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 8
AAB25447
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and protein sequences isolated from eucalyptus (Bucalyptus grandis) or pine (Pinus radiata also known as Monterey pine). The protein sequences are involved in cell signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and development of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and nutrient metabolism. Examples of modifications which can be produced are altered fruit ripening and senescence of leaves and flowers e.g. to delay senescence and prolong the life of cut flowers or enhance senescence of reproductive organs to engineer sterile plants. Other modifications can be used to delay senescence in selected cell types or organs providing fruit and vegetables which have a longer shelf life to the productive organs providing frequency in or to decrease branching frequency in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elongation; survival; disease resistance; nutrient metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    signaling used for generating to external signals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strabala TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JAN-1999;
01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W0200042171-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between harvest and consumption, or to decrease branching frequency in forest tree species giving long stretches of valuable knot free clear wood which can be used in solid timber furniture and veneers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENESIS RES & DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide and protein sequences isolated from eucalyptus (Eucalyptus grandis) or
                                                                                                            Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modifi plant cell signalling; modulation; transgenic plant; pathogen; environmental change; development; cell proliferation; differen elongation; survival; disease resistance; nutrient metabolism.
                                                                                                                                                                                                                                                            Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB25447 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                  27-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                        AAB25447;
WO200042171-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 TGRIPP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TGRIPP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000WO-US00724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nieuwenhuizen
                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                               cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0228986.
99US-0162866.
                                                                                                                                                                                                                                                            signalling involved protein SEQ ID NO:766
                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           red. No. 66;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 155;
                                                                                                                           ion; differentiation;
metabolism.
                                                                                                                                                                                                               modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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PR PF PR XXX
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AAB25432
                                                                                                                                                                                                                                                                                                                                                                                                                  В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and protein sequences isolated from eucalyptus (Eucalyptus grandis) or pine (Pinus radiata also known as Monterey pine). The protein sequences are involved in cell signalling. The polynuclectide and protein cequences sequences can be used to modify the response of plant cells to external certain colls to external certain colls to external cevelopment of a plant. They can be used to modify cell proliferation, colloquence of plants of a plant. They can be used to modify cell proliferation, colloquence of modify cell proliferation, colloquence of modifications which can be produced are cell attreed fruit ripening and senescence of leaves and flowers e.g. to cell attreed fruit ripening and senescence of leaves and flowers or enhance cell senescence of reproductive organs to engineer sterile plants. Other colloquence consumption, or to decrease branching frequency in forest tree species giving long stretches of valuable knot-free clear way wood which can be used in solid timber furniture and veneers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 6
12-JAN-1999;
01-NOV-1999;
                                                                                                                                                                         Eucalyptus grandis; Pinus radiata; Plant cell signalling; modulation; environmental change; development;
                                           11-JAN-2000; 2000WO-US00724
                                                                          20-JUL-2000
                                                                                                                                      Pinus radiata.
                                                                                                       WO200042171-A1
                                                                                                                                                                 elongation; survival;
                                                                                                                                                                                                                                   Pinus radiata cell signalling involved protein SEQ
                                                                                                                                                                                                                                                                          27-NOV-2000
                                                                                                                                                                                                                                                                                                                               AAB25432 standard; Protein; 224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses to external signals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JAN-1999;
01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-476052/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                               126 TGRIPP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGRIPP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to AAA79736 and AAB25100 to AAB25570 represent polynucleotide ein sequences isolated from eucalyptus (Eucalyptus grandis) or nus radiata also known as Monterey pine). The protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 355; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US00724.
990S-0228986
990S-0162866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nieuwenhuizen NJ
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99US-0162866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                      Monterey pine; plant; modification; transgenic plant; pathogen; growth; cell proliferation; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                       ID NO:751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
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RESULT 10
AAY53775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                        (EIDG-) EIDGENOESSISCHE TECH HOCHSCHULE ZUERICH
                                                       11-MAY-1998;
28-APR-1999;
                                                                                                  11-MAY-1999;
                                                                                                                             18-NOV-1999
                                                                                                                                                                                                                                           angiogenesis; vascular proliferation; diabetic retinopathy; age-related macular degeneration; tumour; immunoscintigraphic detection; blood coagulation; blood vessel occlusion: occlusion:
                                                                                                                                                                                                                                                                               scFv; antibody; ED-B domain epitope; fibronectin;
                                                                                                                                                                                                                                                                                                           An antibody with improved specificity for fibronectin
                                                                                                                                                        WO9958570-A2
                                                                                                                                                                                      Homo
                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                              anglogenesis-related
                                                                                                                                                                                                                                                                                                                                                                             AAY53775;
                                                                                                                                                                                                                                                                                                                                                22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                      AAY53775 standard; Protein; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 347-348; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to external signals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-476052/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strabala TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity es 6; Conserv
                                                                                                                                                                                     sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 TGRIPP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TGRIPP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 AA;
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                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                     98US-0075338
99US-0300425
                                                                                                99WO-EP03210
                                                                                                                                                                                                                                   blood vessel occlusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding a polypeptide involved in cell rating transgenic plants with modified responses
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Pred.
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                                                                                                                                                                                                                                                                                    marker;
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Neri D,

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Viti F,

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RESULT 11
AAU40893
THE DRAW THE PRESENT OF THE PRESENT 
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   determining region (CDR) residues located at the periphery of the binding site. The improved antibody is used for rapid targeting markers of angiogenesis, for detecting diseases characterized by vascular proliferation, such as diabetic retinopathy, age-related macular degeneration or tumours. The antibody localizes the respective tissue within 3 to 4 hours after injection. It is used in immunoscintigraphic detection of angiogenesis and for diagnosis and therapy of tumours and diseases characterized by vascular proliferation. The antibody can be conjugated to a molecule which induces blood coagulation and blood vessel occlusion. These conjugates are used in the preparation of injectable compositions for the treatment of angiogenesis-related pathologies, especially caused by or associated with ocular proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a modified human scFv antibody which has specific affinity for a characteristic epitope of the ED-B domain of fibronectin. The affinity of the antibody for this epitope was improved by introducing a number of mutations in the complementarity determining region (CDR) residues located at the periphery of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-039074/03
                                                                                                                                                                                                    21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amalgamation
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                          WPI;
                                                                                                Skeiky YAW,
                                                                                                                                                                                                                                                                                                     20-APR-2001;
                                                                                                                                                                                                                                                                                                                                                    01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                      WO200181581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory lesion; acne vulgaris; enzyme linked immunosorbent dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uveitis; endophthalmitis; bone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAPHO syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Propionibacterium acnes immunogenic protein #1789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU40893
                                                                            L'maisonneuve
N-PSDB; AAS59513.
                                                                                                                                                  (CORI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222
                          2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 this sequence
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                                                                                                                                                     CORIXA
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                                                                                                                                                                                                 ; 2000US-199047P.
; 2000US-208841P.
; 2000US-216747P.
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H
                                                                         Persing DH,
e J, Zhang
                                                                                                                                                                                                                                                                                                        2001WO-US12865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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A
                                                                                                                                                     CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synovitis; acne;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 does not appear
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100
                                                                                                DH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epitope specific antibodies and conjugate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .0%;
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                                                                            Mitcham JL, Wang SS,
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    given
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pustulosis; hypertosis; osteomyelitis;
joint; central nervous system; ELISA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the specification; it claim 10.
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cc sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic cc polypeptides. The proteins and their associated DNA sequences are used in cc the treatment, prevention and diagnosts of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, cc pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. Cc presence is also involved in infections of bone, joints and the central cc nervous system, however it is particularly involved in the inflammatory clesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a cc sample with a binding agent that binds to the proteins of the invention cand determining the amount of bound protein in the sample. The collective specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and ctivity of P. acnes polypeptides and ctivity of P. acnes polypeptides and datapostic agents for determining P. acnes presence, for example, by cenzyme linked immunosorbent assay (ELISA).

Cc enzyme linked immunosorbent assay (ELISA).

Cc at fire winc introduce the protection of the printed contaction, but was obtained in electronic format directly from WIPO and contacting the printed contaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2088; 1069pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
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밁 ΩÃ Matches Query Match Best Local 84 1 TGRIPP 6 Similarity 6; Conserv TGRIPP 89 100.0%; ilarity 100.0%; Conservative 0 Score 34; DB 22; Pred. No. 1.3e+02; Mismatches 0; 22; Length 307; Indels 0; Gaps

0

Sequence

307

A,

at ftp.wipo.int/pub/published_pct_sequences

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RESULT 12
AAU14225
                                      AAU14225 standard;
24-OCT-2001
                   AAU14225;
 (first
                                       Protein; 307
                                        A
A
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Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiastimatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; parkinson's disease; tissue regeneration; Human novel protein #96. immune disorder

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WPI; 2001-451939/48.
N-PSDB; AAS22530.
                                           02-AUG-2001
                                                   WO200155437-A2
                                                          Homo sapiens.
                                   25-JAN-2001; 2001WO-US02623
                   (HYSE-) HYSEQ
                           25-JAN-2000; 2000US-0491404
            YT,
            Liu C,
            Drmanac
             R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC The invention relates to polynucleotides encoding novel human CC proteins or their active domains. The polypeptides, polynucleotides and CC antibodies raised against the polypeptides are used in a method of CC treatment of a mammal and prevention of disorders caused by the aberrant CC protein expression or activity. The polypeptides can be used as CC molecular weight markers, food supplements, and in antibody production. The polypeptides can be used as probes and completely polypeptides. Polynucleotides of the invention are used as probes and CC primers, for sequencing, for chromosome or gene mapping, in the CC primers, for sequencing, for chromosome or gene mapping, in the CC primers, for sequencing, for chromosome or gene mapping, in the CC production of recombinant proteins, and in generating anti-sense DNA or CR has and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to craise antibodies/elicit an immune response, to determine quantitative CC protein levels, as tissue markers, and to isolate receptors or ligands. Sistem call disorders, regenerating bone, cartilage, tendon, the proliferation, differentiation and survival of stem cells, as a alzheimer's, parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                         Human: novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antialtergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis
                (HYSE-) HYSEQ INC
                                                   25-JAN-2000; 2000US-0491404
                                                                                           25-JAN-2001; 2001WO-US02623
                                                                                                                                                                        WO200155437-A2
                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                     t188ue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU14227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU14227 standard; Protein; 312 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                            Human novel protein #98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                   regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TGRIPP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGRIPP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                   immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 22; I
Pred. No. 1.3e+02;
""Asmatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                             asthma; osteoporosis;
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Best Local Similarity
""" 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC The invention relates to polynucleotides encoding novel human CC antibodies raised against the polypeptides, polynucleotides and treatment of a mammal and prevention of disorders caused by the aberrant CC molecular weight markers, food supplements, and in antibody production. The polypeptides are used as probes and CC The polypeptides are used to identify compounds which bind to the CC primers, for sequencing, for chromosome or gene mapping, in the CC primers, for sequencing, for chromosome or gene mapping, in the CC primers, for sequencing, for chromosome or gene mapping, in the CC primers, for sequencing, for chromosome or gene mapping, in the CC primers, for sequencing, for chromosome or gene mapping, in the CC primers, for sequencing, for chromosome or gene mapping, in the CC primers, for sequencing, and in generating anti-sense DNA or CC target drugs to a tumour, in assays to determine biological activity, to CC raise antibodies/molicit an immune response, to determine quantitative CC protein levels, as tissue markers, and to isolate receptors or ligands CC protein levels, as tissue markers, and to isolate receptors or ligands. CC disorders, stem cell disorders, regenerating bone, cartilage, tendon, CC the proliferation, differentiation and survival of stem cells, as a CC contraceptive, treating osteoporosis and osteoarthritis, anaemia, CC alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral CC contraceptive, treating osteoporosis and osteoarthritis, anaemia, CC anti-inflammatory disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection.

The present sequence represents a protein of the invention.
                                                 09-SEP-1999;
                                                                                  06-SEP-2000;
                                                                                                                                                                                                                    Maize; plant disease resistance; crop; soybean; sunflower; sorghum; canola; wheat; alfalfa; cotton; rice; barley; millet; plant cell death; herbicide resistance; ZmLRR1-1; Cf-2; Cf-9.
                                                                                                                                                                                                                                                                                             Maize disease resistance enhancing protein ZmLRR1-1.
                                                                                                                      15-MAR-2001
                                                                                                                                                           WO200118061-A2.
                                                                                                                                                                                             Zea mays.
                                                                                                                                                                                                                                                                                                                                         19-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                AAU00443;
                                                                                                                                                                                                                                                                                                                                                                                                              AAU00443 standard; Protein; 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polypeptides useful nervous system disorders, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 576-577; 894pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TGRIPP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGRIPP 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                2000WO-US24403
                                                 99US-0152988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for treating anti-inflammatory diseases, for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
1.3e+02;
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(PION-) PIONEER HI-BRED INT INC

N-PSDB; ABL09845

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RESULT 15
ABB65742
ABB65742
ABB65742
AC ABB65
XX
AC ABB65
XX
DT 26-M
DT 26-M
DT 26-M
DT 26-M
DT 27-
DT 27-
PD W02
XX
PP W02
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PP 23
PF 23
PF 23
PR 11
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by transforming a plant cell with a recombinant expression cassette which comprises the disease resistance polynucleotide operably linked to a promoter, or by culturing the plant cell under plant growing conditions to produce a regenerated plant, or by inducing expression of the polynucleotide to modulate the disease resistance protein in a plant. The polynucleotides encoding the disease resistance proteins are useful for increasing resistance in a plant to disease, controlling cell death, and conferring resistance to herbicides. They are useful as probes or amplification primers in the detection, quantification, or isolation of gene transcripts. They can be used for recombinant expression of their encoded polypeptides, as immunogens in the preparation and/or screening of antibodies, and in sense or antisense suppression of the polynucleotide in a host cell, tissue or plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a Zea mays gene homologue for a leucine-rich repeat (LLR) containing disease resistance gene of the Cf-2 or Cf-9 type. These novel maize disease resistance polymucleotides and polypeptides are useful for enhancing disease resistance in crops and transgenic plants including maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley or millet. The level of disease resistance protein is increased barley or millet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated maize disease resistance polynucleotide useful for increasing resistance in a plant to disease, controlling cell death, and conferring resistance to herbicides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence representing maize ZmLRR1-1 protein is 1 of 7 novel disease resistance proteins (AAU00443-AAU00449). The ZmLRR1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 24018
   WPI; 2001-656860/75.
                                   Venter JC, Adams M,
                                                                                                       23-MAR-2000;
11-JUL-2000;
                                                                                                                                                        23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                          27-SEP-2001.
                                                                                                                                                                                                                        WO200171042-A2
                                                                                                                                                                                                                                                            Drosophila melanogaster.
                                                                                                                                                                                                                                                                                            pharmaceutical.
                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                 ABB65742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB65742 standard; Protein;
                                                                     (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-226742/23.
DB; AASO1013.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 AA;
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                                                                                                      2000US-191637P.
2000US-0614150.
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                                         Li PWD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB
Pred. No. 1.4
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Search completed: August 20, 2003, 12:33:49
Job time: 14.1928 secs

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                                                                Query Match
Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions – \,
                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 24018; 21pp + Sequence Listing; English
                                                                                                                                      Sequence
 231 TGRIPP 236
                                 1 TGRIPP 6
                                                                                                                                       334 AA;
                                                                   Conservative
                                                                                  100.0%;
                                                                       0,
                                                                   Score 34; DE Pred. No. 1.4
); Mismatches
                                                                                      1.4e+02;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

    protein search, using sw model

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1: /cgn2_6/ptodata/1.

2: /cgn2_6/ptodata/1.

3: /cgn2_6/ptodata/1.

4: /cgn2_6/ptodata/1.

5: /cgn2_6/ptodata/1.

5: /cgn2_6/ptodata/1.
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Match
     328717 seqs, 42310858 residues
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/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/1aa/backfiles1.pep:*
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US-08-605-150A-6
US-08-244-646-17
US-08-244-646-17
US-08-244-646-17
US-08-244-646-17
US-08-244-646-17
US-08-248-646-12
US-08-881-706-2
US-09-881-706-2
US-09-397-238A-12
US-09-397-238A-12
US-09-397-238A-2
US-09-252-991A-20481
US-09-252-991A-24538
US-09-252-991A-21784
US-09-252-991A-217863
US-09-252-991A-217863
US-09-252-991A-18178
US-09-252-991A-23122
US-09-252-991A-25576
US-09-252-991A-18172
                                                                                                                                                                                                                                             US-09-252-991A-24232
US-09-252-991A-26457
US-09-252-991A-31991
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Sequence
Sequence
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2045, Appl
20461, A
292, Appl
29169, A
24538, A
32, Appl
32, Appl
32, Appl
31, Appl
21184, A
18983, A
18983, A
23172, A
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2, Appli
12, Appl
12, Appl
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2, Appli
17, Appl
15, Appl
21, Appl
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24232, A
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US-09-228-986-83
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29 85.3 390 4 US-09-252-991A-24517 29 85.3 396 4 US-09-252-991A-24517 29 85.3 397 4 US-09-252-991A-18709 29 85.3 410 1 US-08-123-343A-7 29 85.3 410 1 US-08-123-343A-7 29 85.3 410 3 US-09-431-573-4 29 85.3 410 3 US-09-431-573-5 29 85.3 421 4 US-09-252-991A-30742 29 85.3 421 4 US-09-252-991A-31018 29 85.3 421 4 US-09-252-991A-31018 29 85.3 421 4 US-09-252-991A-31018 29 85.3 421 4 US-09-252-991A-25851 29 85.3 546 4 US-09-252-991A-28544 29 85.3 788 4 US-09-252-991A-28544 29 85.3 980 2 US-08-473-553A-6 29 85.3 980 2 US-08-473-553A-6 29 85.3 988 4 US-09-252-991A-29699	5	\$	<u>.</u> .	<u>د</u>	42	41	4	. (c	9 0	ى ر 0 -	2 (7	ω G	34	· L) K	<u>د</u> د	ω L	30	2 6	3
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	29699, A		6, Appli	/2/ Appl	•	28544 2	25851 /	3, Appli	31018, /	30742, 1	25017, A	J, Appl	100	A	•	5, Appli	T0/09, A	':	24697	24517.	ZLL33,

ALIGNMENTS

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Sequence 83, Application US/09228986

Patent No. 6359198

GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: And Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 83
LENGTH: 153
TYPE: PRT
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                             US-09-252-991A-24232
; Sequence 24232, Application US/09252991A
; Patent No. 6551795
US-09-252-991A-24232
                         APPLICANT: MATC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107105.136

CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 24232

LENGTH: 457

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 6
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             ORGANISM: Pseudomonas aeruginosa
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Pred. No.
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26457
LENGTH: 196
                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEO ID NOS: 33142
SEO ID NO 31991
LENGTH: 308
TYPE: PRT
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APPLICANT: Marc J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26457, Application US/09252991A Patent No. 6551795
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
ETLE REPERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                     ORGANISM: Pseudomonas aeruginosa
                                                                                                 Local Similarity hes 5; Conserv
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5. 6551795
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                                      TGRLPP 33
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83.3%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DE
Pred. No. 52;
                                                                                                                       Score 32;
Pred. No.
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81;
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COUNTRY:
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US-08-605-150A-6
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                                                                                                                                                                           Sequence 2, Application US/08605150A
Patent No. 6103520
                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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                                                                                                                                                                GENERAL INFORMATION:
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APPLICANT: SChell, JOZef
APPLICANT: SChell, JOZEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT\EP94\02936
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4329827.3
FILING DATE: 03-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-854-5502
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                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Klein & Szekeres
                                                                                       APPLICANT: Schell, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Irvine
                                                                            UMBER OF SEQUENCES:
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nes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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CITY: Irvine STATE: CA
                            STREET:
                                                                                                                                                                                                                                                                        347 TGRLPP 352
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amino acid
agy: linear
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                              4199 Campus Drive, Suite 700
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                                                                                                        GLYCEROL-3-PHOSPHATE DEHYDROGENASE
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Pred. No.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,646
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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APPLICANT:
APPLICANT:
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APPLICATION NUMBER: PCT\EP94\02936
FILLNG DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nucleotide Sequences Coding An TITLE OF INVENTION: Endopolygalacturonase Inhibito
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                            FILING DATE: 06-JUN-1994
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REGISTRATION NUMBER: 28,675
REFERENCE/DOCKET NUMBER: 54
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5370 Manhattan Circle Suite 201
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                                                                                                                                                                                                                                                                                                                                                                                 Salvi, Giovanni
Albersheim, Peter
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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06-DEC-1991
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                                                                                                                                                                                                                                                                                                           Endopolygalacturonase Inhibitor
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RESULT 8
US-08-244-646-15
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INFORMATION FOR SEQ ID NO:
                                                                                                                                           APPLICATION NUMBER: IT RM 91A 000915
FILING DATE: 06-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT:
                           NAME: Sullivan, Sally A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                            FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Nucleotide Sequences Coding An TITLE OF INVENTION: Endopolygalacturonase Inhibitor NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
            TELEPHONE:
                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/244,646 FILING DATE: 06-JUN-1994 CLASSIFICATION: 435
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TOPOLOGY: linear
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5370 Manhattan Circle Suite 201
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(303)499-8089
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Albersheim, Peter
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               (303)499-8080
                                                                                                                 UMBER: WO PCT/IT/00158
04-DEC-1992
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Pred. No. 94;
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INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-244-646-15
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US-08-592-936B-21
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                                           RESULT 10
US-09-111-573-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
               Patent No.
                            Sequence 21,
                                                                                                                                                                Matches
                                                                                                                                                                                            Query Match
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APPLICANT: Kellogg, J
APPLICANT: Bestwick,
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (650) 324-09 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: EVAINS, SUSAIN T.
REGISTRATION NUMBER: 38,443
REFERENCE/DOCKET NUMBER: 4257-0012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/592,936B FILING DATE: 29-JAN-1996 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                              MOLECULE TYPE: PI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bestwick, Richard K.
TITLE OF INVENTION: PLANT TISSUE / STAGE SPECIFIC PROMOTERS FOR
TITLE OF INVENTION: REGULATED EXPRESSION OF TRANSGENES IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity les 5; Conserv
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                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                           amino acid
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                            Application US/09111573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 Cambridge Avenue, Suite 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                       (650) 324-0880
550) 324-0960
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83.3%;
                                                                                                                                                                              91.2%;
83.3%;
                                                                                                                                                                                                                                       predicted amino acid of SEQ ID NO:20
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                                                                                                                                                                               Score 31; DB 1;
Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                     coding
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; INDIVIDUAL ISOLATE: ; INDIVIDUAL ISOLATE: US-09-111-573-21
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Best Local Similarity
Whiches 5; Conservi
                                             ; TYPE: PRT; ORGANISM: Arabidopsis sp. US-08-881-706-2
                                                                                                                                                                                                                                                                                                                US-08-881-706-2
                                                                                                                                                                                                                                                                                                                                   RESULT 11
                                                                                                          NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                             Sequence 2, Application US/08881706 Patent No. 6245969
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                                                            APPLICANT: Chong, Joane
APPLICANT: L1, Jianming
TITLE OF INVENTION: Receptor Kinase BIN1
FILE REFERENCE: 07251/022001
CURRENT APPLICATION NUMBER: US/08/881,706
CURRENT FILING DATE: 1997-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (650) 324-09
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: US/08/592
FILING DATE: 29-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: EVAID, SUSAN T.
REGISTRATION NUMBER: 4257
REFERENCE/DOCKET NUMBER: 4257
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650, 324-0880)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                             LENGTH: 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                  216 TGKIPP 221
                                                                                                                                                                                                                                                                                                                                                                                                            1 TGRIPP 6
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350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kellogg, Jill A.
Bestwick, Richar
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650) 324-0960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLANT TISSUE / STAGE SPECIFIC PROMOTERS FOR REGULATED EXPRESSION OF TRANSGENES IN PLANTS 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.2%;
91.2%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Richard K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  predicted of SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31; DB 2;
Pred. No. 1.4e+02;
 Score 31; DB 3;
Pred. No. 4.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid coding sequence NO:20
               Length 1196;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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US-09-188-469-12
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                                                                                                                                        Sequence 12, Application US/09188469 Patent No. 5989825 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12 Patent No.
                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                  TITLE OF INVENTION: Excitato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,569A FILING DATE: 10-OCT-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy
                                       UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Excitato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TORNEY/AGENT INFORMATION:
NAME: NO. 5882926nan, Kevin
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                             171 TGKVPP 176
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                                                                                                                                                                                                                                                                      1 TGRIPP 6
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5882926
                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                 564 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 South Wacker Drive
                                                                                              Arriza, Jeffrey L
Ellasof, Scott
                                                                                                                                                                                                                                                                                                   Conservative
                                                                               Kavanaugh, Michael P
                                                                                                                           Amara, Susan G
                                                                                                                                                                                                                                                                                                                                                                                        linear
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Arriza, Jeffrey L
Eliasof, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
      McDonnell Boehnen Hulbert & Berghoff
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                        ADDRESS
                                                           Excitatory Amino Acid Transporter Genes
                                                                                                                                                                                                                                                                                                               88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kevin E
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                                                                                                                                                                                                                                                                                                              Pred. No.
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                                                                                                                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                                                                                          Length 564;
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                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-09-188-469-12
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/09397238A Patent No. 6284505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 amino acid
                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
       APPLICATION NUMBER: US/09/397,238A
FILING DATE: 16-Sep-1999
CLASSIFICATION: <UNknown>
ATTORNEY/AGENT INFORMATION:
NAME: No. 6284505nan, Kevin E
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Amara, Susan G
Arriza, Jeffrey L
Eliasof, Scott
                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Excitatory and Uses
                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||::||
| 171 TGKVPP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGRIPP 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                         COUNTRY: USA
ZIP: 60606
                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                         ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                             300 South
                                                                                                                                                                                                                                                                         E ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.2%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                  Michael P
NUMBER: 93,509-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kevin E
                                                                                                                                                                                                                                              Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93,509-F
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Pred. No.
                                                                                                                                                                                                                                                                                                               Amino Acid Transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5e+02;
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RESULT 15
US-09-252-991A-20481
; Sequence 20481, Application US/09252991A
; Patent No. 6551795
; Patent TON:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-397-238A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΩÝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                             ; FEATURE:
; NAME/REY: UNSURE
; LOCATION: (388)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-20481
                                                                                                                      Š
Search completed: August 20, 2003, 12:44:23 Job time : 4.15663 secs
                                                                                    밁
                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20481
LENGTH: 582
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
FRANTIFE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 88.2%;
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                               Query Match 88.2%; Score 30; DB 4; Length 582; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Matches 5; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEPAR: 312-913-0002
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 TGKVPP 176
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94 TGRFPP 99
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Pred. No. 3.5e+02;
2; Mismatches 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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Match
        100.0
100.0
100.0
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94.1
91.2
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Gapop 10.0 , Gapext 0.5
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'Ggn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
'Cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
'Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
'Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
'Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
'Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
'Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
'Cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*
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'Cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*
'Cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*
'Cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*
'Cgn2_6/ptodata/1/pubpaa/USOOE_PUBCOMB.pep:*
'Cgn2_6/ptodata/1/pubpaa/USOOE_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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1 US-09-300-425B-34
1 US-09-300-425B-21
5 US-10-101-464A-63
5 US-10-101-464A-63
5 US-10-101-464A-766
5 US-10-101-464A-751
5 US-10-101-464A-791
5 US-10-101-464A-894
6 US-10-101-464A-891
7 US-10-101-464A-891
8 US-10-101-464A-891
9 US-09-864-73-394-2
1 US-09-863-3-394-2
1 US-09-864-3-394-2
1 US-09-864-3-394-2
1 US-09-864-3-394-2
1 US-09-864-3-394-2
1 US-09-758-269-14
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Compugen Ltd
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    Sequence 344, App Sequence 944, App Sequence 944, App
                                                                        Sequence 34, Appl
Sequence 21, Appl
Sequence 685, Appl
Sequence 685, Appl
Sequence 766, App
Sequence 751, App
Sequence 791, App
Sequence 8911, App
Sequence 8911, App
Sequence 8911, App
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  Sequence
                                                           Sequence 898,
Sequence 2, A
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-10-219-479-	-10-21	0-219-464-	-10-219-075-	-10-219-003-	-10-230-434-	19-076-	-10-227-883-	-10-227-873-	-218-849-6	-10-216-159A	-10-230-4	-10-218-631-	-10-230-338-	-10-230-163-	-10-227-884-	-10-216-163-6	-09-738	US-09-816-664-2	0	-09-764-891-	0-101-464	-10-101-464A-631	56-761-1210	-10-156-761-	-10-080-170-290	-10-101-464A-57	-10-101-464	-10-101-464A-92	US-10-101-464A-896
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ALIGNMENTS

RESULT 1 US-09-300-425B-34

Sequence 34, Application US/09300425B Publication No. US200300456B1A1

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Publication NU.

GENERAL INFORMATION:

APPLICANT: NERI, Dario

APPLICANT: TARLI, Lorenzo

APPLICANT: TARLI, Lorenzo

APPLICANT: VITI, Francesca

APPLICANT: VITI, Francesca

APPLICANT: BIRCHLER, Manfred

TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES

TITLE OF INVENTION: ANGIOGENESIS

FILE REFERENCE: SCH-1739P1

CURRENT APPLICATION NUMBER: US/09/300,425B

PRIOR APPLICATION NUMBER: 09/075,338

PRIOR PELICATION NUMBER: 09/075,338

PRIOR FILING DATE: 1998-05-11

NUMBER: OF SEQ ID NOS: 34
В
                                                                                                                                                    SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 34

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B

OTHER INFORMATION: antibody clone
US-09-300-425B-34
                                   Ş
                                                                                              Query Match
Best Local :
                                                                               Matches
1 TGRIPP
                                     1 TGRIPP 6
                                                                         Similarity 6; Conserv
                                                                   100.0%; Score 34; DB 11; llarity 100.0%; Pred. No. 4.4e+05; Conservative 0; Mismatches 0;
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                                                                                                        Length 6;
                                                                     Indels
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RESULT 2

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US-09-300-425B-21

; Sequence 21, Application US/09300425B

; Publication No. US20030045681A1
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US-10-101-464A-685
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                                                                                                                                                ; ORGANISM: Pinus radiata US-10-101-464A-685
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SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 685, Application US/10101464A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF INVENTION: ANGIGGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: VL antibody OTHER INFORMATION: specific for ED-B domain of fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                       LENGTH: 10
TYPE: PRT
                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-01-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 108
                                                                                                                                                                                                                             , ID NO 685
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                                                                                            Local
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                                                                         Similarity 6; Conserv
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 TGRIPP 26
                                                                         100.0%; ilarity 100.0%; Conservative 0
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                                                                                            Score 34; DB Pred. No. 29;
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US-10-101-464A-645
Query Match
Best Local Similarity
Thes 6; Conserv
                                                                                            ; ORGANISM: Eucalyptus US-10-101-464A-645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                     NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-11-01
PRIOR PELICATION NUMBER: 09/228,986
PRIOR PELICATION NUMBER: 09/228,986
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR PELICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/101,464A CURRENT FILING DATE: 2002-03-18
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                                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US00/00724
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 11000.1020c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                          LENGTH: 155
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                Conservative
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                                     100.0%;
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                                       Score 34;
Pred. No.
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                    red. No. 40;
Mismatches
                                                            DB 15; Length 155;
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; ORGANISM: Pinus radiata 
US-10-101-464A-751
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; Sequence 766, Application US/10101464A
; Publication No. US20030046728A1
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CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR APPLICATION NUMBER: F07/US00/00724
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
                                                                                                                                             NUMBER OF SEQ ID NOS: 989
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 751
LENGTH: 224
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 766
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APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Strabala, Timothy APPLICANT: Nieuwenhuizen, N APPLICANT: Higgins, Colleen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Strabals, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
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TYPE: PRT
ORGANISM: Pinus radiata
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  100.0%;
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Score 34;
Pred. No.
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Pred. No. 42;
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DB 15;
58;
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                   Length 224;
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                                     ; ORGANISM: Streptomyces avermitilis US-10-156-761-8911
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US-10-101-464A-894
US-10-ence 894, Application US/10101464A
; Sequence 894, Application US/20101464A
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CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR APPLICATION NUMBER: 09/162,866
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
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                                                                          NUMBER OF SEQ ID NOS:
SEQ ID NO 8911
LENGTH: 598
TYPE: PRT
Query Match
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SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 894
LENGTH: 705
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Best Local :
                                                                                                                                           PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                         PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                     APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
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TYPE: PRT
ORGANISM: Pinus radiata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Strabala, Timothy APPLICANT: Nieuwenhuizen, N
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HORIKAWA, HIROSHI
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SAKAKI, YOSHIYUKI
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94.18;

Score 32;

B 15;

Length 598

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US-10-101-464A-701
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Matches
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SOFTWARE: FastSEQ for
SEQ ID NO 701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their, Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT PELICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR PILING DATE: 2001-1-01
PRIOR PILING DATE: 2009-01-12
PRIOR PILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-01-01
PRIOR PILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 00/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
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                                                                             SEQ ID NO 898
                                                                                                                                    PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
CURRENT FILING DATE: 2007-04,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
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                                                                                               NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
ORGANISM: Pinus radiata
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                                   TYPE: PRT
                                                     ENGTH: 383
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nes 5; Conservative
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5; Conserv
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L; Mismatches
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Pred. No.
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thes 0;
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Best Local
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LENGTH: 1196
; TYPE: PRT
; ORGANISM: Arabidopsis
US-09-823-394-2
            PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09823394 Publication No. US20030041344A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 5; Conserv
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PRIOR FILING DATE: 1997-06-24
NUMBER OF SEC. TO TO THE PRIOR FILING DATE: 1997-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jianming, Li
APPLICANT: Salk Institute for Biological Studies
TITLE OF INVENTION: RECEPTOR KINASE, BIN 1
FILE REFERENCE: SALKINS.012CP1
CURRENT APPLICATION NUMBER: US/09/823,394
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-55-23
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 TGKIPP 213
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Chen, Wensheng
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2001-01-30
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83.3%;
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Pred. No. 3.5e+02;
1; Mismatches 0
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Pred. No.
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1.1e+03;
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                                                       CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33825
LENGTH: 63
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APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Strabala, Timothy
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
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RIOR FILING DATE: 2001-01-30
RIOR APPLICATION NUMBER: PCT/US01/00663
RIOR FILING DATE: 2001-01-30
RIOR APPLICATION NUMBER: PCT/US01/00662
RIOR APPLICATION NUMBER: PCT/US01/006662
RIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-01-30
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FastSEQ for Windows Version 4.0
                                           SEQ ID NOS
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5; Conserv
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EST_HUMAN
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EXPRESSED IN PLACENTA, SIGNAL = 1.1
EXPRESSED IN BT474, SIGNAL = 8.4
EXPRESSED IN BT474, SIGNAL = 8.4
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83.3%;
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IN HBL100, SIGNAL = 1.5
IN FETTAL LYVER, SIGNAL = 1.8
IN HELA, SIGNAL = 2.1
IN ADULT LYVER, SIGNAL = 1.2
IN ADULT LYVER, SIGNAL = 1.2
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Pred. No. 95;
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HEART, SIGNAL = 1.3
T: A124380.1, EVALUE 8.60e+00
T: Q13085, EVALUE 1.00e-30
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Search completed: August 20, 2003, 13:16:48 Job time: 7.50602 secs

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                                                                                                         ; ORGANISM: Zea mays US-09-758-269-14
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                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-09-758-269-14
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US-10-101-464A-944
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Best Local Similarity bs...
Thes 5; Conservative
                                                        Matches
                                                                  Query Match
Best Local
                                                                                                                                                                 SOFTWARE: P.
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 944
LENGTH: 370
                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09758269 Patent No. US20020104120A1
                                                                                                                                                                                         PRIOR APPLICATION NUMBER: JP PRIOR FILING DATE: 2000-01-13 NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/758,269
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: JP 2001-003476
PRIOR FILING DATE: 2001-01-11
                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: TRANSGENIC PLANTS CARRYING NEOXANTHIN TITLE OF INVENTION: CLEAVAGE ENZYME GENE FILE REFERENCE: 3914-3
                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                             APPLICANT: IUCHI, APPLICANT: KOBAY
                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
142 SGRIPP 147
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                           1 TGRIPP 6
                                                                                                                                                  604
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                                                     Similarity 5; Conserv
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                                                                                                                                                                                                                                                                                                                               KOBAYASHI, MASATOMO
SHINOZAKI, KAZUO
                                                     Conservative
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                                                                 88.2%;
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                                                  Score 30; DB 10;
Pred. No. 8.4e+02;
1; Mismatches 0;
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Pred. No. 5.2e+02
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Sequence:
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                                                                                             Score
           100.0
                                                                                        Match
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Gapop 10.0 , Gapext 0.5
                                                                                                                       Query
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US-09-300-425B-34
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                                                                 Description
Sequence 34,
Sequence 34,
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US-09-075-338C-34
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equence 2088, equence 144095	2088, A e 2088,	equence 1, Ap	e 171478 e 6784	equence 2943,	equence 2943, A	D O	e 42835,	equence 78827,	equence 783	equence 783	equence 155	751	e /51	751, 7	e 221	766,	equence 766,	Sequence	quence 766,	equence	equence 645,		sequence 83,	equence 83, App	equence	quence 83, Appl	equence 4223,	equence 1676	equence 685	equence 685.	e 685. Ap	quence 685. App	equence 21. App	equence 21, App	quence 21.	Ana

ALIGNMENTS

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Sequence 34 Application US/09075338C

Sequence 34 Application US/09075338C

Sequence 34 Application US/09075338C

APPLICANT: MERI, Dario

APPLICANT: TARLI, Lorenzo

APPLICANT: TARLI, Lorenzo

APPLICANT: BIRCHLER, Manfred

ITILE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY

FILE REFERENCE: SCH-1733

CURRENT APPLICATION NUMBER: US/09/075,338C

CURRENT FILING DATE: 1998-05-11

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin Ver. 2.1

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B

OTHER INFORMATION: antibody clone

US-09-075-338C-34

Query Match

Best Local Similarity 100.0%; Score 34; DB 14; Length 6;

Best Local Similarity 100.0%; Pred. No. 5.2e+06;
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Best Local Similarity
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                                    ; FEATURE; OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B; OTHER INFORMATION: antibody clone US-09-512-082-34
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US-09-512-082-34
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SEQ ID NO 34
LENGTH: 6
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Query Match
                                                                                                                                                                  SEQ ID NO 34
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CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
PRIOR FILING DATE: 1998-05-11
                                                                                                                                                                                                                                                                                     APPLICANT: TARLÍ, LOTENZO
APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, Manfred
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
TITLE OF INVENTION: ANGIOGENESIS
FILE REFERENCE: SCH-1733P2
CURRENT APPLICATION NUMBER: US/09/512,082
CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF TITLE OF INVENTION: ANGICE
                                                                                                                                                                                                 PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-C
NUMBER OF SEQ ID NOS: 34
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                                                                                                                                                                                     SOFTWARE:
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ORGANISM: Artificial Sequence
                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: anti-ED-B OTHER INFORMATION: antibody clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                               ENGTH:
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VITI, Francesca
BIRCHLER, Manfred
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APPLICANT: NERI, D
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SOFTWARE: PATENTIN VEI. 2.1
SEQ ID NO 21
LENGTH: 108
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SEQ ID NO 21
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APPLICANT: BIRCHLER,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/09300425B GENERAL INFORMATION:
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                                 Matches
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FILE REFERENCE: SCH-1/33

CURRENT APPLICATION NUMBER: US/09/075,338C

CURRENT FILING DATE: 1998-05-11

CURRENT FILING DATE: 34
                                                 Query Match
Best Local Similarity
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APPLICANT: BIRCHLER, Manfired
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY
FILE REFERENCE: SCH-1733
                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
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                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                   LENGTH: 108
TYPE: PRT
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                                                                                                                   ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: VL antibody
OTHER INFORMATION: specific for ED-B domain of fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity les 6; Conserv
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1 TGRIPP 6
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                                                                                                                                                                                                                                                                                                                                                                                                      VITI, Francesca
BIRCHLER, Manfred
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                                   Conservative
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                                                 100.0%; Score 34; DB 17; 100.0%; Pred. No. 4.8e+02;
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Pred. No. 4.8
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hes 0;
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                                                                                                                                                           ) ORGANISM: Pinus radiata PCT-US00-00724-685
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                                                                                                                                                                                                    SEQ ID NO 685
LENGTH: 109
TYPE: PRT
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LENGTH: 108
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Best Local Similarity
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CURRENT FILING DATE: 2000-01-11
EARLIER APPLICATION NUMBER: 09/228,986
EARLIER FILING DATE: 1999-01-12
EARLIER APPLICATION NUMBER: US 60/162,866
EARLIER FILING DATE: 1999-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020C1PCT
                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 1322
SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR TILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
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NUMBER OF SEQ ID NOS:
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                                                                            Local Similarity
les 6; Conserv
21
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TGRIPP 26
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VITI, Francesca
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                                                                                              100.0%;
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Pred. No.
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RESULT 10
US-60-162-866-685
; Sequence 685, Application US/60162866
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
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GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolass
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c1U
CURRENT APPLICATION NUMBER: US/09/704,302A
CURRENT FILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 1402
SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 685
LENGTH: 109
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Best Local Similarity
Matches 6; Conserv
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SOFTWARE: FastSEQ for
SEQ ID NO 685
LENGTH: 109
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APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 1100,1020c2
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/728,986
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
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Best Local :
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Pred. No. 4.8e+02;
Pred. No. 4.8e+02;
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Pred. No.
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hes 0;
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RESULT 11
US-10-424-599-167644
; Sequence 167644, Application US/10424599
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US-60-162-866-685
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US-09-513-999C-4223
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SEQ ID NO 685
LENGTH: 109
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APPLICANT: Dumas Milne Edwards, J.B.
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SEQ ID NO 167644
LENGTH: 114
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Best Local Similarity
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Best Local
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               SOFTWARE: Patent.pm
SEQ ID NO 4223
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                                                 CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26 NUMBER OF SEO ID NOS: 36681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
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CURRENT APPLICATION NUMBER: US/60/162,866
CURRENT FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 1275
                                                                                                                                                       APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and
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APPLICANT: Kovalic David K
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LOCATION: (1)..(114)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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LENGTH: 144
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Pred. No.
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Pred. No. 4.8e+02;
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                                                                                                                                                                    Encoded Human Proteins
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US-09-704-302A-83
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PCT-US00-00724-83
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                                  US-09-704-302A-83
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                                                                                                                                                                                                                                                                              Sequence 83, Application US/09704302A GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 83, Application PC/TUS0000724
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
                                                                                                       SEQ ID NO 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                         APPLICANT: Nieuwenhuizen, Nicolaas
TITLE OF INVENTION: Compositions Isolated from Plant Cells.
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c1U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: PCT/US00/00724
CURRENT FILING DATE: 2000-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Compositions Isolated from Plant Cells TITLE OF INVENTION: and Their Use in the Modification of P. FILE REFERENCE: 11000.1020C1PCT
                                                                                                                     NUMBER OF SEQ ID NOS: 1402
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                               APPLICANT: Strabala, Timothy APPLICANT: Nieuwenhuizen, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: US 09/228,986
EARLIER FILING DATE: 1999-01-12
EARLIER APPLICATION NUMBER: US 60/162,866
EARLIER FILING DATE: 1999-11-01
                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/704,302A CURRENT FILING DATE: 2002-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 153
TYPE: PRT
ORGANISM: Pinus radiata
                                                 ORGANISM: Pinus
                                                                    TYPE: PRT
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                                                                                    LENGTH: 153
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seq ATVLLLSFGSVAA/SH
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Pred. No. 6.3e+02;
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Pred. No. 6.7e+02;
 Score
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 34;
 DВ
 21;
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Length 153;
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GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Nieuwenhuizen, Nicolated from Plant Cells
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: And Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT FILING DATE: 1000-01-01
PRIOR APPLICATION NUMBER: 09/704.302
PRIOR APPLICATION NUMBER: 09/704.302
PRIOR FILING DATE: 2000-01-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR APPLICATION NUMBER: 05/162,866
PRIOR APPLICATION NUMBER: 05/162,866
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR SEQ ID NOS: 989
SEQ ID NOS: 989
SEQ ID NOS: 989
SEQ ID NOS: 989
LENGTH: 153
TYPE: PRT
ORGANISM: Pinus radiata
US-10-101-464A-83
Search completed: August 20, 2003, 13:13:46 Job time: 62.4096 secs
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US-10-101-464A-83
; Sequence 83, Application US/10101464A
; GENERAL INFORMATION:
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126 TGRIPP 131
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126 TGRIPP 131
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Result
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Maximum DB
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Perfect score:
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length: 2000000000
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1: /cgn2_6/ptcdata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptcdata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptcdata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/1/paa/US08_NEW_COMB.pep:*

6: /cgn2_6/ptcdata/1/paa/US08_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/1/paa/US08_NEW_COMB.pep:*
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1 TGRIPP 6
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Maximum Match 100%
Listing first 45 summaries
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US-10-408-765A-2802
US-10-258-898A-3022
US-10-258-898A-3022
US-10-258-898A-6594
US-10-613-520-1196
US-10-613-520-1378
US-09-674-546A-1529
US-09-674-546A-1529
US-09-674-546A-1529
US-09-673-20480-18
PCT-US03-20480-18
PCT-US03-20480-15
US-10-268-897-6954
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1527, Ap
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16954, Ap
6954, Ap
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9, Appl
193, Appl
1931, App
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2802, Ap
3022, Ap
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65	<u></u>	4		Sequence 2, Appli		3552	577		10255,		1775,	6114,				e 3366,	272	Sequence 16, Appl

ALIGNMENTS

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Sequence 1, Application US/10336041A
GENERAL INFORMATION:
APPLICANT: Schering AG
TITLE OF INVENTION: New methods for diagnosis and
FILE REFERENCE: 27041P_WOAS
CURRENT APPLICATION NUMBER: US/10/336,041A
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: EP02 000 315.8
PRIOR FILING DATE: 2002-01-03
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2002-02-25
NUMBER OF SEQ ID NOS: 13
SOSTWARE: Patentin Ver. 2.1
RESULT 2
US-10-336-041A-10
; Sequence 10, Application US/10336041A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: recombinant; OTHER INFORMATION: antibody fragment US-10-336-041A-1
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US-10-336-041A-1
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LENGTH: 238
TYPE: PRT
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Matches
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LOCATION: (117)..(130)
OTHER INFORMATION: Linker
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                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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222 TGRIPP 227
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100.0%; Pred. No. 7.8;
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                                                                                                                                                                                                 RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/10350041A
GENERAL INFORMATION:
APPLICANT: Schering AG
TITLE OF INVENTION: New methods for diagnosis
FILE REFERENCE: 27041P_WOAS
                                                                                                                                      Sequence 11, Application US/10336041A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 240
TYPE: PRT
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Best Local :
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
APPLICANT: Schering AG
TITLE OF INVENTION: New methods for diagnosis and treatment of tumours
FILE REFERENCE: 27041p WOAS
CURRENT APPLICATION NUMBER: US/10/336,041A
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: EPO2 000 315.8
PRIOR FILING DATE: 2002-01-03
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CURRENT APPLICATION NUMBER: US/10/336,041A
CURRENT FILING DATE: 2003-01-03
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TITLE OF INVENTION: New methods for diagnosis
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NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
                                                                                                                                                                                                                                   Sequence 9, Application US/10336041A GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
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           SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
                                                                 CURRENT APPLICATION NUMBER: US/10/336,041A CURRENT FILING DATE: 2003-01-03 PRIOR APPLICATION NUMBER: EP02 000 315.8 PRIOR FILING DATE: 2002-01-03 PRIOR APPLICATION NUMBER: US60/358702 PRIOR APPLICATION NUMBER: US60/358702 PRIOR FILING DATE: 2002-02-25
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TITLE OF INVENTION: New methods for diagnosis and treatment of tumours
FILE REFERENCE: 27041P_WOAS
                                                                                                                                                                                 APPLICANT: Schering AG
TITLE OF INVENTION: New methods for diagnosis
FILE REFERENCE: 27041P_WOAS
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PRIOR APPLICATION NUMBER: US60/358702
PRIOR FILING DATE: 2002-02-25
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CURRENT FILING DATE: 2003-01-03
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                                                    NUMBER OF SEQ ID NOS: 13
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ORGANISM: Homo sapiens
US-10-408-765A-1931
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US-10-291-265-332
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PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FREESEQ for Windows Version 3.0
SEQ ID NO 332
                                                      SEQ ID NO 1931
LENGTH: 311
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APPLICANT: Fahy, E
APPLICANT: Zhang,
APPLICANT: Glbson,
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APPLICANT: Tang et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
                                                                                                                              CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
                                                                                                                                                                 APPLICANT: Glbson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
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PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
                                                                                         NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 8.
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APPLICANT: Tang et al
TITLE OF INVENTION: NOVel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
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US-10-612-783-4490
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                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT4577_129850C.1.pep US-10-612-783-4490
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SEQ ID NO 334
LENGTH: 312
TYPE: PRT
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APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53373)
                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/612,783
CURRENT FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 7098
SEQ ID NO 4490
LENGTH: 518
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                                                        Score 33; DB
Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB Pred. No. 10;
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                                                                        Length 518;
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                                         Indels
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504 TGRVPP 509

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                                                                                                          ; TYPE: PRT; ORGANISM: Homo sapiens US-10-286-897-3022
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US-10-286-897-3022
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US-10-408-765A-2802
Query Match
Best Local Similarity 83...
**Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity bo...
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                SOFTWARE: pt_FL_genes_b Versions 1.0
SEQ ID NO 3022
LENGTH: 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ghosh, Soumitra APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US/09/620,312
PRIOR FILING DATE: 2000-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/286,897
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hyseq Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784FLPCT
                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 7143
                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US/09/727,344 PRIOR FILING DATE: 2000-11-29
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US/09/662,191
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US/09/693,036
PRIOR FILING DATE: 2000-10-19
PRIOR FILING DATE: 2000-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US/09/552,317
PRIOR FILING DATE: 2000-04-25
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                                                88.2%;
83.3%;
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    Mismatches

                                                  Score 30; DB Pred. No. 72;
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                               Indels
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US-10-258-898A-3022
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GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Hyseq In
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SEQ ID NO 3022
LENGTH: 334
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Best Local
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PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US09/653,450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/258,898A
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US/9552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/286,897
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR FILING DATE: 2000-01-21
                                                                                                                                 PRIOR APPLICATION NUMBER: US/09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US/09/653,450
PRIOR FILING DATE: 2000-08-31
                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US/09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US/09/598,042
PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US09/727,344
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US/09/727,344 PRIOR FILING DATE: 2000-11-29
                                                PRIOR APPLICATION NUMBER: US/09/693,036 PRIOR FILING DATE: 2000-10-19
                                                                                        PRIOR APPLICATION NUMBER: US/09/662,191 PRIOR FILING DATE: 2000-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hyseq Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-08-31
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                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US09/693,036 FILING DATE: 2000-10-19
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5; Conserve
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Pred. No.
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Gaps

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Page 5
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CORRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR PLICATION NUMBER: US09/552,317
PRIOR APPLICATION NUMBER: US09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US09/653,450
PRIOR APPLICATION NUMBER: US09/652,191
PRIOR APPLICATION NUMBER: US09/662,191
PRIOR APPLICATION NUMBER: US09/652,191
PRIOR APPLICATION NUMBER: US09/693,036
PRIOR APPLICATION NUMBER: US09/693,036
PRIOR APPLICATION NUMBER: US09/793,036
PRIOR APPLICATION NUMBER: US09/793,036
PRIOR APPLICATION NUMBER: US09/793,036
PRIOR FILING DATE: 2000-10-19
PRIOR FILING DATE: 2000-11-29
NUMBER OF ESQ ID NOS: 7143
SOFTWARE: Pt_FL_genes_b Versions 1.0
SEQ ID NO 6594
LENGTH: 365
TYPE: PRT
ORGANISM: Homo Sapiens
Search completed: August 20, 2003, 12:45:15 Job time: 1.73494 secs
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US-10-258-898A-6594
Sequence 6594, Application US/10258898A
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
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: SEQ ID NO 6594
: LENGTH: 365
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-286-897-6594
                                                                                                                                                                  Query Match 88.2%;
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 88.2%;
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides FILE REFERENCE: 784FLPCT CURRENT APPLICATION NUMBER: US/10/258,898A CURRENT FILING DATE: 2002-10-29
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||:|||
305 TGQIPP 310
                                                                                    305 TGQIPP 310
                                                                                                                              1 TGRIPP 6
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Result
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Perfect score:
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No. 1s the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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length: 2000000000
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Match
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34
1 TGRIPP 6
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      T39507
T01258
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H97423
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AD1889
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T09356
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C81216
G81793
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                                                                                                                                                                                                                                                       SUMMARIES
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receptor protein k
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hypothetical prote
conserved hypothet
hypothetical prote
probable ATP synth
hypothetical prote
                  UDP-galactose 4-ep
UDP-galactose 4-ep
alpha-1,2-N-acetyl
alpha 1,2 N-acetyl
            adenylate cyclase
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Om(2D) protein - f
                                                                                                                                           FAD synthase NMA06 polygalacturanase-penicillin-binding
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cylicin I - bovine
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                                                                                                                      probable receptor-
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29	29	29	29	29	29	29	29	29	29	30	30	30	30	30	30
85.3	85.3	85.3	85.3	85.3	85.3	85.3	85.3	85.3	85.3	88.2	88.2	88.2	88.2	88.2	88.2
149	134	133	121	100	99	86	79	75	57	4767	2346	2339	2324	1123	1109
2	Ν	N	N	N	N	N	ب	N	N	N	N	N	ب	N	N
F91217	JC5572	S10038	G75604	F82453	B87374	D65181	PJHUSB	A69010	S10782	T31345	I38928	S41121	A29924	D96756	T18536
	₽	_	hypothetical prote	conserved hypothet	transcription requ	hypothetical prote	proline-rich pepti	hypothetical prote	salivary protein P		acetyl-CoA carboxy	acetyl-CoA carboxy	acetyl-CoA carboxy	receptor-like prot	receptor-like prot

ALIGNMENTS

acetoin catabolism protein AcoX - Alcaligenes eutrophus (strain H16) C;Species: Alcaligenes eutrophus C;Date: 24-7ul-1992 #sequence_revision 24-Jul-1992 #text_change 30-Sep-1993 C;Accession: A42462

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RESULT A42462

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cylicin I - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change
C;Accession: B40713; S35920
R;Hess, H.; Heid, H.; Franke, W.W.
J. Cell Biol. 122, 1043-1052, 1993
A;Title: Molecular characterization of mammalian cylicin, a basi
A;Reference number: A40713; MUID:93359502; PMID:8354692
A;Accession: B40713
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
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B40713
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A;Title: Identification and molecular characterization of A; Reference number: A42462; MUID:91286190; PMID:2061286; A; Accession: A42462

A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-359 < PRID:
                                                                                                                          C; Keywords: cytoskeleton
                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-598 <HES>
A;Cross-references: GB:222780; NID:g396104; PIDN:CAA80457.1; PID:g396105
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Best Local S
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Best Local :
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                                                          Similarity
5; Conserv
TGRVPP 549
                                                            Conservative
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                                                                           97.1%;
83.3%;
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                                                                         Score 33;
Pred. No.
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Pred. No.
                                                       Mismatches
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                                                                      DB 45;
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                                                                                     Length 598
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                                                          Indels
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cylicin I - bovine
Cyspecies: Bos primigenius taurus (cattle)
Cyspecies: Bos primigenius taurus (cattle)
Cybate: 12-May-1994 #sequence_revision 12-May-1994 #text_change (cybates)
Cybate: 12-May-1994 #text_change (cybates)
Cybates: 12-May-1994 #text_change (cybates)
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SXAD97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hexon-associated protein (IX) - human adenovirus 3
C;Species: Mastadenovirus h3 (human adenovirus 3)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C;Accession: B03854; A03854
R;Engler, J.A.
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SXAD93
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C;Speciles: Mastadenovirus h7 (human adenovirus 7)
C;Speciles: Mastadenovirus h7 (human adenovirus 7)
C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 05-Jun-1998
C;Accession: A03854
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A; Residues: 1-667 <HES>
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                                                                                                                                                                                                                  A;Cross-references: GB:J01962; NID:g209966; C;Superfamily: adenovirus hexon-associated C;Keywords: hexon-associated protein
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C; Superfamily: adenovirus hexon-assoc
C; Keywords: hexon-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 13, 375-385, 1981
A;Title: The gene for polypeptide IX of human adenovirus
A;Reference number: A91480; MUID:81261948; PMID:6266923
A;Recession: A03854
A;Rocession: A03854
A;Residues: 1-138 <DIJ>
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A; Residues: 1-138 <ENG>
                                                                                                                                                                                                                                                                                                                                                                                           A; Title: The nucleotide sequence of the polypeptide IX A; Reference number: A91481; MUID:81261949; PMID:7262560
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 13, 387-394, 1981
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                                                   TGRIPP
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                                                                                                      Pred. No. 15;
1; Mismatches
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protein (IX)
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regulatory protein nask - Klebsiella pneumoniae
C;Species: Klebsiella pneumoniae
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 04-Mar-2000
C;Accession: A55859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A55859
                                                                                                                                                                                                                                                                                                             R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Elsen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755; PMID:10710307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Goldman, B.S.; Lin, J.T.; Stewart, J. Bacteriol. 176, 5077-5085, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                    riboflavin kinase/FMN adenylyltransferase NMB1834 [imported] - Neisseria mei C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: H81036
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A; Residues: 1-393 <GOL>
Ъ
                                 Q_{Y}
                                                                                                                                                A; Gene: NMB183
C; Superfamily:
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A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: H81036
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A;Accession: A55859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 176, 5077-5085, 1994 A; Title: Identification and structure of the mask
                                                                                                                                                                                                        A; Experimental source: serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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ce: serogroup B, strain MC58
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83.3%;
                                                                                                                                                  hypothetical protein HI0963
                                                                                             91.2%;
83.3%;
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Pred. No.
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                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein nasR
                                                                                                                   2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                               0;
                                                                                                                 Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                               Indels
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                                                                               0;
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                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                 0,
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C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: A81982

Neisseria meningitidis (; (EC 2.7.7.2); riboflavin

(strain Z2491 in kinase (EC :

l serogroup 2.7.1.26)

ð

R; Parkhill,

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Achtman,

Ξ

James,

K.D.;

Bentley,

S.D.;

Churcher,

Klee,

. R.;

8

RESULT A81982

FAD synthase NMA0621 [similarity]

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C;Accession: H71803
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: H71803
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-613 <ARN>
                                                                                                                                                                                                                                                                                       H71803

penicillin-binding protein - Helicobacter pylori (strain J99)

c;Species: Helicobacter pylori
A;Variety: strain J99

c;Date: 12-Peb-1999 #sequence_revision 12-Feb-1999 #text_change 17-Mar-2000
                                                     A; Experimental source: C; Genetics:
                                                                                         A; Cross-references: GB: AE001568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X64769; NID:g21028; PIDN:CAA46016.1; PID:g21029
A;Note: it is uncertain whether Met-1 or Met-10 is the initiator
C;Superfamily: polygalacturanase-inhibiting protein; leucine-rich alpha-2-glycoprotein
F;274-297/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-342 < TOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Toubart, P.; Desiderio, A.; Salvi, G.; Cervone, F.; Daroda, 1 Plant J. 2, 367-373, 1992
A;Title: Cloning and characterization of the gene encoding the A;Reference number: S23764; MUID:93272053; PMID:1303801
A;Recession: S23764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polygalacturanase-inhibiting protein precursor - kidney bean
C;Species: phaseolus vulgaris (kidney bean)
C;Date: 05-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S23764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; A;Experimental source: serogroup A, strain Z2491 C;Genetics: A;Gene: ribF; NMA0621 C;Superfamily: conserved hypothetical protein HI0963 C;Keywords: nucleotidyltransferase; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete DNA sequence of a serogroup A strain of A;Reference number: A81775; MUID:20222556; PMID:10761919 A;Accession: A81982
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A; Residues: 1-318 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TGRIPP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGKIPP 221
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5; Conser
            penicillin-binding protein
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83.3%;
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83.3%;
                                                                                       GB:AE001439;
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61;
                                                                                   NID: g4156083; PIDN: AAD07044.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                      Doig, P.C.;
ylor, D.E.; v
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                                                                                 PID:g41560
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                                                                                                                                                                                                                                                       D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bergma
                                                                             RESULT 13
C84527
probable receptor-like protein kinase [imported] - C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-reb-2001 #sequence_revision 02-Feb-2001 C;Accession: C84527
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S51599
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                                                                                                                                                                                                                                                                                                                                                   Genetics:
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A;Gene: FlyBase:Dana/Om(2D)
A;Cross-references: FlyBase:FBgn0010400
                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-671 <YOS>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                C;Acc.
R;Yoshida, K.,
Cen. Genet.
                                                                                                                                                                                                                                                                                                                                                                            Om(2D) protein - fruit fly (Drosophila ananassae)
C;Species: Drosophila ananassae
C;Date: 15-Jul-1995 #sequence_revision Ol-Sep-1995 #text_change 07-May-1999
C;Accession: S51599
                                                                                                                                                                                                                                                                                          A; Title: Retrotransposon-induced ectopic expression of the Om(2D) gene causes A; Reference number: S51599; MUID:95107256; PMID:7808408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-615 <TOM>
A;Cross-references: GB:AE000653; GB:AE000511; NID:g2314733; PIDN:AAD08596.1; PID:g231
C;Superfamily: penicillin-binding protein 3
                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                  A; Accession: S51599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            son, J.D.; Kelley, J.M.; Cotton, M.D.; Dudson, K.; Khalak, H.G.; Glodek, A.; Mature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fras A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKe son, J.D.; Kelley; J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 17-Mar-2000 C;Accession: D64714
                                                                          Query Match
Best Local S
Matches 5
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 5
  431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 TGKIPP
                                                                                                                                                                                                                                                                                                                                          K.; Juni, N.; Awasaki,
Benet. 245, 577-587, 199
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                                    1 TGRIPP
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                                                                        Similarity
5; Conser
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TGKIPP 436
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein - Helicobacter pylori (strain 26695)
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                      EMBL:D26553;
                                                                                                                                                                                                                                                                                                                                N.; Awasaki, T.; Tsuriya, Y.; Shaya, N.; Hori, S.H. 577-587, 1994
                                                                                      91.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.2%;
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                                                                    Score 31; DB
Pred. No. 1.46
1; Mismatches
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Pred. No. 1.3e
1; Mismatches
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Pred. No. 1
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                                                              DB 2; Lc..
1.4e+02;
~ 0;
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1.3e+02;
0;
                                                                                                                                                                                                  PID:d1006095; PID:g443770
                                                                                                        Length 671
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Arabidopsis thaliana #text_change 02-Feb-2001

euss, D.; Nierman, W.C.; Nature 402, 761-768, 1999

in, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, s, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Town, C

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hypothetical protein T9N14.3 [imported] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C.Accession: C96745
R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.R.; Dewar, K.;
Ansen, N.F.; Hughes, B.; Huizar, L.
A.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
R.Izzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.; Reference number: A86141; MUID:21016719; PMID:11130712
A.; Accession: C96745
A.; Accession: C96745
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A;Molecule type: DNA
A;Residues: 1-744 <5TO>
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A;Gene: At2g15300
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                                                                                                                       R;Yamamoto, E.; Karakaya, H.C.; Knap, H.T. Biochim. Biophys. Acta 1491, 333-340, 2000 A;Title: Molecular characterization of two
                                                                                                                                                                                                                     receptor protein kinase homolog [imported] - soybean
C;Species: Glycine max (soybean)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
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                                                                           A; Reference number: 225262
A; Accession: T50851
                                                                                                                                                                                                   C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-977 <STO>
A; Residues: 1-981 <YAM>
                       A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
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Pred. No. 2.1e+02;
1; Mismatches 0
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A;Cross-references: EMBL:AF197946; PIDN:AAF59905.1
C;GenetLcs:
A;Gene: CLV1A
                                                         C; Superfamily: protein kinase Xa21; leucine-rich alpha-2-glycoprotein repeat homology
Query Match
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"heres 5; Conserv
            Conservative
                       91.2%;

    Mismatches

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Search completed: August 20, 2003, 12:42:28 Job time: 6.19277 secs

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34
1 TGRIPP 6
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        ACOX, ALCEU
GPIB_HUMAN
CYIL_HUMAN
CYIL_BOVIN
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GPDA_CUPLA
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PGI2_PHAVU
PGI2_PHOVIN
TIZ2_MOUSE
RBL2_MOUSE
RBL2_MOUSE
RBL2_HUMAN
COAL_BOVIN
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ALIGNMENTS

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MEDIZINE-98024174; PubMed=9356492; MEDIZINE-98024174; PubMed=9356492; Yu J., Nagarajan S., Knez J.J., Udenfriend S., Chen R., Medof M.E.; Yn J., Nagarajan S., Knez J.J., Udenfriend S., Chen R., Medof M.E.; The affected gene underlying the class K glycosylphosphaticylinositol (GPI) surface protein defect codes for the GPI transamidase."; (GPI) surface protein defect codes for the GPI transamidase."; Natl. Acad. Sci. U.S.A. 94:12580-12585(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Benghezal M., Benachour A., Ru
"Yeast Gpi8p is essential for
EMBO J. 15:6575-6583(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=97133287; PubMed=8978684;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (hGPI8).
PIGK OR GPI8.
Hydrolase;
ACT_SITE
ACT_SITE
CONFLICT
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                                     PRINTS; PR00776;
Hydrolase; Thiol
                                                                                   MEROPS; C13.005;
                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content ified and this statement is not removed. Usage by and ities requires a license agreement (See http://www.isb-send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                 protein.

PATHWAY: GPI-anchor biosynthesis.
SUBUNIT: Associates with PIGS and PIGT.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C13.
                                                                                                                                                                                                                                                                                                                  Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

FUNCTION: Mediates GPI anchoring in the endoplasmic reticulum, replacing a protein's C-terminal GPI attachment signal peptide with a pre-assembled GPI. During this transamidation reaction, GPI transamidase forms a carbonyl intermediate with the substra
                                                                                                 605087;
                                                                                                                        AF022913; AAB81597.1;
BC020737; AAH20737.1;
                                                            pro; IPR001096; Legumain.
pr01650; Peptidase_C13; 1.
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T.J., Udenfriend S.,
                                      protease;
                                                   HEMOGLOBNASE.
   164
206
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                                      GPI-anchor biosynthesis.
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   MAVT -> SI
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     SLHEA (IN
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                    InterPro; IPR002314; tRNA-synt_2k
InterPro; IPR002320; tRNA-synt_tk
InterPro; IPR006195; tRNA_11gase_
Pfam; PF03129; HGTP_anticodon; 1.
Pfam; PF032824; TGS; 1.
Pfam; PF00587; tRNA-SYNTHTHR.
PRINTS; PR01047; TRNASYNTHTHR.
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30-MAY-2000
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                             some structural and kinetic properties.";
Biochimie 76:71-77(1994).
-I- CATALYTIC ACTIVITY: ATP + L-threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence analysis and modular organization of threonyl-tRWA synthetase from Thermus thermophilus and its interrelation with threonyl-tRWA synthetases of other origins."; Eur. J. Biochem. 267:379-393(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-HB8 / ATCC 27634;
MEDLINE-20098514; PubMed-10632708;
                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                        diphosphate + L-threonyl-trna(Thr).
-!- COFACTOR: Binds 1 zinc ion per subunit.
-!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- DOMAIN: THE C-TERMINAL DOMAIN RECOGNIZES THE ANTICODON BASES.
-!- SIMILARITY: Belongs to class-II aminoacyl-trna synthetase fam
                                                                                                                                            EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                Ehresmann C., Ehresmann B.;
"Threonyl-tRNA synthetase from Thermus
                                                                                                                                                                                                                                                                                                                                                                                                    zheltonosova J., Melnikova E., Garber M., Reinbolt J.,
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=HB8 / ATCC 27634;
MEDLINE=94304998; PubMed=8031907;
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Bacteria; Deinococcus-Thermus;
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; P00955; 1EV
P; MF_00184;
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Rel. 41, Last annotation updat
synthetase (EC 6.1.1.3) (Thre
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tRNA_ligase_II.
                                                                                              tRNA-synt_2b
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RESULT 4
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ID CYL1_HI
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Matches
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01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cylicin I (Multiple-band polypeptide I) (Fragr
CYLC1 OR CYL1 OR CYL.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertel
Mammalia; Eutheria; Primates; Catarrhini; Hom.
NCBL_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as modified and this statement is not removed. Us entities requires a license agreement (See http or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular characterization of mammalian cylicin, a basic the sperm head cytoskeleton.",
J. Cell Biol. 122:1043-1052(193).
I-FUNCTION: POSSIBLE ARCHITECTURAL ROLE DURING SPERMATO BE INVOLVED IN SPERMATID DIFFERENTIATION.
I-SUBCELLULAR LOCATION: CALYX; SPERM HEAD CYTOSKELETAL
I-TISSUE SPECIFICITY: Testis.
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DOMAIN 234
DOMAIN 338
METAL 349
METAL 400
METAL 529
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                                                                                                                                                                                                                                                                                                                             EMBL; Z22780;
PIR; B40713; E
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SEQUENCE
                                                                                                                                                                                                            Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- DEVELOPMENTAL STAGE: SPECIFIC TO LATE SPERMATOGENESIS.
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P35663;
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GO:0005198; F:structural molecu
GO:0007283; P:spermatogenesis; I
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I) (Fragment).
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                                                                                                                                                                                                                                                                                                                                "Molecular characterization of mammalian cylicin, a basic the sperm head cytoskeleton.;
J. Cell Biol. 122:1043-1052(1993).
-I- FUNCTION: POSSIBLE ARCHITECTURAL ROLE DURING SPERMATOG BE INVOLVED IN SPERMATID DIFFERENTIATION.
-I- SUBCELLULAR LOCATION: CALYX; SPERM HEAD CYTOSKELETAL S-I- TISSUE SPECIFICITY: Testis.
                                                                             SEQUENCE
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                                                                                                                                                                    REPEAT
REPEAT
                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
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01-JUN-1994 (Rel.
01-NOV-1997 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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TGRVPP
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5; Conserv
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94 (Rel. 29, Last sequence update)
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(Multiple-band polypeptide I).
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83.3%;
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Pred. No.
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CBF66EA462243D91 CRC64;
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RESULT

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RESULT 7
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DE Glycer
GN GPDH.
OS Cuphea
OC Eukary
OC Sperma
OC MCBL_T
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EMBL; J01962; AAA42510.1; -.
PIR; A03854; SXAD97.
PIR; B03854; SXAD93.
InterPro; IPR005641; Adeno_PIX.
Pfam; PF03955; Adeno_PIX; 1.
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21-JUL-1986
15-DEC-1998
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01-OCT-1996
01-OCT-1996
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hexon-associated PIX.
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Human adenovirus type
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
Glycerol-3-phosphate dehydrogenase [NAD+] (
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                                                                             Eukaryota; Viridiplantae; Streptophyta; Embry, Spermatophyta; Magnoliophyta; eudicotyledons; eurosids II; Myrtales; Lythraceae; Cuphea.
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                                                                                                                                         Cuphea lanceolata.
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      Hausmann L.,
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                                                             NCBI_TaxID=3930;
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PubMed=7262560;
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(In) Kader J.-C., Mazliak P. (eds.);
Plant lipid metabolism, pp.534-536,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phaseolus vulgaris (Kidney bean) (French bean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
NCBI_TaxID=3885;
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                                                                                                                                                                                                                                                               Toubart P., Desiderio A., Salvi G., Cervone F., Daroda L de Lorenzo G., Bergmann C., Darvill A.G., Albersheim P.; "Cloning and characterization of the gene encoding the endopolygalacturonase-inhibiting protein (PGIP) of Phase
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SE(
STRAIN-CV. Saxa; TISSUE-Hypocotyl;
MEDLINE-93272055; PubMed-1303801;
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28-FEB-2003 (Rel.
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P35334;
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  Leckie F., Mattei B., Capodicasa C., Hemmings A., Nuss L. De Lorenzo G., Cervone F.; De Lorenzo G., Cervone F.; "The specificity of polygalacturonase-inhibiting protein single amino acid substitution in the solvent-exposed beta-strand/beta-turn region of the leucine-rich repeats
                                                                                                               SEQUENCE FROM N.A., AND MUTAGENESIS STRAIN=CV. Pinto; TISSUE-Hypocotyl; MEDLINE-99246261; PubMed=10228150; MEDLINE-99246261; PubMed=10228150;
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EMBL; A23205; CAA01664.1; -
PIR; S23764; S23764.
InterPro; IPR001611; LRR.
InterPro; IPR007090; LRR_pl
Pfam; PF00560; LRR; 4
   PGI2_PHAVU
P58822;
28-FEB-2003
28-FEB-2003
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MO1. Plant Microbe Interact. 10:852-860(1997).

-i- FUNCTION: Inhibitor of fungal polygalacturonase. It is an important factor for plant resistance to phytopathogenic fungi.
Substrate preference is polygalacturonase (PG) from A. niger >> |

of F.oxysporum, A.solani or B.cinerea. Not active on PG from
F.moniliforme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE-97449843; PubMed-9304859;
Desiderio A., Aracri B., Leckie F.,
Van Roekel J.S., Baulcombe D.C., Me)
Cervone F.;
                                                                          PHAVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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5; Conserv
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18:2352-2363(1999).
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   (Rel. 41, (Rel. 41,
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83.3%;
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   sequence, update)
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LRR 2.
LRR 3.
LRR 4.
LRR 5.
LRR 6.
LRR 7.
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t-1 or Met-10 is the initiator.
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STRAIN-cv. Pinto; TISSUE-Hypocotyl;
MEDLINE-99246261; PubMed-10228150;
Leckie F., Mattel B., Capodicasa C., Hemmings A., Nuss L., Arac.
De Lorenzo G., Cervone F.;
"The specificity of polygalacturonase-inhibiting protein (PGIP)
single amino acid substitution in the solvent-exposed
beta-strand/beta-turn region of the leucine-rich repeats (LRRs)
confers a new recognition capability.";
EMBO J. 18:2352-2363(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phaseolus vulgaris (Kidney bean) (French bean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseo
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Pfam; PF00560; LRR;
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                                                                                                                                                                                                                                                                                                                                   Glycoprotein;
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    Last annotation update)
    inhibitor 2 precursor (Polygalacturonase-inhibiting

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Q->K: NO EFFECT.
A->S: NO EFFECT;
ASSOCIATED WITH G
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N-LINKED (GLCNAC
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V->G: NO EFFECT;
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                                                                              REASE OF ACTIVITY; LOSS OF ASSOCIATED WITH G-181 OR
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           T; NO EFFECT WHEN H G-181; LOSS OF F D WITH K-253.
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H K-253;
H S-326.
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TGKIPP

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                                                                                                                                                                                                                                                                                                                                         -i- TISSUE SPECIFICITY: Found in suspension-cultured lesser extent in hypocotyls, leaves and flowers.
-i- SIMILARITY: BELONGS TO THE POLYGALACTURONASE-INHI
                                                                                                                                                                                                                                                                                                                                                                          Plant J. 2:367-373(1992).

- FUNCTION: Inhibitor of fungal polygalacturonase.

- important factor for plant resistance to phytopat

- i SUBCELLULAR LOCATION: Cell-wall associated.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Toubart P., Desiderio A., Salvi G., Cervone F., Daroda L., de Lorenzo G., Bergmann C., Darvill A.G., Albersheim P.; de Lorenzo and characterization of the gene encoding the "Cloning and characterization of the gene encoding the endopolygalacturonase-inhibiting protein (PGIP) of Phaseolus vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-cv. Pinto; TISSUE-Hypocotyl; MEDLINE-93272053; PubMed-1303801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein) (PGIP-2)
PGIP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Polygalacturonase inhibitor 3 precursor (Poly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHAVU
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InterPro; IPR007090;
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                      Similarity
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                       Conservative
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83.3%;
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BY SIMILARITY.
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MEDLINE=20083488; PubMed=10617198;
Mayer K.F.X., Schueller C., Wambutt R.,
Mayer K.F.X., Duesterhoeft A., Stiekema W.,
Pohl T., Duesterhoeft A., Stiekema W.,
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Weichselgartner M., de Simone V., Obermaier B., Mache R.,
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Feldmann K.A., Tax I
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RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R., Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S., RA Chefdor F. Cooke R., Berger C., Monfort A., Casacuberta E., Ra Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E., Ra Chefdor F., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., Pernel B., Bent E., Johnson S., Tacon D., Jesse T., Ra Perper P., Heber S., Tacon D., Jesse T., Ra Prishman D., Hasse D., Lemcke R., Wewes H.-W., Stocker S., Schwarz S., Scholler P., Heber S., Francs P., Bielke C., Ra Zaccaria P., Bevan M., Milson R.K., de la Bastide M., Habermann K., Ra Zaccaria P., Bevan M., Milson R.K., de la Bastide M., Habermann K., Ra Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J., Ra Schoneking T., Kalicki J., Graves T., Harmon G., Edwards J., Lancelle P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., Ra Schon J., Fulton B., Miller N., Greco T., Kemp K., Ra Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L., Ra Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., Ra Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ra Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R., Ra Swaby I. K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Ra Chen E., Marra M., Martienssen R., McCombie W.R.; "Sequence and analysis of chromosome 4 of the plant Arabidopsis of chromosome 4 of the plant Arabidopsis
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MEDLINE-20336852; PubMed-10875920;

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[5]
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InterPro; IPR007090; LR
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PRINTS; PR00019; LEURICHRPT.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISCELLANEOUS: A 70 amino acid island between the 20th and the 21th LRR is essential for the binding of brassinosteroids.

MISCELLANEOUS: Binding of brassinosteroid induces intramolecular autophosphorylation of BRII. Interaction with BAKI activates both receptor kinases and the full activation of either receptor kinases and the full activation of either receptor kinase requires transphosphorylation by their partners. Optimum in vitro phosphorylation of the substrate requires arg or Lys residues at P-3, P-4, and P+5 (relative to the phosphorylated amino acid at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: Phosphorylated on at least 12
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DOMAIN: Contains one 1
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DEVELOPMENTAL STAGE: Expressed constitutively
  429
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                                       \vdash
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TGKIPP 434
                                       TGRIPP 6
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                         repeat;
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                                                                                                                                                               1196
813
121
146
169
197
221
221
268
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; Prot_kinase.
; Ser_thr_pkinase.
                                                                                           91.2%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein;
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d Cys (Cys pair 1 and
                                                                     Score 31; DB
Pred. No. 1e+0
1; Mismatches
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LRR 1.
LRR 2.
LRR 3.
LRR 4.
LRR 5.
LRR 6.
LRR 7.
LRR 7.
LRR 8.
                                                                                                                                                                                                                                                                                                                                             BRASSINOSTEROID
                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation
                                                                                             1e+02;
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                                                                                                                 DB 1;
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1 2) invol
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RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Ra Altschul S.F., Zeebbrg B., Buetcow K.H., Schaefer C.F., Bhat N.K., Ra Altschul S.F., Zeebbrg B., Buetcow K.H., Schaefer C.F., Bhat N.K., Ra Altschul S.F., Zeebbrg B., Buetcow K.H., Schaefer C.F., Bhat N.K., Ra Altschul S.F., Zeebbrg B., Buetcow K.H., Schaefer C.F., Bhat N.K., Ra Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Ra Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Ra Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Ra Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Ra Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Ra Brownstein M.J., Wackernan K.J., Malek J.A., Gunaratne P.H., Ra Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Ra Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Ra Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Ra Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Ra Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Ra Richards S., Worley K.C., Hale S., Sarchen A., Rodrigues S., Sanchez A., Whiting M., Maddan A., Young A.C., Shevchenko Y., Bouffard G.G., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Ra Schnerch A., Schein J.E., Jones S.J.M., Warra M.A.;

"Generation and mouse cDNA sequences", 1977 1000 full-length human and mouse cDNA sequences."
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Proline-serine-threonine phosphatase-interacting protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Wagatsuma M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.,
"NEDO human cDNA sequencing project.",
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: Binds to F-actin. May be involved in regulation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 112-333 FROM N.A. (ISOFORM 1). ISOGAI T., Ota T., Hayashi K., Sugiyama T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                               Genew; HGNC: 9581; PSTPIP2
InterPro; IPRO01060; Cdc1:
Pfam; PF00611; FCH; 1.
SMART; SM00055; FCH; 1.
                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932;
PROSITE;
                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                         EMBL; AK023100; BAB14404.1; EMBL; BC035395; AAH35395.1;
                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                             Note=No experimental confirmation available; pTM: phosphorylated on tyrosine (By similarity). SIMILARITY: Contains 1 FCH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 actin cytoskeleton (B SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q9H939-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9H939-2; Sequence=VSP_004070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISOFORM 2).
                                                                                Cdc15_Fes_CIP4
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NN: Cytosolic and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugiyama T., Otsuki T.,
S., Shiratori A., Sudo I
Y., Kodaira H., Kondo H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shiratori A., Sudo H.,
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RESULT 13
TIZ2_MOUSE
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                          "Identification: "Identification of TSC22.";
genes related to TSC22.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSCRIPTIONAL REPRESSOR (BY SIMILARITY).
-!- FUNCTION: TRANSCRIPTIONAL REPRESSOR (CAN FORM AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9EQN3;
                                                                                                                              InterPro; IPR000580; TSC-22_Dip_Bun. pfam; PF01166; TSC22; 1. proDom; PD007152; TSC-22_Dip_Bun; 1. proSITE; PS01289; TSC22; 1.
                                                                                                                                                                               HSSP; P80220; 1DIP.
MGD; MGI:1926079; 0610009M14Rik.
                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                              "Identification and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001
16-OCT-2001
                                                                                               SEQUENCE
                                                                                                          DOMAIN
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                                                             Local
                                                                       Match
                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear (Potential). SIMILARITY: BELONGS TO THE TSC-22/DIP/BUN FAMILY.
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 246 TGKVPP 251
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
ed inducible leucine zipper protein
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MYEQVERKSLEMCSIQROIEYEN/ORKTGQIPPAPIMHENFY
SSGKNAVPAGKATGPNLARRGELPIPKSSPDDPNYSLVDDY
SILVQ -> HESCMRISTPPRRMQSQQERLQGLTWQGEDPS
QFLKAHQMIPITLWLMTTVCSISKINETRAFSG (in
                                                 Score 30; DB:
Pred. No. 50;
2; Mismatches
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0A8C9FD4C419A2B8
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

REQUIRE 96203998; PubMed=8622859;

RA Lecouter J.E., Whyte P.F.M., Rudnicki M.A.;

RA Lecouter J.E., Whyte P.F.M., Rudnicki M.A.;

RT "Cloning and expression of the Rb-related mouse pl30 mRNA.";

CC "I- FUNCTION: MAY HAVE A FUNCTION IN CELL CYCLE REGULATION. BINDS TO CC AND MAY BE INVOLVED IN THE TRANSFORMING CAPACITY OF THE ADENOVIRUS CC E1A PROTEIN. MAY ACT AS A TUMOR SUPPRESSOR. POTENT INHIBITOR OF CC E2F-MEDIATED TRANS-ACTIVATION, ASSOCIATES. PREFERENTIALLY WITH CC E2F-MEDIATED TRANS-CATIVATION, ASSOCIATES. PREFERENTIALLY WITH CC E2F5. BINDS TO CYCLINS A AND E (BY SIMILARITY).

CC -I- SUBCELLULAR LOCATION: Nuclear.

CC -I- PTM: Phosphorylation on Ser-669 in G1 leads to its ubiquitin-

Ammendent proteolysis (By similarity).
                                  DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                          Phosphorylation; Anti-oncogene
DOMAIN 414 1021 PM
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Q64700;
30-MAY-2000
                                                                                                                                                                                                                                                                                                    MGD; MGI:105085; Rb12.
InterPro; IPR006670; Cyclin.
InterPro; IPR002720; RB_A.
InterPro; IPR002719; RB_B.
                                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                                                                          TRANSFAC; T02972; MGD; MGI:105085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning, expression, and developmental characterization the murine retinoblastoma related gene Rb2/p130."; Cell Growth Differ. 5:1659-1664(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. B101.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDILINE-96199216; PubMed-8621630;

Chen G., Guy C.T., Chen H.W., Hu N., Lee E.Y.H.P.,

"Molecular cloning and developmental expression of
member of the retinoblastoma gene family.";

J. Biol. Chem. 271:9567-9572(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Retinoblastoma-like protein 2 (130 kDa
protein) (PRB2) (P130) (RBR-2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                       PF01858; RB_A; 1.

PF01857; RB_B; 1.

; SM0385; CYCLIN; 2.

cription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                               U36799; AAB48991.1; -. U50850; AAC52598.1; -. U47333; AAC52555.1; -. P06400; IGUX.
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A., de Luca A.,
POCKET (BINDS E1A).
DOMAIN A.
SPACER.
DOMAIN B.
POLY-PRO.
POLY-ALA.
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Sciurognathi; Muridae; Murinae; Mus
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RESULT 15
COAC_CHICK
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Best Local S
Matches
                                                                                                                                                                                                    acetyl-CoA carboxylase.";
FEBS Lett. 212:98-102(1987).
-I- FUNCTION: CATALYZES THE RATE-LIMITING REACTION IN THE BIOGENESIS OF LONG-CHAIN FATTY ACIDS. THIS PROTEIN CARRIES THREE FUNCTIONS:
BIOTIN CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetyl-CoA carboxylase (EC 6.4.1.2) (ACC) [Incarboxylase (EC 6.3.4.14)].
                                                                                                                                           -!- CATALYTIC ACTIVITY:
                                                                                                                                                                                 CARBOXYLTRANSFERASE.
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CONFLICT
CONF
                                                                                                                                                                                                                                                                                                           Takai T., Wada K., Tanabe T.; "Primary structure of the biotin-binding site
                                                                                                                                                                                                                                                                                                                                                MEDLINE-87106011; PubMed-2879745;
                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Liver
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 493-820 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           from cDNA sequence.";
J. Biol. Chem. 263:2651-2657(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takai T., Yokoyama C., Wada K., Tana
"Primary structure of chicken liver
from cDNA sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-88139305; PubMed-2893793;
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Eukaryota; Metazoa; Cho
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DOMAIN
         SUBCELLULAR LOCATION: Cytoplasmic SIMILARITY: PARTIAL TO CARBAMOYL F
                                                                                                          - ADP + phosphate + COFACTOR: BIOTIN.
                                                                    PATHWAY:
                                                              ENZYME REGULATION: BY PHOSPHORYLATION. PATHWAY: Long-chain fatty acid biosynthesis;
                                                                                                                                                                 + malonyl-CoA.
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83.3%;
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POLY-GLU.

PHOSPORYLATION (BY SIMILARITY).

MISSING (IN REF. 3).

A -> P (IN REF. 2).

A -> P (IN REF. 1).

R -> T (IN REF. 1).

S -> T (IN REF. 1).

O -> R (IN REF. 2).

O -> R (IN REF. 2).
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A -> R (IN REF. 1)
P -> A (IN REF. 3)
PT -> RA (IN REF.
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Pred. No. 1.6e+02;
1; Mismatches 0
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                                                                                                                                           biotin-carboxyl-carrier
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I (IN REF. 1)
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SO THE TENT WE WERE
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DR InterPro; IPR005482; Biotin_lipoyl.

DR InterPro; IPR000089; Biotin_lipoyl.

DR InterPro; IPR000089; Carboxyl_trans.

DR InterPro; IPR005481; CPase_L_N.

DR InterPro; IPR005481; CPase_L_N.

DR Pfam; PF002785; Biotin_carb_C; 1.

DR Pfam; PF002785; Biotin_carb_C; 1.

DR Pfam; PF00789; CPase_L_D2.

DR Pfam; PF00789; CPase_L_chain; 1.

DR Pfam; PF00789; CPase_L_chain; 1.

DR Pfam; PF00786; CPase_L_D2; 1.

DR Pfam; PF00786; CPase_L_D2; 1.

DR PROSITE; PS00188; BIOTIN; 1.

DR PROSITE; PS00186; CPASE_L; 1.

R PROSITE; PS00867; CPASE_L; 1.

R PROSITE; PS00867; CPASE_S; Biotin; Ligase; Multifunctional enzyme;

W ATP-binding; Phosphorylation.

The Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of t
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EMBL; X05019; CAA28675.1; -.
PIR; A29924; A29924.
HSSP; P24182; IDVI.
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BY SIMILARITY.
BIOTIN.
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
COENZYME A-BINDING (BY SIMILARITY).
7 MW; 3F1C541F01BBBEF6 CRC64;
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Pred. No. 3.3e+02;
Vienmatches 0; Indels
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Result
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length:
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34
1 TGRIPP 6
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Match
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1: sp_archea:*
2: sp_bacter1a
3: sp_fung1:*
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sp_bacteria:*
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136.423 Million cell updates/sec
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Q9vnu2 drosophila
Q3417 pseudomonas
O82432 malus domes
O81826 glycine max
Q91826 glycine max
Q81hw9 oryva sativ
Q92865 rhizobium m
Q8bxx3 mus musculu
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| 0958726 094CC4 0946C24 094652 08H1P9 09A530 08MS94 094L67 09JYY5 09BW035 09BW035 09BW035 09BW035 09BW035 09BW036                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 958726 941C4 094CC4 094L67 094L67 094L67 094L67 094L67 094L67 094L67 094L67 094L67 092J51 026078 08L272 08L272 08L272 08L272 08L272 08L277 08S700 09SH06 09C7T7 09SH06 09C7T7 09SH06 09C7T7 09M6AB 09M27 09SH06 09C7T7 09M6AB 09M27 09SH06 09C7T7 09H6AB 09M27 09SH06 09C7T7 09H6AB 09M27 09SH06 09C7T7 09H6AB 09M27 09SH06 09C7T7 09H6AB 09M27 09SH06 09C7T7 09M6AB 09M27 09M6AB | 1299<br>2427<br>85<br>100            |                                                | 671<br>717<br>737<br>744<br>977<br>981                   | 306<br>318<br>358<br>613<br>633                          | 496<br>505<br>505<br>778<br>81                                                         |
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## ALIGNMENTS

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RESULT
Q9VNU2
ID Q9
AC Q9
DT 01
DT 01
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Best Local Similarity
Matches 6; Conserv
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01-MAY-2000 (TrEMBLrel. 13, 1
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CG11440 protein (HL01743p).
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Signal peptidase I (EC 3.4.21.89).
SIPC OR LA3754.
 Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases EMBL; AE011531; AAN50952.1; -. Hydrolase; Complete proteome. SEQUENCE 198 AA; 22758 MW; 5D8B8F7351B65237 CRC64;
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STRAIN-56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
 Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
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Last annotation update)
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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 Adams M.D., Celniker S.E., Holt R.M., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., E. Richards S., Ashburner M., Henderson S.M., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Ephydroidea; Drosophilidae; Drosophila.
 Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., Ghampe M., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 Submitted (JUN-2002) to the EMBL; AE003597; AAF51828.1; EMBL; AY119567; AAM50221.1;
 Patel S., Phouanenavong
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 "A leucine-rich repeat receptor-like protein induced in Malus x domestica by Venturia inae salicylic acid treatment "; plant Mol. Biol. 40:945-957(1999).

--- SIMILARITY: BELONGS TO THE SER/THR FAMILY EMBL; AF053127; AAC36318.1; --
Interpro; IPR001611; LRR.
Interpro; IPR007099; LRR.plant.
 rseudomonas aeruginosa PAO during cloning of the arylsulfatase gene Eur. J. Biochem. 229:385-394(1995)
 033417
 Malus domestica (Apple) (Malus sylvestris).
Eukaryota; Viridiplantae; Streptophyta; Embry.
Spermatophyta; Magnoliophyta; eudicotyledons;
 ATSB
 InterPro;
InterPro;
 Pseudomonas
Bacteria; Pi
 ABC-type
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 MEDLINE=99454543; PubMed=10527419; Komjanc M., Festi S., Rizzotti L.,
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Bacteria; Proteobacteria;
Pseudomonadaceae; Pseudomo
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001 (TrEMBLrel. 19, Last annotation update)
transporter, putative membrane subunit.
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 IPR000719;
 Florina;
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(TIEMBLrel. 08, Last sequence update)
(TIEMBLrel. 23, Last annotation update)
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 5F8B669560AF81BB CRC64;
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 Mol. Biol. Evol. 18:1522-1531(2001).

Mol. Biol. Evol. 18:1522-1531(2001).

-!- SIMILARTY: BELONGS TO THE SER/THR FAMII
EMBL; AF244888; AAF91322.1; -.

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InterPro; IPR004838; NHtransf_1.

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ATP-binding; Kinase; Serine/threonine-proteil
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Q9LKZ6;
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Q1-CCT-2000 (TrEMBLrel. 15, Last
Q1-MAR-2003 (TrEMBLrel. 23, Last
Receptor-like protein kinase 1.
 PRINTS: PRO0019; LEURICHRPT.
PRINTS: PRO0109; TYRKINASE; 1.
PRODOM; PD000001; PROT_KINASE; 1.
PROSITE; PS50502; LRR_PS; 5.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00111; PROTEIN_KINASE_DOM;
PROSITE; PS00108; PROTEIN_KINASE_ST; 1
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae; Glycine CEI_TaxID-3847;
 a gene family.
Mol. Biol. Evo
-!- SIMILARITY
 RLK1.
Glycine max (Soybean).
 Yamamoto E., Knap
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 ATP-binding; Kinase; Receptor;
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R InterPro; IPRO06025; Zn_MTpeptdse.
R InterPro; IPRO06025; Zn_MTpeptdse.
R Ffam; PF00050; LRR; 19.
R Pfam; PF00009; pkinase; 1.
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DR PRONTS; PR000109; TYRKINASE.
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DR PROSITE; PS00142; ZINC_PROTEASE; 1.
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Sasaki T., Matsumoto T., Yamamo;
Sasaki T., Matsumoto T., Yamamo;
"Oryza sativa nipponbare(GA3) gr
clone:P0022B05.";
Submitted (OCT-2001) to the EMB;
EMBL; AP004262; BAC10827.1; -.
 01-OCT-2000
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01-MAR-2003
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 Q9LKZ4
Q9LKZ4;
 Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Etreptophyta; Ex
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
 -!- SIMILARITY: BELONGS TO THE EMBL; AF244890; AAF91324.1; -. HSSP; P12931; 1FMK.
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 Hypothetical P0022B05.33.
 InterPro; IPR001611; LRR.
InterPro; IPR007090; LRR_
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 a gene family.
Mol. Biol. Evo
 Glycine max (Soybean)
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 'Soybean receptor-like
 Biol. Evol.
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Tyr_pkinase.
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Hypothetical protein R01632.
R01632 OR SMCQ0940.
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01-MAR-2003
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SEQUENCE 1016 AA; 110741 MW; 533584DBCC6EA686 CRC64;
 Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batubolistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.";
 InterPro; IPR001245; Tyr_p:
Pfam; PF00560; LRR; 1.
Pfam; PF00069; pkinase; 1.
 InterPro;
InterPro;
 Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; AL591787; CAC46211.1; -.
Hypothetical protein; Complete proteome.
 Sinorhizobium meliloti strain
 Bacteria; Proteobacteria; A
Rhizobiaceae; Sinorhizobium
 Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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 MEDLINE=21396507; PubMed=11481430;
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Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
[1]
 the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome b 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK077893; BAC37051.1;
EMBL; AK087803 BAC37051.1;
SEQUENCE 395 AA; 44895 MW; 4765ADD
 01-MAR-2003 (TrEMBLrel.
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Nature 420:563-573(2002)
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Mammalia; Eutheria;
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 Mus musculus (Mouse)
 GPI transamidase homolog
 Q8BH63
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STRAIN-Nipponbare;

MCCombie W.R., de la Bastide M., Spiegel L., Preston R., Kirchoff K.,

MCCombie W.R., de la Bastide M., Santos L., Zutavern T., Miller B.,

Kuit K., Mascimento L., Baker J., Santos L., Zutavern T., Miller B.,

Cunnius D.M., Katzenberger F., Muller S., Bell M., Balija V., Shah R.,

King L., Yang C., Dike S., O'Shaughnessy A., Palmer L., Dedhia N.,

"Genomic sequence for Oryza sativa, Nipponbare strain, clone

OSJNBb0023M11, from chromosome 10, complete sequence.";
 QBRU53;
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2002 (TrEMBLrel. 22,
 Q8BL63;
Q8BL63;
Q1-MAR-2003
Q1-MAR-2003
Q1-MAR-2003
 Oryza sativa (Rice).

Gukaryota; Viridiplantae; Str.

Spermatophyta; Magnoliophyta;

Ehrhartoideae; Oryzeae; Oryza

NCBI_TaxID=4530;
 SEQUENCE FR. Wing R.A., Currie J.,
 OSJNBB0023M11.14.
 Putative cytochrome
 Q8RU53
 the RIKEN Genome Exploration Research analysis of the mouse transcriptome b 60,770 full-length cDNAs.";
Nature 420.563-573(2002).
EMBL: AK046246; BAC32653.1; -
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
 The
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Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahl B.B.,
Jin S.S., Koo H., Zismann V., Hislao J., Blunt S., Vanaken S.S.,
Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.,
Potyza sativa chromosome 10 BAC OSJNBb0038A07 genomic sequence.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC092389; AAM86826.1;
EMBL; AC113948; AAM94518.1;
Gramene; Q8L4U4;
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Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
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In S.S., Koo H., Zismann V., Hslao J., Blunt S., Vanaken S.S.,
Utterback T.T., Feldblyum T.V., Yang Q.O., Haas B.J., Suh B.B.,
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"Oryza sativa chromosome 10 BAC OSJNBa0053C23 genomic sequence."
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ProDom; PD000001; Prot_Kinase; 1.

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SMART; SM00219; TYFKC; 1.

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InterPro; IPR001245; Tyr.pkinase.
Pfam; PF00069; pkinase; 1.
 Oryza sativa (japonica cultivar-group).
Eukaryota; Viriddiplantae; Streptophyta; Embryophyt
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 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative receptor-like protein kinase (Hypothetical
OSJNBA0055C23.12 OR OSJNBB0038A07.18
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 01-OCT-2002
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 "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";

Mesorhizobium loti.";

DNA Res. 7:331-338(2000).

EMBL; AP002996; BAB48475.1; ...

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Pfam; PF00532; Peripla_BP_like; 1.

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Complete proteome.

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Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Kimura T., Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Kishida Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Tabeta S.;
 01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Transcriptional regulator.
MLR1005.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986 DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988 DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998 DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990 DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991 DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991 DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992 DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992 DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993 DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993 DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995 DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997 DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999 DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990 DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000 DAT: *
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001 DAT: *
| SIDS1/gcgdata/ge
 A_Geneseq_19Jun03:*
 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen
 116
238
238
307
363
117
116
240
 DB
 21
22
23
24
24
24
 AAY53772
AAE08817
AAY53775
AAU14225
AAU14228
ABB050533
ABB95999
AAY02472
ABB95997
 IJ
 SUMMARIES
 Ltd
 1107863
 VH component of an Human scFV L19 ant An antibody within Human novel protei Human novel protei Fibronectin isofor HSA antibody relat A single chain ant
 Description
Human serum albumi
```

| XX<br>XX<br>Vd                                                                        | PR<br>PR<br>XX                                           | XX<br>3d                   | XX<br>XX     | PN            |                          | XXX<br>WW<br>WW<br>WW<br>WW<br>WW                                                                                                                                                                                                                                                              | XX<br>DE                                                               | DT.                       | - AC      | RE XX                                                                |            | -                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                                                | _                        |                          | •                                                    |                                |                          |                                |                            |                                                        |                          |                                    |                                                          |                          | <del></del>                                                  |                          | <del></del>                               | _                              | •                                          |                                         |                                   |                                        |                                                        |
|---------------------------------------------------------------------------------------|----------------------------------------------------------|----------------------------|--------------|---------------|--------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------|---------------------------|-----------|----------------------------------------------------------------------|------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------|--------------------------|--------------------------|------------------------------------------------------|--------------------------------|--------------------------|--------------------------------|----------------------------|--------------------------------------------------------|--------------------------|------------------------------------|----------------------------------------------------------|--------------------------|--------------------------------------------------------------|--------------------------|-------------------------------------------|--------------------------------|--------------------------------------------|-----------------------------------------|-----------------------------------|----------------------------------------|--------------------------------------------------------|
| (EIDG-) EIDGENOESSISCHE TECH HOCHSCHULE ZUERICH. Neri D, Tarli L, Viti F, Birchler M; | 11-MAY-1998; 98US-0075338.<br>28-APR-1999; 99US-0300425. | 11-MAY-1999; 99WO-EP03210. | 18-NOV-1999. | WO9958570-A2. | Synthetic. Homo sapiens. | scFv; antibody; ED-B domain epitope; fibronectin; marker; angiogenesis; vascular proliferation; diabetic retinopathy; age-related macular degeneration; tumour; immunoscintigraphic detection; blood coagulation; blood vessel occlusion; ocular angiogenesis; angiogenesis-related pathology. | VH component of an antibody with improved specificity for fibronectin. | 22-FEB-2000 (first entry) | AAY53772; | RESULT 1<br>AAY53772<br>ID AAY53772 standard; Peptide; 116 AA.<br>XX | ALIGNMENTS | and the second s | 44 538.5 88.6 221 24 ABRO1506 Human anti-TIMP-1 45 538 88.5 118 23 AAO18441 Anti-GD2 anti-bod- | 539 88.7 281 18 AAW27560 | 539 88.7 120 24 ABJ18675 | 539 88.7 125 22 AAE07013<br>539 88.7 120 18 AAW27553 | 540 88.8 293 22 AAG65715 Amino | 540 88.8 240 22 AAB46038 | 540 88.8 240 22 AAB46010 Human | 540.5 88.9 240 21 AAY15125 | 541 89.0 367 24 ABP55467<br>540.5 88.9 240 21 AAY15124 | 541 89.0 240 22 AAB46040 | 541 89.0 136 24<br>541 89.0 239 23 | 541.5 89.1 123 22 AAE07019<br>541.5 89.1 217 24 ABR01504 | 542 89.1 124 22 AAB72879 | 542.5 89.2 121 22 AAEO7029 Human 542.5 89.2 121 24 ARESESSO7 | 543 89.3 224 24 ABRO1511 | 544 89.5 131 18 AAW13520 Anti-melanoma an | 545 89.6 220 24 ABR01517 Human | 545.5 89.7 245 22 AAB67620 Human leukocyte | 549 90.3 220 24 ABR01519 Human anti-TIV | 551 90.6 240 22 AAB46042 Human TF | 558 91.8 116 23 AAO21548 Antibody scre | 560.5 92.2 313 22 AAU14320<br>558 91.8 116 23 ABG69320 |

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```
RRESULT 2
AAEOBB 7
ID AAEOB
XX AAEOB
XX AAEOB
XX AAEOB
XX 19-N
XX 19-N
XX COAB
XX COAB
XX COAB
XX HOME
XX HOME
XX HOME
XX AAEO
PM WO20
 νQ
 Š
 밁
 밁
 The present sequence represents the VH component of a modified human of scFv antibody which has specific affinity for a characteristic epitope of the ED-B domain of fibronectin. The affinity of the antibody for this epitope was improved by introducing a number of mutations in the complementarity determining region (CDR) residues located at the periphery of the binding site. The improved antibody is used for rapid targeting markers of angiogenesis, for detecting diseases characterized by vascular proliferation, such as diabetic retinopathy, age-related by vascular proliferation or tumours. The antibody localizes the respective constant of the first and diseases characterized by the first and diseases characterized by the respective constant of the preparation of diseases characterized by vascular proliferation. The antibody can be conjugated to a molecule which induces blood coagulation and blood vessel occlusion. These conjugates are used in the preparation of injectable compositions for the treatment of angiogenesis-related pathologies, especially caused by or associated
 Query Match
Best Local (
 Matches
 Claim 10;
 Fibronectin
 Sequence
 WPI; 2000-039074/03.
 19-NOV-2001
 with ocular angiogenesis.
 Neri
 angiogenesis; blood
 Human; ScFv; single-chain variable antibody fragment; cancer; cytotoxic; coagulant; ED-B domain; fibronectin; tumuor; ocular disorder; psoriasis; vascular proliferation; rheumatoid arthritis; blood vessel occlusion; anglogenesis; blood coagulation; variable heavy chain; VH.
 AAE08817 standard; Protein; 116
 An antibody,
ED-B domain
 (EIDG-)
 24-FEB-2000;
 23-FEB-2001;
 30-AUG-2001
 WO200162800-A1
 Homo sapiens
 Human scFV L19 antibody variable heavy chain region.
 Ò
 2001-541701/60
 116;
 61
 61
 Similarity
 EIDGENOESSISCHE TECH
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS
 EVQLLESGGGLVQPGGSLRLSCAASGFTESSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS
 Tarli L,
 Page 38;
 116 AA;
 ED-B domain epitope specific antibodies and conjugate
 of fib
 Conservative
 2000US-0512082
 2001WO-EP02062
 (first entry)
 ith specific fibronectin
 59pp; English.
 Viti
 100.0%;
 'n
 affinity
for the t
 0
 Birchler
 Score
Pred.
 HOCHSCHULE
 Mismatches
 e 608; DB 21;
. No. 5.8e-49;
smatches 0;
 for a characteristic treatment of diseases
 ×
 Indels
 Length 116;
 epitope of the characterized
 0;
 Gaps
 116
 116
 60
 60
 0;
```

```
RRESULT 3
AAX153775
IID AAX15
XX AAX15
XX AAX15
XX AAX15
XX SCFV
XX SCFV
XX Angl
XX Fibi
Pri anti
XX Cla
XX
 밁
 δÃ
 Вр
 QΥ
 Query Match
Best Local
 Matches
 The invention relates to an antibody with specific affinity for a characteristic epitope of the ED-B domain of fibronectin, where the antibody has improved affinity to ED-B. The invention also relates to conjugates comprising antibodies with a suitable photoactive molecule useful in the detection and/or coagulation of blood vessels. An antibody with improved affinity to the ED-B domain is useful for diagnosis and therapy of tumours and diseases characterised by vascular proliferation, cancer, rheumatoid arthritis, neo-vasculature associated ocular comprises the injection of conjugates comprising antibody and a molecule capable of inducing blood coagulation and blood vessel occlusion. The present sequence is single-chain variable antibody fragment (scFV) L19 antibody variable heavy chain (VH) region related to the invention.
 Claim 10;
 by vascular proliferation
 angiogenesis; vascular proliferation; diabetic retinopathy; age-related macular degeneration; tumour; immunoscintigraphic detection; blood coagulation; blood vessel occlusion; ocular angiogenesis;
 An antibody with improved specificity for fibronectin
 Sequence
 angiogenesis-related
 22-FEB-2000
 AAY53775
 AAY53775 standard; Protein;
 11-MAY-1998;
28-APR-1999;
 Homo
 Synthetic
 Claim
 Fibronectin
 WPI; 2000-039074/03.
 11-MAY-1999;
 18-NOV-1999
 WO9958570-A2
 (EIDG-)
 Ď
 sapiens.
 10;
 antibody;
 al Similarity
116; Conserv
 61
 61
 Н
 ۲
 EIDGENOESSISCHE TECH HOCHSCHULE
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
 EVQLLESGGGLVQPGGSLRLSCAASGFTESSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
 Tarli
 Page
 Page -;
 116
 Conservative
 ED-B domain
 (first entry)
 AA;
 36;
 L, Viti
 98US-0075338.
99US-0300425.
 99WO-EP03210
 ED-B domain epitope;
 73pp;
 59pp; English.
 100.0%;
 Ä
 epitope
 English
 238
 0,
 Birchler
 Score 608; DB 22;
Pred. No. 5.8e-49;
); Mismatches 0;
 A
 specific
 fibronectin;
 antibodies
 marker;
 Indels
 Length
 and conjugate
 116;
 0;
 Gaps
 60
 60
```

The present sequence represents

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modified human

SCFV

antibody which

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 8888888888888888888888888888888888888
 CC has specific affinity for a characteristic epitope of the ED-B domain CC improved by introducing a number of mutations in the complementarity content of the conten
 Best Loca
Matches
 Query Match
 Isolated polypeptides useful for treating anti-inflammatory diseases nervous system disorders, and for regenerating bone and cartilage -
 Example 4;
 Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antialiergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
 WPI; 2001-451939/48
 (HYSE-)
 25-JAN-2000; 2000US-0491404
 25-JAN-2001; 2001WO-US02623.
 02-AUG-2001
 WO200155437-A2
 Homo sapiens.
 Human novel protein #96.
 24-OCT-2001
 AAU14225 standard; Protein; 307 AA
 Sequence
 amalgamation
 roca1
 13
 116;
 this sequence does not appear in the specification; it is smatten of the sequences given in claim 10.
 regeneration;
 AAS22530
 ۲
 μ
 HYSEQ INC
 Similarity
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
 Liu c,
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116
 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKPEPYEDYWGQGTLVTVSS 116
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
 Page
 238 AA;
 (first entry)
 Conservative
 575;
 Drmanac RT
894pp; English
 100.0%;
 immune disorder.
 0
 Score 608;
Pred. No. 1
 Mismatches
 DB 21;
.3e-48;
 0;
 Length
 238;
 0
 Gaps
 an
 60
 60
 0,
```

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RESULT 5
AAU14228
 밁
 Ş
 밁
 Q
 *6588888888888888888888888888888888
 cc proteins or their active domains. The polypeptides, polynucleotides and thodoles raised against the polypeptides are used in a method of curatment of a mammal and prevention of disorders caused by the aberrant complexities are used in a method of curatment of a mammal and prevention of disorders caused by the aberrant complexities are used as protein a method of curatment of a mammal and prevention of disorders caused by the aberrant curatment of a mammal and prevention of disorders caused by the aberrant curatment of a mammal and preventides can be used as protein an antibody production. The polypeptides can be used as probes and curatment of compounds which bind to the primers, for sequencing, for chromosome or gene mapping, in the curatment of the proteins, and in generating anti-sense DNA or curate drugs to a tumour, in assays to determine biological activity, to curate antibodies/elicit an immune response, to determine quantitative curatment of the invention may also be useful in treating platelet curatment and/or nerve tissue, wound healing, treating burns, promoting curatment and/or nerve tissue, wound healing, treating burns, promoting curatment and/or nerve tissue, wound healing, treating burns, promoting contraceptive, treating osteoporosis and osteoarthritis, anaemia, cartification, differentiation and survival of stem cells, as a curative of the proliferation or from autoimmunity, cancer, allergy, asthma, cartification and survival and infection. The present sequence represents a protein of the invention.
 Matches
 Query Match
Best Local
 Tang
 immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis.
 (HYSE-)
 25-JAN-2000;
 25-JAN-2001; 2001WO-US02623
 WO200155437-A2
 Homo sapiens.
 Human novel protein #99.
 24-OCT-2001
 AAU14228 standard; Protein; 363
 Sequence
 proteins or their active
 The invention relates
 YT,
 116;
 novel protein; Antianaemic; osteopathic; antiinflammatory;
 08
 61
 20
 ۲
 HYSEQ INC.
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116
 Similarity
Liu C,
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
 307 AA;
 2000US-0491404
 Conservative
 (first entry)
Drmanac
 100.0%; Score 608; DB 22; 100.0%; Pred. No. 1.7e-48;
 polynucleotides encoding novel human domains. The polypeptides, polynucleo
 disorder
 0
 æ
 Mismatches
 Length
 Indels
 0
 Gaps
 60
 79
 0
```

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cc molecular watersawou or accuracy in preparation of molecular weight markers, food supplements, and in antibody production. CC The polypeptides are used to identify compounds which bind to the CC productions. Polynucleotides of the invention are used as probes and CC production of recombinant proteins, and in generating anti-sense DNA or CR RNA and in gene therapy. Polypeptides of the invention can be used to CC target drugs to a tumour, in assays to determine biological activity, to CC traise antibodies/elicit an immune response, to determine quantitative CC protein levels, as tissue markers, and to isolate receptors or ligands. CC disorders, stem cell disorders, and to isolate receptors or ligands. CC ligament and/or nerve tissue, wound healing, treating burns, promoting CC ligament and/or nerve tissue, wound healing, treating burns, promoting CC ligament and/or nerve tissue, wound healing, treating burns, promoting CC alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral CC graft-versus host disease, eczema, haemophilia, thrombosis, and infection. CC anti-inflammatory diseases, nervous system disorders, and infection. CC The present sequence represents a protein of the invention.
RESULT 6
ABB05053
ID ABB0
XX ABB05053
AC ABB0
XX ABB0
XX Fib
DT 26-b
CY Fib
XX Fib
XX Fib
XX Onio
XX O
 B
 δÃ
 밁
 Qy
 Query Match
Best Local S
Matches 116
 The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as protein expression or activity.
 Example 4; Page 577; 894pp; English
 Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
 N-PSDB; AAS22533
 Sequence
 26-MAR-2002
 ABB05053;
 ABB05053 standard;
 angiogenesis;
 Fibronectin
 Fibronectin
 15-JUN-2000; 2000US-211677P
 08-JUN-2001; 2001WO-EP06533.
 20-DEC-2001
 WO200196599-A2
 Unidentified
 2001-451939/48
 116;
 61
 80
 Similarity
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 135
 363
 Conservative
 isoform B; B-FN; extra domain B;
 isoform
 (first entry)
 A
 Protein; 117
 B specific binding antibody VH domain protein.
 100.0%;
 tumour; detection.
 0
 Score 608; DB 2
Pred. No. 2e-48;
; Mismatches
 A
 22;
 ED-B;
 0;
 Length 363;
 Indels
 antibody; VH domain;
 method of by the aberrant
 0;
 Gaps
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Matches Query Match Best Local

113;

Conservative

Indels

7;

Gaps

60

116 60 Similarity

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The present invention describes a method for detecting the presence of fibronectin isoform B (B-FN) in body fluid of an individual. The method convolves passing the fluid over a solid support (SS) to which gelatin that binds FN is attached, such that if FN is present, it is retained on SS by binding gelatin, and determining the presence of B-FN on SS by comparison of B-FN is a stratched, such that if FN is present, it is retained on SS by binding the ability of a specific binding member for extra domain B comparison of B-FN in a body fluid taken or collected quantitative determination of B-FN in a body fluid taken or collected from an individual. Other methods from the present invention can be used: from an individual. Other methods from the present invention can be used: for quantitating the amount of an insoluble marker protein in a sample cof tissue or tumour; for determining the grade or severity of neoplasia in a sample of tissue or tumour. An elevated level of B-FN in a body comparison in the clinic present in diagnostic and prognostic situations. The methods are useful in diagnostic and prognostic situations. The methods can be readily applied to small biopsy samples constant in the clinic, thereby providing valuable information without componing to the patients or complications for the Clinic binding antibody molecule, which is used in the exemplification of a B-FN ED-B clinic binding antibody molecule, which is used in the exemplification
 Detecting fibronectin isoform B in body fluid of an individual, by binding fibronectin to gelatin on solid support, and determining ability of specific binding member for Extra Domain B to be retained support -
 (PHIL-)
(CAST/)
(ZARD/)
 N-PSDB;
 Castellani P,
 Disclosure;
 (ZIJL/)
 Sequence
 2002-098076/13.
DB; ABA92717.
 PHILOGEN SRL.
CASTELLANI P.
 ZARDI L.
ZIJLSTRA A.
 present invention.
 117
 Page 54; 72pp; English
 Zardi
 A
 Ļ
 92.8%;
 Zijlstra
Score 564.5; DB 23
Pred. No. 6.4e-45;
0; Mismatches 0;
 Α
 DB 23;
 Length 117;
```

on

```
ABP95999
 RESULT
 antiinflammatory; antianaemic; immunosuppressive; neuroprotective; dual-specific ligand; cancer; HIV infection; hepatitis; rubella;
 01-MAY-2003
 ABP95999 standard; Protein;
 Homo sapiens
Synthetic.
 dual-specific ligand; anaemia; inflammation;
 HSA antibody
 АВР95999;
 Crohn's disease;
 Ligand; human serum albumin;
 related VH chain
 (first entry)
 myasthenia
 autoimmune disorder; multiple sclerosis;
 gravis.
 HSA; antibody; cytostatic;
 VH dummy.
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 The present invention describes a dual-specific ligand (I) comprising:

CC (a) a first single immunoglobulin variable domain with a binding

CC specificity to a first antigen or epitope; and (b) a second complementary

CC antigen or epitope. The binding domain with a binding activity to a second

CC antigen or epitope. The binding domains are mutually complementary, and

CC the first and second domains lack mutually complementary domains that

CC antininilammatory, immunosuppressive and neuroprotective activities. The

CC disare the same specificity. (I) has cytostatic, anti-HIV, antianaemic,

CC dual-specific ligand is useful for treating, preventing or diagnosing

CC diseases, e.g. cancer, HIV infection, hepatitis, rubella, anaemia,

CC disease or myasthenia gravis). The dual-specific ligand may be used to

CC also useful for monitoring the efficacy of drugs, as well as for

CC also useful for monitoring the efficacy of drugs, as well as for

CC albumin (HSA) related antibody VH sequence, which is used in an example
 Matches
 Query Match
Best Local
 Screening; functional polypeptide; enrichment; single chain antibody;
 W09920749-A1
 Unidentified
 A single chain antibody (Scrv).
 AAY02472 standard; Protein;
 15-JUL-1999
 AAY02472;
 Sequence
 myasthenia gravis
 Dual-specific ligand having immunoglobulins with binding specificity different antigens or epitopes, useful for treating, preventing or diagnosing diseases, e.g. cancer, HIV infection, inflammations, or
 Example 1; F1g 3; 84pp; English.
 Winter G,
 28-JUN-2001; 2001GB-0015841
 WPI; 2003-210246/20
 28-JUN-2002; 2002WO-GB03014.
 WO2003002609-A2
 the present invention.
 61
 13
 107; Conservative
 1
 MEDICAL RES COUNCIL.
 116
 Ignatovích O,
 (first entry)
 A,
 92.48;
 Tomlinson I;
 240
 <u>ن</u>
 Score 562; DB 24;
Pred. No. 1.1e-44;
 Ş
 Mismatches
 ligand; non-functional;
ScFv.
 4
 Length 116;
 Indels
 0;
 116
 ç
 0
```

```
RESULT 9
ABP95997
ID ABP9
XX ABP9
XX ABP9
XX ABP9
XX Liga
DE Huma
XX Liga
KW Anti
KW Guali
KW
 В
 20
 망
 ρy
 The specification describes a method for screening for functional C polypeptides which bind a ligand. The method comprises contacting a crepertoire of polypeptides with a generic ligand, and then acreening selected functional polypeptides with a target ligand. The method comprises contacting a contacting and then acreening selected functional polypeptides with a target ligand. The method comprises the removal from a chosen repertoire of polypeptides, those compression of the introduction of the introduction of the compression of the compre
 Query Match
Best Local Similarity 92.2
 28-JUN-2002; 2002WO-GB03014
 09-JAN-2003
 WO2003002609-A2
 Homo sapiens.
Synthetic.
 Crohn's disease; myasthenia gravis
 Ligand; human serum albumin; HSA; antibody; cytostatic; anti-HIV; antiinflammatory; antianaemic; immunosuppressive; neuroprotective; dual-specific ligand; cancer; HIV infection; hepatitis; rubella; anaemia; inflammation; autoimmune disorder; multiple sclerosis;
 Human serum albumin antibody related protein #1.
 01-MAY-2003
 ABP95997 standard; Protein; 240
 Sequence
 Disclosure; Fig 2; 67pp;
 Screening for functional polypeptides which bind a ligand
 21-NOV-1997;
20-OCT-1997;
 Tomlinson
 (MEDI-) MEDICAL RES COUNCIL
 13-NOV-1997;
 20-OCT-1998;
 61 ADSVKGRETISKDNSKNTLYLOMNSLRAEDTAVYYCAKPEPYEDYWGOGTLVTVSS 116
 _
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSYGAFDYWGQGTLVTVSS 116
 240 AA;
 (first entry)
 Winter
 97US-0066729.
97GB-0022131.
97US-0065428.
 98WO-GB03135
 92.4%;
 English.
 ÇI
T
 Score 562; DB 20;
Pred. No. 2.4e-44;
 Mismatches
 DB 20;
 Length 240;
 Indels
 0;
 Gaps
 60
 60
```

28-JUN-2001; 2001GB-0015841

```
The present invention describes a dual-specific ligand (I) comprising:

(C) (a) a first single immunoglobulin variable domain with a binding

(C) specificity to a first antigen or epitope; and (b) a second complementary

(C) immunoglobulin single variable domain with a binding activity to a second

(C) antigen or epitope. The binding domains are mutually complementary, and

(C) the first and second domains lack mutually complementary domains that

(C) share the same specificity. (I) has cytostatic, anti-HIV, antianaemic,

(C) antiinflammatory, immunosuppressive and neuroprotective activities. The

(C) diseases, e.g. cancer, HIV infection, hepatitis, rubella, anaemia,

(C) diseases, e.g. cancer, HIV infection, hepatitis, rubella, anaemia,

(C) diseases or myasthenia gravis). The dual-specific ligand may be used to

(C) calso useful for monitoring the efficacy of drugs, as well as for

(C) consistoring toxicity. The present sequence represents a human serum

(C) albumin (HSA) related antibody sequence, which is used in an example
RESULT 10
AAU14320
ID AAU14
XX AU14
AC AAU14
XX 24-OC
XX 24-OC
XX Human
XX Human
KW Human
KW inmuur
KW inmuur
KW antis
KW antis
KW enrik
KW enrik
KW enrik
KW thron
OS Homo
XX
XX
YX
PF 02-AU
XX
PF 25-JJ
 밁
 γQ
 В
 δÃ
 Matches
 Query Match
Best Local
 Dual-specific ligand having immunoglobulins with binding specificity different antigens or epitopes, useful for treating, preventing or diagnosing diseases, e.g. cancer, HIV infection, inflammations, or
 WPI; 2003-210246/20.
N-PSDB; ABZ76706.
 myasthenia
 Example 1; Fig 1; 84pp; English.
 diagnosing
 (MEDI-) MEDICAL RES COUNCIL.
 Sequence
 Human novel protein #191.
 24-OCT-2001
 AAU14320 standard; Protein;
 Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
 25-JAN-2001; 2001WO-US02623
 02-AUG-2001
 WO200155437-A2
 tissue
 immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
 Parkinson's disease;
 thrombolytic;
 sapiens.
 107;
 61
 61
 -
 ب
 regeneration;
 Similarity
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116
 EVQLLESGGGLYOPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
 gravis
 diseases, e.g. cancer,
 Ignatovich
 240
 Conservative
 (first entry)
 immunogen; antibody; gene ther
isease; inflammatory disorder;
 AA;
 92.4%;
 Ó
 immune disorder
 Tomlinson
 antibody; gene therapy; neurological disorder;
 Score 562; DB Pred. No. 2.4e 5; Mismatches
 5
 313 AA
 DB 24;
 4;
 Length
 Indels
 0;
 osteoporosis,
 Gaps
 to
 60
 60
 0
```

```
CC proteins or their active domains. The polypeptides, polynucleotides and CC proteins or their active domains. The polypeptides, polynucleotides and CC antibodies raised against the polypeptides are used in a method of CC treatment of a mammal and prevention of disorders caused by the aberrant CC treatment of a mammal and prevention of disorders caused by the aberrant CC protein expression or activity. The polypeptides can be used as CC protein expression or activity. The polypeptides can be used as CC polypeptides. Polynucleotides of the invention are used as probes and CC primers; for sequencing, for chromosome or gene mapping, in the CC polypeptides. Polynucleotides of the invention are used as probes and CC protein of recombinant proteins, and in generating anti-sense DNA or CC target drugs to a tumour, in assays to determine biological activity, to CC target drugs to a tumour, in assays to determine duantitative CC protein levels, as tissue markers, and to isolate receptors or ligands. CC protein levels, as tissue markers, and to isolate receptors or ligands. CC protein levels, as tissue markers, and to isolate receptors or ligands. CC protein levels, as tissue markers, and to isolate receptors or ligands. CC disorders, stem cell disorders, regenerating bone, cartillage, tendon, CC disorders, stem cell disorders, regenerating bone, cartillage, tendon, CC disorders, parkinson's and Huntington survival of stem cells, as a cc the proliferation, differentiation and survival of stem cells, as a cc contraceptive, treating osteoporosis and osteoarthritis, anaemia, CC allebraic's, Parkinson's and Huntington's diseases, amylotrophic lateral cc contraceptive in the Example 4; Page 630-631; 894pp; English.
 Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
 Tang
 (HYSE-) HYSEQ INC
 25-JAN-2000; 2000US-0491404
 N-PSDB;
 WPI; 2001-451939/48
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 Drmanac
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Matches
 Local
 109;
 61
 61
 Н
 Similarity
 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKPFP-----
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSHPGYYYDSSGYSYYFDYWGQG
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
 Conservative
 92.2%;
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Query Match

4;

Score 560.5; Pred. No. 4.3e 4; Mismatches

3e-44; DB 22; ω

Indels Length

Gaps

--YFDYWGQG

109

120 60

313; 11;

Sequence

313

AA;

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121 110 181

QΥ

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TLVTVSS TLVTVSS 116

187

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RESULT 11
ABG69320
ABG69320 standard; Protein; 116
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21-OCT-2002
 (first entry)
```

ABG69320;

Antibody DP47 heavy chain variable region.

Sequence arrayed library; SAL; antibody library; protein identification;  $\mathtt{DP47}$ ;  $\mathtt{DPK22}$ .

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RESULT 12
AAO21548
ID AAO21
XX AAO20
XX Unide
XX
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 Query Match
Best Local S
Matches 107
 Screening antibody; 2-D electrophoresis; antibody library; proteomics.
 The invention relates to screening an antibody against a specific protein in an objective structure sample containing a protein group in high efficiency, comprising reacting an objective structure sample containing a protein group or a portion containing an objective protein in the sample with an antibody library, recovering the antibody combined with the protein, replicating the recovered antibody and reacting it with the objective protein at least once. The method is used for the identification of an objective protein. The present sequence is an antibody chain (derived from the DP47 heavy chain, the DPK22 light chain) used in the method of the invention.
 05-JUN-2001; 2001WO-JP04732
 30-MAY-2002
 Unidentified
 (NISC-) JAPAN SCI & TECHNOLOGY CORP.
(NINA-) JAPAN NAT CENT NEUROLOGY & PSYCHIATRY
 24-NOV-2000;
 Sequence
 WO200242774-A1
 Antibody screening method related protein VH(DP-47).
 02-SEP-2002
 AA021548
 AAO21548 standard; Protein;
 Example 8; Fig 1; 43pp; Japanese.
 Screening of an antibody used protein in high efficiency -
 ÆPI:
 07-DEC-2000; 2000JP-0373259
 07-DEC-2000;
 21-JUN-2002
 JP2002174635-A
 Homo
 (KOKU-)
 (KAGA-)
 Local Sim
hes 107;
 2002-579732/62
 sapiens
 61
 61
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 ب
 KAGAKU GIJUTSU SHINKO JIGYODAN.
KOKURITSU SEISHIN SHINKEI CENT
 Similarity
 ABK99213
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFDYFDYWGQGTLVTVSS 116
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSS1SGSSGTTYY
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKXXXXFDYWGQGTLVTVSS
 116
 91.8%;
nilarity 92.2%;
Conservative
 2000JP-0358539
 (first entry)
 2000JP-0373259
 ₹
 116
 Score 558; DB 23;
Pred. No. 2.5e-44;
4; Mismatches 5;
 for
 ₿
 the
 identification
 SOCHO
 plural protein; protein spot;
 Length 116;
 Indels
 of an objective
 0;
 Gaps
 116
 60
 60
```

```
RESULT 13
ABJ36939
ID ABJ36
XX ABJ36
XX ANT1
DT 01-M
XX ANT1
KW ANT1
KW Human
KW dend
KW dend
KW Human
KW OS Uni
XX
YN WO2
XX
PN WO2
XX
PP WO2
XX
PP 8 11
PR 26
XX
PR 11
PR 26
XX
PR 27
PR 27
PR 26
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PR 27
PR 36
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PR 36
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PR 36
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PR 46
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 SXCCCCCCCCCX PX PT X RRXX
 Matches
 Query Match
 27-APR-2001; 2001WO-US13672.
11-MAY-2001; 2001JP-0142482.
05-OCT-2001; 2001JP-0310535.
26-OCT-2001; 2001US-0040244.
 The invention relates to a novel method for screening an antibody, comprising performing 2-D electrophoresis on plural proteins in a sample. Individual protein spots are separated by reacting them with an antibody library and then replicating the bound antibodies before reacting them with the spot proteins again. The method is useful for screening an antibody specific for a target protein, e.g. from a phage antibody library, which is useful in proteomics for studying various protein and complementary deoxyribonucleic acid (cDNA) expression libraries as well as gene functions, and in other biological and medical sciences. This sequence is a protein relating to the antibody screening method of the
 N-PSDB; ABT31881
 WPI; 2003-120463/11.
 Mikayama T,
 immunoactivator; anti-tumour agent;
autoimmune disease; coagulation fac
 (KIRI) KIRIN BEER KK.
 07-NOV-2002
 Antiallergic; haemostatic; immunomodulator; cytostatic; a
human CD40; II-12; LPS; lipopolysaccharide; InNgamma; int
dendritic cell; hlgh G28-5; CD95 expression; high G28-5;
immunoactivator; anti-tumour agent; immunosuppressant; al
autoimmune disease; coagulation factor VIII inhibitor; an
 Antiallergic; haemostatic; human CD40; IL-12; LPS; lip
 01-MAY-2003
 Screening an antibody using 2-D electrophoresis samples for separating individual protein spots antibody library useful in proteomics and other
 26-APR-2002; 2002WO-JP04292
 WO200288186-A1
 Unidentified
 Anti-CD40 monoclonal antibody related protein
 АВЈ36939;
 ABJ36939 standard; Protein; 177 AA.
 Disclosure; Fig 1; 78pp; Japanese.
 WPI; 2002-471742/50.
N-PSDB; AAL39119.
 Sequence
 Kaneko K;
 Local
 107;
 61
 61
 _
 ب
 Similarity
 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKXXXXFDYWGQGTLYTVSS
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
 116 AA;
 Conservative
 Yoshida
 (first entry)
 Ħ,
 91.8%;
92.2%;
 Force
 4
 Score 558; DB 23;
Pred. No. 2.5e-44;
Mismatches 5
 ₩R,
 Chen
 ×
 23;
 Takahashi
 SEQ
 5.
 on plural proteins to react with an biological sciences
 Length 116;
 ID No
 Indels
 interferon
 anti-CD40
 antibody;
 64
 B cell line;
 0
 Gaps
 H
 60
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Disclosure; Page 11; 36pp;

German.

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RESULT 14
AAB46042
ID AAB46
XX
AC AAB4
XX
DT 23-M
XX
DT 23-M
XX
MUC
KW MUC
KW ant
XX
AV
PN WO
XX
PFR (
XX
PFR (
XX
PFR (
XX
PFR XX
PFT
PT
PT
PT
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PT
PT
PT
XX
 QΥ
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 Query Match
Best Local
 Matches
 The invention relates to an antibody to human CD40, or its functional fragment, has at least one of the following properties: acting on dendritic cells to produce II-12 in the presence of LPS (lipopolysaccharide) and IrNgamma (interferon gamma); acting on dendritic cells to activate maturity of the dendritic cells with high G28-5 antibody; and activating CD95 expression with high G28-5 antibody against B cell line. Such antibodies or functional fragments can be used as immunoactivators, anti-tumour agents, immunosuppressants, and as remedies for autoimmune diseases, allergy or coagulation factor VIII inhibitors
 MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer; antiidiotypic antibody; cytostatic; virucidal; antibacterial; TF antige antiparasitic; infectious disease.
 Claim
 diseases or cancer
 Anti-CD40 monoclonal antibody with antagonist/agonist or functional fragment, is useful in the treatment of
 Human TF
 Sequence
 monoclonal
 syndrome. This sequence represents a protein relating to the anti-CD40
 Vaccines against conformation-dependent or non-peptide antigens, on DNA encoding peptide which mimics the antigen, useful e.g. as
 07-DEC-2000
 23-MAR-2001
 AAB46042;
 AAB46042 standard; Peptide; 240 AA
 Goletz
 (DELB-) DELBRUECK CENT
 27-MAY-1999;
09-SEP-1999;
 29-MAY-2000;
 WO200073430-A2
 140
 113
 2001-049937/06
 108;
 15;
 80
 61
 20
 \vdash
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 Similarity
 anti-idiotype antibody fragment H1.
 TVSS
 TVSS 116
 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKDGGYYGSGSYGYEDYWGQGTLV
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK--
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
 EVQLLESGGGLVQPGGSLRLSCAASGTTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
 vaccines
 antibody of the invention
 177 AA;
 Conservative
 2000WO-DE01809
 (first entry)
 143
 59,
 99DE-1024405.
99DE-1043016.
 94pp;
 ₫
 91.6%;
87.1%;
 MOLEKULARE MEDIZIN MAX
 Japanese
 Score 557; DB Pred. No. 4.9e 5; Mismatches
 DB 24;
 Length
 Indels
 -----PFPYFDYWGQGTLV
 activity to CD40, e.g. autoimmune
 8
 TF antigen;
 based
 60
 79
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 \begin{array}{c} \mathbb{Z} \times \mathbb{R} \times \mathbb
 ce encodes a region of an antidiotypic antibody (Ab2) or another peptide cowhich: (a) specifically binds to the binding site of an antibody (Ab1) or another peptide cowhich: (a) specifically binds to the binding site of an antibody (Ab1) corn an antigen binding molecule; and (b) immunologically mimics the corn an antigen binding molecule; and (b) immunologically mimics the cinitial antigen. The epitope is partially or completely conformation-dependent, and has an immunogenic structure defined by a specific spatial conformation of amino acids. (I) is used in the form confined to circular naked DNA and/or with a viral vector and/or confined and antiparasitic. The invention have cytostatic, virucidal, contibes can antibody vaccine (V2) against antigens which are not proteins or peptides, as defined above but which have epitopes which show an corresponding vaccine (V2) against antigens which are not proteins or peptides, as defined above but which have epitopes which show an communogenic structure; (2) preparing (V1) and (V2); (3) human confidency in the specification; (4) MUC1-conformation epitope mimics antily one of 31 approximately 60 residue amino acids sequences, all fully defined in the specification; (4) MUC1-conformation epitope mimics can tigen having one of 24 approximately 200 residue amino acid sequences, all fully defined in the specification; (6) TF carbohydrate epitope mimetics having one of 25 7-13 residue amino acid sequences, all fully defined in the specification; (6) TF carbohydrate epitope mimetics can period of the specification; (7) DNA sequences and fully defined in can sequence and parasites. The vaccines are effective in cases where vaccination has consorbly are used to treat cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria and province viruses and consorbly are used to treat cancer.
 conformation-dependent antigens (CDA) comprising DNA (I) antibody, or peptide which immunologically imitates CDA,
 not been possible.
 240 AA;
 describes
 a novel vaccine (V1) against
 DNA (I) and/or
 S.
 new.
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B QΥ δÃ 밁 Matches 105; Query Match Best Local 61  $\vdash$ 1 Similarity ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSSITELGRSTQY Conservative 90.5%; 6; Pred. No. 2.56 6; Mismatches Score 551; DB 22; Pred. No. 2.5e-43; Length 240; Indels 0; Gaps 60 60

Sequence

ABR01519 standard; Protein;

16-APR-2003 (first entry)

Human anti-TIMP-1 antibody heavy chain #17.

RESULT 15
ADRO1519
ID ADRO1
XX
AC ADRO1
XX
DT 16-A
DT 16-A
XX
DT Humae
XX
Humae
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H Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3; matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis; alcoholic liver disease; cardiac fibrosis; acute coronary syndrome; lupus nephritis; glo idiopathic pulmonary glomerulosclerotic renal disease; nary fibrosis; benian process

Homo sapiens.

WO200286085-A2

31-OCT-2002

24-APR-2002; 2002WO-US12801

24-APR-2001; 2001US-285683P

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Search completed: August 20, 2003, 12:33:39 Job time: 256.06 secs
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 The invention relates to a novel purified preparation of a human CC antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1) cc and neutralises a matrix metalloprotease (MMP)-inhibiting activity of TMP-1. The antibody comprises a variable heavy chain (VMC)DR3 region and CC a variable light chain (VLC)DR3 region. An antibody preparation of the CC invention has hepatotropic, cytostatic, nephrotropic and cardiant CC invention has hepatotropic, cytostatic, nephrotropic and cardiant CC activity. The human antibody is useful for decreasing an MMP-inhibiting CC symptoms of a disorder in which TIMP-1 is eleverated, e.g. liver CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic CC uncer. The antibody is also useful for detecting a TIMP-1 in a test C preparation, or in diagnosing a disorder in which a TIMP-1 level is clevated. The sequences shown in ABRO1502-ABRO1545 represent the heavy can contain regions of a human anti-TIMP-1 antibody of the invention.
 Query Match 90.3%;
Best Local Similarity 89.7%;
Matches 104; Conservative
 Sequence
 New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung cancer
 WPI; 2003-129114/12.
N-PSDB; ABZ74790.
 Claim 20; Page 159-160; 228pp; English.
 Pan C,
 (FARB) BAYER CORP. (MORP-) MORPHOSYS AG.
 5
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116
 Knorr AM, Schauer M,
 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARLIGYFDLWGQGTLVTVSS 116
 220 AA;
 Score 549; DB 24;
Pred. No. 3.4e-43;
7; Mismatches 5;
 Hirth-dietrich C,
 5
 Length 220;
 Indels
 Kraft S,
 0;
 Krebs B;
 Gaps
 0
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Result
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Total number of hits satisfying chosen parameters:
 Database
 Minimum DB
Maximum DB
 Scoring table:
 Title:
Perfect score:
 OM protein - protein search, using sw model
 ö
 Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 562
552.5
542.5
542.5
542.5
540.5
539.5
 seq length: 0 seq length: 2000000000
 100.0
92.4
92.4
92.4
92.6
91.6
91.9
90.9
90.9
90.9
89.2
89.2
89.1
88.9
88.9
88.9
88.7
 Query
Match
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 August 20, 2003, 12:40:51 ; Search time 125.783 Seconds (without alignments) 121.698 Million cell updates/sec
 497079 seqs, 131961718 residues
 US-09-512-082-19
608
 Published_Applications_AA: *
 : /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa/USO9A_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa/USIOB_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/USIOB_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/USIOB_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/USIOB_NEW_PUB.pep:*
 EVQLLESGGGLVQPGGSLRL.....AKPFPYFDYWGQGTLVTVSS 116
 GenCore version Copyright (c) 1993 - 2003
 /Ggn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
 /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
 Length DB
 124
123
120
121
121
123
239
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288
123
123
123
 10
12
15
10
10
10
10
11
11
10
10
 US-09-968-561A-2
US-10-968-744A-2
US-10-040-244-16
US-10-269-805-59
US-09-840-459-85
US-09-840-459-82
US-09-880-748-1922
US-09-880-748-1922
US-09-818-247-22
US-09-818-247-22
US-09-818-247-25
US-09-840-459-76
US-10-025-687-4
 US-09-300-425B-19
US-09-192-854-2
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 SUMMARIES
 5.1.6
Compugen Ltd.
 Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 16, Appli
Sequence 59, Appli
Sequence 85, Appli
Sequence 82, Appli
Sequence 82, Appli
Sequence 23, Appli
Sequence 34, Appli
 Description
 Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
 Sequence 19, Appl
Appli
Appli
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| 45                 | 44      | 43                | 42     | 41      | 40     | 9        | 38            | 37      | 36          | 35            | 34             | ω<br>ω       | 32           | 31              | 30           | 29       | 28                 | 27               | 26              | 25           | 24           | 23             | 22           | 21              | 20             | 19             | 18            | 17               | 16                |
|--------------------|---------|-------------------|--------|---------|--------|----------|---------------|---------|-------------|---------------|----------------|--------------|--------------|-----------------|--------------|----------|--------------------|------------------|-----------------|--------------|--------------|----------------|--------------|-----------------|----------------|----------------|---------------|------------------|-------------------|
| 524                | 524.5   | 524.5             | 525    | 525     | 525    | 526.5    |               | 528     | 528         | ž             | 529.5          | 530          | 531          | 531             | 531          | 531      | 531                | ω                | 532.5           | 32           | 533          | 533            | 534          | 534             | 534            | 534.5          | 536           | 37               | 537.5             |
|                    | 86.3    |                   |        |         |        |          |               |         |             |               |                |              |              |                 |              |          |                    |                  |                 |              |              |                | 7            | 7               | 7              | 7              |               | æ                | 8                 |
| 249                | 240     | 130               | 443    | 239     | 124    | 125      | 250           | 128     | 128         | 249           | 130            | 246          | 283          | 283             | 263          | 263      | 239                | 127              | 119             | 119          | 239          | 118            | 247          | 246             | 116            | 449            | 239           | 224              | 113               |
| 11                 | 11      | 15                | 9      | 1       | 10     | 10       | 11            | 10      | 10          | 13            | 15             | 1            | 10           | 10              | 10           | 10       | 11                 | 10               | 15              | ဖ            | 11           | 15             | 드            | 11              | 10             | 10             | 11            | 11               | 9                 |
| US-09-880-748-1856 | 0-748-2 | US-10-118-100-53  | -410-4 | 0-748-2 | 0-459- | 0-459-84 | -09-880-748-1 | -09-840 | -09-840-459 | -10-039-785-5 | -10-118-100-54 | -09-880-748- | -09-985-442- | US-09-983-580-6 | -09-956-087- | <b>ٺ</b> | US-09-880-748-2023 | US-09-840-459-87 | US-10-268-501-6 | 09-811-123-3 | -09-880-748- | -10-001-934-39 | -09-880-748- | -09-880-748-197 | -09-840-459-80 | -09-736-371B-2 | -09-880-748-2 | US-09-972-656-68 | US-09-056-160B-11 |
|                    | 2013    | Sequence 53 April | ۰.     | 202     | 90     |          | 142           | 79. App | 77          | J (           |                | 198          | , ر          | <u>ئ</u> د      | . س          |          | 202                | 87. App          | D               | w            | 202          |                | 193          | 1975            | 80             | 21             | 20            | e 68             | •                 |

## ALIGNMENTS

RESULT 1 US-09-300-425B-19

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 Вb
 Qy
 ; OTHER INFORMATION: Description of Artificial Sequence: H antibody specific ; OTHER INFORMATION: for ED-B domain of fibronectin US-09-300-425B-19
 GENERAL INFORMATION:
APPLICANT: NERI, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: VII, Francesca
APPLICANT: BIRCHLER, Manfred
TITLE OF INVENTION: SPECIFIC B
TITLE OF INVENTION: CONTAINING
TITLE OF INVENTION: ANGIOGENES
FILE REFERENCE: SCH-1733P1
 TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF FILE REFERENCE: SCH-1733P1
CURRENT FILING DATE: 1999-04-28
CURRENT FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial Sequence
 Matches 116;
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Best Local Similarity
 Sequence 19, Application US/09300425B Publication No. US20030045681A1
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 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY 60
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 100.0%; ilarity 100.0%; Conservative 0;
 0;
 Score 608; DB 11;
Pred. No. 7.7e-47;
Mismatches 0;
 Indels
 0;
 Gaps
 60
 0
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В

61

ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116

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RESULT 2
US-09-192-854-2
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 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-2
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 US-09-968-561A-2
 Sequence 2, Application US/09192854 Patent No. US20020068276A1
 SOFTWARE: PatentIn Ver. SEQ ID NO 2
 Matches 107;
 Query Match
Best Local Similarity
 GENERAL INFORMATION:
 Sequence 2, Application US/09968561A Patent No. US20020164642A1
 APPLICANT: Tomlinson, Ian TITLE OF INVENTION: Methods for Selecting FILE REFERENCE: 3789/72916
CURRENT APPLICATION NUMBER: US/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
 Matches 107; Conservative
 SEQ ID NO 2
 Query Match
 PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR FILING DATE: 1998-10-20
 APPLICANT: Tomlinson, Ian M
APPLICANT: Winter, Gregory
TITLE OF INVENITION: Wethod to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1073B
 EARLIER FILING DATE: 1997-11-21 NUMBER OF SEQ ID NOS: 212
 APPLICANT: Winter, Greg
 CURRENT APPLICATION NUMBER: US/09/968,561A CURRENT FILING DATE: 2001-10-01
 NUMBER OF SEQ ID NOS: 350 SOFTWARE: PatentIn version 3.1
 PRIOR APPLICATION NUMBER: US 09/511,939 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: GB 9722131.1 PRIOR FILING DATE: 1997-10-20
 TYPE: PRT ORGANISM: Homo sapiens
 ENGTH: 240
 LENGTH: 240
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116
 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
 Similarity
 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKSYGAFDYWGQGTLVTVSS 116
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY 60
 Conservative
 92.4%;
 92.4%;
 for Selecting Functional Peptides
 Score 562; DB 10;
Pred. No. 1.9e-42;
5; Mismatches 4
 Score 562; DB 9; Pred. No. 1.9e-42;
 Mismatches
 Length 240
 Length 240;
 Indels
 0;
 Gaps
 Gaps
 60
 60
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 QΥ
 US-09-968-744A-2
 SEQ ID NO 2
LENGTH: 240
TYPE: PRT
 GENERAL INFORMATION:
 Sequence 2, Application US/09968744A Publication No. US20030148372A1
 Sequence 16, Application US/10040244 Publication No. US20030059427A1
 Matches
 Query Match
Best Local
 PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
 APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
FILE REFERENCE: 8039/1073
 SEQ ID NO 16
LENGTH: 124
 CURRENT APPLICATION NUMBER: US/09/968,744A CURRENT FILING DATE: 2003-01-13
 FILE REFERENCE: 021286/0272501
CURRENT APPLICATION NUMBER: US/10/040,244
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/200,601
PRIOR FILING DATE: 2000-4-28
PRIOR APPLICATION NUMBER: PCT/US01/13672
 NUMBER OF SEQ ID NOS: 350.
 APPLICANT: TAKAHASHI, NOBUAKI
APPLICANT: MIKAYAMA, TOSHIFUMI
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTI
 APPLICANT: KIRIN BEER KABUSHIKI KAISHA APPLICANT: FORCE, WALKER F.
 PRIOR APPLICATION NUMBER: 09/844,684
PRIOR FILING DATE: 2001-04-27
 PRIOR FILING DATE: 2001-04-27
 SOFTWARE:
 NUMBER OF SEQ ID NOS:
 ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
 TYPE: PRT
 APPLICATION NUMBER: US 09/511,939
 FILING DATE: 1998-10-20
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS
 107;
 61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKSYGAFDYWGQGTLVTVSS 116
 61 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGOGTLYTVSS 116
 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
 1 EVOLLESGGGLYQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
 PatentIn version 3.1
 Similarity
 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKSYGAFDYWGQGTLVTVSS 116
 PatentIn Ver.
 Conservative
 92.4%;
 Score 562; DB 12;
Pred. No. 1.9e-42;
 Mismatches
 Length 240;
 Indels
 0;
 Gaps
 60
 60
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GENERAL INFORMATION:

APPLICANT: LaROSB, Gregory J.

APPLICANT: Horvath, Christopher

APPLICANT: Horvath, Christopher

APPLICANT: Jones, S. Tarran

APPLICANT: Jones, S. Tarran

APPLICANT: O'Berien, Siobhan H.

APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: METHODS OF USE THEREFOR

TITLE OF INVENTION: METHODS OF USE THEREFOR

FILE REFERENCE: 1055.1052-012

CURRENT APPLICATION NUMBER: US/09/840,459

CURRENT FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: PCT/US01/03537
 RESULT 7
US-09-840-459-85
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 ; ORGANISM: Homo sapiens US-10-269-805-59
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 US-10-040-244-16
 Sequence 85, Application US/09840459 Patent No. US20020150576A1
 PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
SEQ ID NO 59
 Sequence 59, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
 Query Match 90.9%;
Best Local Similarity 87.8%;
Matches 108; Conservative
 Query Match
Best Local Similarity
 APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOTETIN-2 SPECIFIC BINDING
FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
 Matches 108;
 LENGTH: 123
TYPE: PRT
 121
 114 VSS 116
 121
 113 TVSS 116
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKETISFSTFSGYFDYWGQGTLVT 120
 61 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKP------FPYFDYWGQGTLVT 113
 61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKDGGYYGSGSYGYFDYWGQGTLV 120
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK-------PFPYFDYWGQGTLV 112
 VSS 123
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 4
 Score 552.5; DB 15; Length Pred. No. 6.7e-42;
 Score 557; DB 15; Length 124; Pred. No. 2.7e-42;
 Mismatches
 Mismatches
 Indels
 7;
 Gaps
 Gaps
 60
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APPLICANT: Newman, Walter

APPLICANT: O'Brien, Slobhan H.

APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMBER: US/09/840,459
CURRENT APPLICATION NUMBER: PCT/US01/03537
CURRENT APPLICATION NUMBER: PCT/US01/03537
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/359,193
 ; ORGANISM: HOMO
US-09-840-459-92
 ; ORGANISM: Homo sapiens US-09-840-459-85
 PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR TRIING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 92
LENGTH: 121
 Matches 105; Conserv
 Query Match
 GENERAL INFORMATION:
 SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 85
LENGTH: 120
 Query Match
Best Local Similarity
Matches 106; Conserv
 Patent No. US20020150576A1
 APPLICANT:
 APPLICANT: LaRosa,
 TYPE: PRT
116 S 116
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDISWGDLEGLDYWGQGTLVTVS
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPY-----FDYMGQGTLYTVS 115
 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY 60
 1 EVQLLESGGGLVQPGGSLRLSCAASGETFSSFSNSWVRQAPGKGLEWVSSISGSSGTTYY
 FastSEQ for Windows Version
 Lakosa,
Horvath, cama
Taman, Walter
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
 Application US/09840459
 Conservative
 Conservative
 Gregory J.
 Christopher
 89.2%;
 89.5%;
 5; Mismatches
 Score 542.5; DB
Pred. No. 5e-41;
6; Mismatches
 Score 544; DB 10;
Pred. No. 3.7e-41;
 DB 10;
 5
 5
 Length 120;
 Indels
 Indels
 Length 121;
 4
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 Gaps
 Gaps
 60
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121

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RESULT 10
US-09-880-748-1922
; Sequence 1922, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
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 Q
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 US-09-840-459-82
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 В
 ; TYPE: PRT; ORGANISM: Homo sapiens US-09-840-459-82
 SOFTWARE: F
 Matches 108;
 Query Match
Best Local
 GENERAL INFORMATION:
 Sequence 82, Application US/09840459 Patent No. US20020150576A1
 PRIOR
PRIOR
 FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
 APPLICANT: Ruben et al. TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
 CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
 TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES TITLE OF INVENTION: METHODS OF USE THEREFOR FILE REFERENCE: 1855.1052-012
 NUMBER OF SEQ ID NOS: 107
 CURRENT APPLICATION NUMBER: US/09/840,459
 APPLICANT:
 PRIOR FILING DATE: 2000-06-15
 PRIOR APPLICATION NUMBER: 60/212,210
 APPLICANT:
 APPLICANT:
 APPLICANT:
 ENGTH:
 APPLICATION NUMBER: 09/359,193
FILING DATE: 1999-07-22
APPLICATION NUMBER: 09/121,781
FILING DATE: 1998-07-23
 APPLICATION NUMBER: 60/:
FILING DATE: 2001-03-16
APPLICATION NUMBER: 60/:
 APPLICATION NUMBER: 60/240,816
FILING DATE: 2000-10-17
APPLICATION NUMBER:
 FILING DATE: 2001-03-21
 113
 120 TVSS 123
 61
 123
 Similarity
 FastSEQ for Windows Version
 TVSS 116
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKK-PGDYGSGSYYLDYWGQGTLV 119
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFP------
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGYTTYY
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY 60
 Horvath, Christ
Newman, Walter
Jones, S. Tarra
 O'Brien, Siobhan H.
O'Keefe, Theresa
 Conservative
 Gregory J.
 Christopher
 89.1%;
87.1%;
60/293,499
 60/277,379
 60/276,248
 υ
••
 Score 541.5; DB 10;
Pred. No. 6.3e-41;
 Mismatches
 4.
 Indels
 Length
 123;
 -YFDYWGQGTLV 112
 Gaps
 60
```

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 ; TYPE: PRT; ORGANISM: Homo sapiens US-10-269-805-23
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 ; ORGANISM: Homo sapiens US-09-880-748-1922
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 RESULT 11
US-10-269-805-23
 RESULT 12
US-09-818-247-22
 밁
 Sequence 23, Application US/10269805 Publication No. US20030124129A1 GENERAL INFORMATION:
 SOFTWARE: PatentIn version 3.1 SEQ ID NO 23
 Matches 103; Conservative
 SEQ ID NO 1922
LENGTH: 239
 GENERAL INFORMATION:
 Sequence 22, Application U Patent No. US20020102657A1
 Query Match
Best Local Similarity
 Query Match
Best Local S
 Matches 105;
 PRIOR APPLICATION NUMBER: US 60/328,604 PRIOR FILING DATE: 2001-10-11
 NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
 APPLICANT: Chapin, Steven J.
APPLICANT: Richman-Eisenstat, Janice
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Ligands Directed to the No. US20020102657A1-Secretory
TITLE OF INVENTION: No. US20020102657A1-Stalk Region of pIgR and Methods
FILE REFERENCE: 18062E-000910US
 NUMBER OF SEQ ID NOS: 76
 CURRENT FILING DATE: 2002-10-10
 APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
 CURRENT APPLICATION NUMBER: US/09/818,247
CURRENT FILING DATE: 2001-03-26
 APPLICANT: Mostov, Keith E. APPLICANT: Chapin, Steven
 FILE REFERENCE: A-722
 TYPE: PRT
 LENGTH:
 Local Similarity
 121
 114 VSS 116
 61
 61
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS 116
 61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKP-----FPYFDYWGQGTLVT 113
 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY 60
 123
 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKETISFSTFSGYFDYWAOGTLYT 120
 EVQLVDSGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
 Conservative
 123
NUMBER: WO PCT/US01/09699
 88.9%;
85.4%;
 89.0%;
 US/09818247
 8; Mismatches
 6; Mismatches
 Score 540.5; DB 1
Pred. No. 7.7e-41;
 Score 541; DB 11;
Pred. No. 1.4e-40;
 DB 15;
 US20020102657Al-Secretory Componen Region of pIgR and Methods of Use T
 5;
 Length 239;
 Indels
 Length 123;
 7;
 0;
 Gaps
 Gaps
 60
 60
 60
 0;
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 ; ORGANISM: Homo sapiens US-09-840-459-76
 CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
 FRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/192,197
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/192,198
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 22
LENGTH: 288
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 US-09-818-247-22
 NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 76
LENGTH: 125
 Matches.
 Query Match
 GENERAL INFORMATION:
 Sequence 76, Application US/09840459
 Query Match
Best Local Similarity
 PRIOR FILING DATE: 1998-07-23
 PRIOR APPLICATION NUMBER: 09/121,781
 TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND TITLE OF INVENTION: METHODS OF USE THEREFOR FILE REFERENCE: 1855.1052-012
 APPLICANT: O'Brien, Siobhan H. APPLICANT: O'Keefe, Theresa
 APPLICANT: LaROSA, Gregory J.
APPLICANT: Horvath, Christop
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
 FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence:Pelb/4AF/myc/6HIS
 ORGANISM: Artificial Sequence
 Local
 61
 61
 61 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKDEP----YEDYWGQGTLVTVSS
 h 88.7%;
Similarity 84.8%;
O6; Conservative
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKP-----FPYF---DYWGQGTL 111
 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKDIEDTAMFPYYYGMDVWGQGTT 120
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSFTVNSGYFQHWGQGTLVTVSS 142
 Conservative
 Gregory J.
h, Christopher
 85.8%;
 Score 539.5; DB 1
Pred. No. 9.6e-41;
 9;
 Score 540; DB 1
Pred. No. 2e-40;
9; Mismatches
 Mismatches
 DB 10;
 DB 10;
 4
 4.
 Indels
 Length 288;
 Length
 Indels
 9
 4.
 Gaps
 Gaps
 60
 116
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 ; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-125-687-4
 RESULT 15
US-10-125-687-4
 Š
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 Qy
 ; OTHER INFORMATION: Human consensus antibody heavy chain variable US-10-025-687-4
 RESULT 14
US-10-025-687-4
 В
 γ
 CURRENT APPLICATION NUMBER: US/10/125,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
 Sequence 4, Application US/10125687 Publication No. US20030054407A1 GENERAL INFORMATION:
 Matches 105;
 Query Match
 CURRENT APPLICATION NUMBER: US/10/025,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
 Matches
 Query Match
Best Local
 Sequence 4, Application US/10025687
Publication No. US20020142255A1
 GENERAL INFORMATION
 TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY FILE REFERENCE: 26050-705
 LENGTH: 1:
TYPE: PRT
 APPLICANT: Luo, Peter
 APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
 ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
 FEATURE:
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Result
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 GenCore version 5.1.6
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| , 92                      | EMBL; M355 PIR; A020 PIR; A020 PIR; A020 PIR; A020 PIR; A020 PIR; A020 RGO: GO: GO: GO: GO: GO: GO: GO: GO: GO:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | SEQUENCE FROM SEQUENCE FROM METLY SEENS ("Structure an heavy chain "Froc. 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| imilarity<br>Conser       | EMBL; J00236; AAAS EMBL; M35415; AAAS PIR; A02047; H3HU2 PDB; 1HOU; 23-DEC- Genew; HGNC:5545; C: GC; GC:0005576; C: GC; GC:0006955; F: INTERPRO; IPRO0791 INTERPRO; IPRO0390 INTERPRO; IPRO0390 INTERPRO; IPRO0390 PFAM; PF00047; 19; SMART; SMO0406; IG PROSTTE; PS50835; IMMUNGTER INTERMOPPOBLIN V; SIGNAL 1 CHAIN 20 DOMAIN 20 DOMAIN 17 SEQUENCE 117 AA;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLINE-81101090; pubMed-6450418  Matthyssens G., Rabbitts T.H.;  "Structure and multiplicity of g heavy chain variable region.";  Proc. Natl. Acad. Sci. U.S.A. 77                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | LIT 1  LHUMAN LHUMAN STANDA P01764; 21-JUL-1986 (Rel. 01, 21-JUL-1980 (Rel. 01, 15-SEP-2003 (Rel. 42, Ig heavy chain V-III Homo sapiens (Human). Eukaryota; Metazoa; C Mammalia; Eutheria; P NCBL_TaxID-9606; | 677.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| \ <u>{</u>                | AAA58735.1; AAA58735.1; AAA58735.1; AAA58735.1; AAA58735.1; AAA58735.1; AAA58735.1; AAA68735.1; AAA687                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Rabbe multimultimultimultimultimultimultimulti                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | STANDARD; 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| Pred.<br>4; Mis           | EMBL; J00236; AAA33516.1; EMBL; M35415; AAA58735.1; PIR; A02047; H3HU26. PDB; 1HOU; 23-DEC-99. Genew, HGNC:5545; GEYVE. GO; GO:0005576; C:extracellular; NAS. GO; GO:0005576; P:immune response; NAS. InterPro; IPR007110; Ig-like. InterPro; IPR007110; Ig-like. InterPro; IPR003596; Ig_MHC. InterPro; IPR003596; Ig_W. Pfam; PF00047; Li; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG_LIKE; 1. Immunoglobulin V region; Signal; 3D-structure. SIGNAL Inmunoglobulin V region; Signal; 3D-structure. SIGNAL Inguistation of the structure of the structure. SIGNAL Inguistation of the structure. Inguistation of the structure. 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It is produce some and the Swiss Institute of Bioinformatics and the Swiss Institutes as long as if ited and this statement is not removed unities requires a license agreement (See https://doi.org/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.10 | P P P P P P P P P P P P P P P P P P P                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
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 MEDLINE=77100368; PubMed=401950; Adetugbo K., Milstein C., Secher D.S.; "Molecular analysis of spontaneous som Nature 265:299-304(1977).
 SEQUENCE OF 17-136.
 antibodies: somatic mu
Cell 24:625-637(1981).
 "Heavy chain variable region antibodies: somatic mutation
 Baltimore
 MEDLINE-81234548; PubMed-6788376; Bothwell A.L.M., Paskind M., Reth
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Mus musculus (Mouse)
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 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAK
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EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
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 Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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 15071 MW;
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 Score 470;
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 RESULT 4
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GO: GO:000576; C:extracellular; NAS.
GO: GO:0003823; F:antigen binding activity; NA
GO: GO:0006955; P:immune response; NAS.
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InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_WC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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15 heavy chain V-III region TIL.
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HSSP; P01772; 2FB4.
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 MEDLINE=78005528; PubMed=409716;
Wang A.-C., Wang I.Y., Fudenberg H.H.;
 SEQUENCE
 NCBI_TaxID=9606;
 Homo sapiens (Human)
 -!- SIMILARITY: Contains 1 immunoglobulin-like
 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
 'Immunoglobulin
MEDLINE-81013859;
 SEQUENCE.
 HOILO
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mo sapiens (Human)
 BIO1. Chem. 252:7192-7199(1977).
MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
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 Pred. No. 3.1e-40;
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 HV3B_HUMAN STANDARD; PRT; 114
P01763;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence upda
15-SEP-2003 (Rel. 42, Last annotation upda
19 heavy chain V-III region WEA.
Homo sapiens (Human).
 Query Match
Best Local :
 Matches
 Goni F., Frangione B.;

"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";

Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983)

-1- MISCELANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
WALDENSTROM'S MACROGLOBULINEMIA.

-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 InterPro; lrv...
InterPro; lrv...
InterPro; lrv...
InterPro; lrv...
InterPro; lrv...
InterPro; lrv...
InterPro; lrv...
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 999
 HSSP;
 InterPro;
 SEQUENCE
 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
 HUMAN
 MEDLINE-83273707;
 NCBI_TaxID-9606;
 InterPro; IPR007110; Ig-1ike
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 HSSP; P01772; 2FB4.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0003823; F:antigen binding activity;

GO; GO:0006555; P:immune response; NAS.
 "Amino acid sequence of the variable region of a location of a possible JH segment."; Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980)
-.!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FR
 PIR; A02051; M3HUAM.
 PATIENT WITH MACROGLOBULINEMIA.
-!- SIMILARITY: Contains 1 immunoglobulin-like
 Lehman
"Amino
 ; A02046; W3HUWE.
P; P01772; 2FB4.
G0:0005576; C:extracellular; NAS.
G0:0003823; F:antigen binding activity;
G0:0006955; P:immune response; NAS.
G0:0006955; P:imy-ike.
 115
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 D.W., Putnam F.W. acid sequence of
 Similarity
 SS
 - s
 ABSVKGRFTISRDBSKBTLYLQMNSLRAEBTAVYYCARDRPLYGBYRAFNYWGQGTLYTV
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPY-----FDYWGQGTLVTV
 .W., Putnam F.W.;
 122
122
 116
 Conservative
 PubMed=6410398;
Ig_MHC.
 76.6%;
72.1%;
 15;
 Score 466;
Pred. No. 7
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 PYRROLIDONE CARBOXYLIC ACID
 A42D0F17D252F1C2 CRC64;
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HV3F_HUMAN
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Matches 89
 InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
 DOMAIN
NON_TER
SEQUENCE
 PIR; A02050; A2HUBU.
HSSP; P01789; 1MCP.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding act
GO; GO:0006555; P:immune response; NA
 Torano A., Putnam F.W.;

"Complete amino acid sequence of the alpha 2 heavy IgA2 immunoglobulin of the A2m (2) allotype.";

Proc. Natl. Acad. Sci. U.S. A. 75:966-969(1978).

-I- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2W REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.

-I- SIMILARITY: Contains 1 immunoglobulin-like doma
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
19 heavy chain V-III region BUT.
 MEDLINE=78137069; PubMed=416441; Torano A., Putnam F.W.;
 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
 Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Pyrry
DOMAIN 1 112
 NCBI_TaxID-9606;
 Homo sapiens (Human)
 SEQUENCE
 HV3F_HUMAN
P01767;
 MOD_RES
 SEQUENCE
 60
 61
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 87;
 61
 61
 Similarity
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
ADSVKGRFTISRDDSRBTVYLQMBSLRAEDTAVYYCARDLAAARLFGKGTTVTVSS
 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKPEPYEDYWGQGTLVTVSS 116
 Similarity
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYWGQGTLVTVSS
 115
115
115 AA;
 Conservative
 114 AA;
 Conservative
 STANDARD;
 115
12379 MW;
 114
; 12256 MW;
 73.6%;
75.0%;
 76.0%;
76.7%;
 Pyrrolldone carboxylic acid.
IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID
 Score 447.5;
Pred. No. 4.9e
13; Mismatches
 14;
 IG-LIKE.
 Craniata; Vertebrata; Catarrhini; Hominidae;
 Score 462;
Pred. No. 1
 208876A7DF52DCF4 CRC64;
 PRT;
 D88294FB418A07B7 CRC64;
 Mismatches
 activity;
 NAS.
 update)
on update)
 115
 .9e-38;
 DB 1;
.7e-39;
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 DB 1;
 NAS
 15;
 domain
 A2M(2)
 Length 114;
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 Indels
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 Euteleostomi;
 115;
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RESULT 7
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Matches 88
 Pfam; PF00047; 19; 1.
SMART: SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1
Immunoglobulin V region.
DOMAIN 1 111
 Capra J.D., Hopper J.E.;

Capra J.D., Hopper J.E.;

Capparative studies on monotypic IgM lambda and IgG kappa from an "Comparative studies on monotypic IgM lambda and IgG kappa from an individual patient. III. The complete amino acid sequence of the vergion of the IgM paraprotein.";

Immunochemistry 13:995-999(1976).

-I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
 MEDLINE=77117674; PubMed=65324; Capra J.D., Hopper J.E.;
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 21-JUI-1986 (Rel. 01, Created)
21-JUI-1986 (Rel. 01, Last Sequence up
15-SEP-2003 (Rel. 42, Last annotation
15 heavy chain V-III region BRO.
 P01766;
 HV3E_HUMAN
 Homo sapiens (Human).
 GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activ
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 NCBI_TaxID=9606;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
15 heavy chain V-III region HIL.
Homo sapiens (Human)
 HUMAN
 SEQUENCE .
 Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
 HV3J_HUMAN
P01771;
 EQUENCE
 Chiu Y.-Y.H.,
 MEDLINE=79124695; PubMed=420800;
Chiu Y.-Y.H., Lopez de Castro J.A.,
 SEQUENCE
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 SIMILARITY:
 120
 111 Ļ 111
 P01772; 2FB4.
 60
 61
 88;
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 Similarity
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKP------FPYFDYWGQGT 110
 r.
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYYNMNWVRQVTGKGLEWVSAI-GTAGDQYY
 120
 120 AA;
 Conservative
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 мзнивы.
 Lopez
 STANDARD;
 Contains 1 immunoglobulin-like domain
 STANDARD;
 Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
 120
 Chordata;
Primates;
 13227 MW;
 73.1%;
72.7%;
 11;
 Score 444.5; DB 1;
Pred. No. 1e-37;
 PRT;
 IG-LIKE.
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 D3F0428F7C2E6410 CRC64;
 Mismatches
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 IgG kappa from an
sequence of the VH
 Length
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 HV3A_HUMAN
 Matches
 Query Match
Best Local
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
 "Amino acid sequence of the VH res
cryoimmunoglobulin IgG Hil.";
Biochemistry 18:53-560(1979).
-!- MISCELLANEOUS: THIS CHAIN WAS
 MOD_RES
 HSSP: P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
 PIR; A02054;
 -!- SIMILARITY: Contains 1
 SEQUENCE
 DOMAIN
 PIR; A02045; AlHUTR.
HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding actions of GO; GO:0003825; P:immune response; NAS
GO; GO:0006955; P:immune response; NAS
 "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.), II. The amino acid sequence of the H-chain, alpha-type, subgroup III; structure of the complete IgA-molecule."; Structure of the complete IgA-molecule."; Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).

--- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.

--- SIMILARITY: Contains 1 immunoglobulin-like domain.
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up. 15-SEP-2003 (Rel. 42, Last annotation Ig heavy chain V-III region TRO.
 HV3A_HUMAN
P01762;
 mmunogiobulin V regin; Pyrrolidone carboxylic acid
 InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
 SEQUENCE (MYELOMA PROTEIN TRO).
MEDLINE-76023781; PubMed-809331;
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 Hilschmann N.
 Kratzin H.,
 NCBI_TaxID=9606;
 Homo sapiens (Human)
 9
 115 SS 116
 120
 61 GDSVKGRFTISRDNSKRTLYMZMNSLRTEDTAVYYCARD-PDILTAFSFDYWGQGVLVTV
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFP-----
 Н
 86;
 Similarity
 SS 121
 121
121 AA;
 Conservative
 Altevogt P., Ruban
 GIHUHL.
; ig; 1.
6; IGv; 1.
 STANDARD;
 121
 ; Chordata; Primates;
 13566 MW;
 73.1%;
 immunoglobulin-like domain
 13;
 Score 444.5;
Pred. No. 1e-3
13; Mismatches
 IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
 Craniata; V
Catarrhini;
 PRT;
 region
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 Vertebrata; Euteleostomi;
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 Hominidae;
 DB 1;
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 CRC64;
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Matches 80
 Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv;
PROSITE; PS50835; IG.
 _HUMAN
HV3T_HUMAN
P01781;
 GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:1mmune response; NAS.
InterPro; IPR0071110; Ig-like.
InterPro; IPR003006; Ig_MHC.
 SEQUENCE
 Immunoglobulin V region.
DOMAIN 1 112
NON_TER 116 116
 PIR; A02064; M3HUGL.
HSSP; P01772; 2FB4.
 Submitted (JUN-1975) to
 MEDLINE=75059123; PubMed=4803843; Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.; "The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain type), subgroup H III. Architecture of the complete IgM-molecule. Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
 21-JUL-1986 (Rel. 01, Creater
21-JUL-1986 (Rel. 01, Last s
15-SEP-2003 (Rel. 42, Last a
To heavy chain V-III region
 -1- SIMILARITY: Contains 1 immunoglobulin-like domain
 Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Homo sapiens (Human)
Eukaryota; Metazoa;
 MOD_RES
 Hilschmann N.;
 SEQUENCE
 NCBI_TaxID=9606;
 REVISION TO 28-33.
 SEQUENCE
 DOMAIN
 Immunoglobulin
 Local
 MACROGLOBULIN.
 115
 121
 61
 51
 80;
 Similarity
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
 : IPR007110;
: IPR003006;
: IPR003596;
 Similarity
 SS
 SS 116
 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKPEPY-----FDYWGQGTLVTV
 QVQLVQSGGLVKPGGSLRLSCVASGFSFRDFYMSWIRZTPGKGLZWVSYIGGSGSTLYY
 PS50835; IG_LIKE; 1.
obulin V region; Pyrr
1 108
 116
116
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 Conservative
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 STANDARD;
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 01, Last sequence up 42, Last annotation
 IG_LIKE;
 12730 MW;
 72.9%;
 13472 MW;
 Ig_v.
 73.0%;
 the PIR data
MU CHAIN WAS
 Pyrrolidone carboxylic
 10;
 18;
 GAL.
 Score 443; DB 1;
Pred. No. 1.4e-37;
0; Mismatches 21
 Score 444; DB
Pred. No. 1.2e
L8; Mismatches
 IG-LIKE
 PYRROLIDONE CARBOXYLIC ACID
 2C67CA9AAAAA1282 CRC64;
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RESULT 11

HV3H_HUMAN

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 RESULT 12
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 MOD_RES
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 GO; GO:0005576; C:extracel
GO; GO:0003823; F:antigen
GO; GO:0006955; P:immune r
 SEQUENCE
 PROSITE;
 -!- SIMILARITY: Contains 1
 Biochemistry 13:2482-2498(1974).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 Immunoglobulin
 MEDLINE=74175307; PubMed=4208843; Florent G., Lehman D., Putnam F.W.;
 21-JUL-1986 (Rel. 01, Create
21-JUL-1986 (Rel. 01, Last s
15-SEP-2003 (Rel. 42, Last a
If heavy chain V-III region
 HV3H_HUMAN P01769;
 NCBI_TaxID=9606;
 Homo sapiens (Human)
 The switch point in mu heavy chains of human IgM immunoglobulins.";
Miochemistry 13:2482-2498(1974).
 MACROGLOBULIN.
 115
 PF00047; 19; 1.
[; SM00406; IGv; 1.
[TE; PS50835; IG_LIKE; 1.
noglobulin V region; Pyrrolidone carboxylic acid.
IN 1 112 IG-LIKE.
 A02052; M3HUGA.
 121
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 Similarity
 SS
 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAK-----PFPYFDYWGGGTLYTV 114
 SS 116
 QVZLVZSGGGAVZPGRSLRLSCAASGFSFSTYAMHWVRQAPGKGLZWLSVISYBGBBZYY
 AASVKGRFTISRBBSKBTMYLEMNSLRAENTAVYYCARSGIALGSVAGTDYWGZGTLVTI 120
 VDSVKGRFTISRDNAKNSLYLQMNSLRVEDTALYYCARGWGGGDYWGQGTLVTVST 116
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPFPYFDYMGQGTLYTVSS
 EVQLVESGGDLVQPGRSLRLSCAASGFBFBBLGMTWVRQAPGKGLEWVANIKZBGSZZBY
 122
122 AA;
 122
 Conservative
 STANDARD;
 P:immune response;
 C:extracellular; NAS. F:antigen binding act
 122'
13166 MW;
 Primates;
 71.48;
65.68;
 Chordata;
 Created)
 20;
 immunoglobulin-like
 annotation
 sequence
 GA.
 Score 434;
Pred. No. 1
 PYRROLIDONE CARBOXYLIC
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 74E5B6959E84100A CRC64;
 Mismatches
 activity;
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 update)
 Vertebrata; Euteleostomi;
Ostariophysi; Cypriniformes;
 Vertebrata;
 DB 1;
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 domain
 Length 122;
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DOMAIN
 HV3I_HUMAN
P01770;
 HUMAN
 HSSP;
 SEQUENCE FROM N.A.
MEDLINE-88144476; PubMed-3125551;
Wilson M.R., Middleton D., Warr G.W.;
 Cyprinidae; Carassius NCBI_TaxID=7957;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).

-i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2004 (Rel. 11) region NIE.
 CHAIN
 SIGNAL
 and family relationships of two genes and a
 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
 Homo sapiens (Human)
 DOMAIN
 PROSITE;
 InterPro;
 InterPro;
 InterPro;
 "Immunoglobulin heavy chain
 NCBI_TaxID=9606;
 Immunoglobulin
 MEDLINE=77070267; PubMed=1002129;
 DISULFIDE BOND.
 SEQUENCE
 PF00047; ig; 1; sm00406; IGV;
 P01772; 2FB4
 Natl. Acad.
 79
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 66;
 , PS50835; Ib___
; PS50835; Ib__
; "lin V region; to 19
 Similarity
 IPR007110;
; IPR003006;
; IPR003596;
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAK 98
 EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQPPGKGLEWVSVIY-SGGSTYY
 116
116
 Conservative ·
 20
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20
20
41
41
 ΑA;
 STANDARD;
 Sci. U.S.A.
 IG_LIKE;
 116
49
54
68
84
116
114
 71.3%;
 12808
 Ig-like.
Ig_MHC.
 Ig_v.
 Signal
 MW;
 variable region
 4;
 Score 433.5;
Pred. No. 1.
 COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3.
BY SIMILARITY.
 COMPLEMENTARITY-DETERMINING-1 FRAMEWORK-2.
 FRAMEWORK-1
 Craniata; Vertebrata; Catarrhini; Hominidae;
 IG HEAVY CHAIN V REGION 5A.
 85:1566-1570(1988).
 PRT;
 9C2279E2DF199B12 CRC64;
 Mismatches
 119
 A
 Hominidae;
 pseudogene in
 gene evolution: structure
 Indels
 Length
 Euteleostomi;
 a teleost
 1;
 Gaps
 78
 60
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RESULT 14
HV02_CANFA
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 Query Match
Best Local S
Matches 84
 MOD_RES
DISULFID
NON_TER
 Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LI
 -i- SIMILARITY: Contains 1 immunoglobulin-like PIR; A91668; G1HUNI. HSSP; P01772; 2FB4.
 SEQUENCE
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 Immunoglobulin V region.
 Pfam; PF00047; ig; 1
SMART; SM00406; IGv;
 PIR; A90403; MHDGMO.
HSSP; P01772; 2FB4.
 Wasserman R.L., Capra J.D.;
"Primary structure of the variable immunoglobulin heavy chains.";
Biochemistry 16:3160-3168(1977).
 SEQUENCE OF 1-112.
MEDLINE-77242268; PubMed-407924;
Wasserman R.L., Capra J.D.;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
 HV02_CANFA
P01785;
 Immunoglobulin V region; Pyrrolidone carboxylic acid
DOMAIN 1 112 IG-LIKE.
 -!- MISCELLANDOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 "The complete amino-acid sequence of a canine mu chain."; Mol. Immunol. 16:565-570(1979).
 MEDLINE=80077682; PubMed=117299; McCumber L.J., Capra J.D.;
 SEQUENCE OF 113-117
 NCBI_TaxID=9615;
 Canis familiaris (Dog).
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 PROSITE;
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 I5-SEP-2003 (Rel. 42, Last a
Ig heavy chain V region MOO.
 21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
 GO:0005576; C:extracellular; NAS. GO:0003823; F:antigen binding acti GO:0006955; P:immune response; NAS
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 EVQLLESGGGIVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY
 PS50835;
 IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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119 AA;
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42, Last annotation updat
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 71.3%;
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 Score 433.5;
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 MEDLINE-79223895; PubMed-111245;
Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
"Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins and its potential role in generating diversity in
 InterPro; IPR007110; Ig-11;
InterPro; IPR003006; Ig_MH
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
 THAT BINDS GALACTAN.
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 complementarity-determining regions.";
proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 PIR; A02077; AVMSX4.
HSSP; P01810; 2FBJ.
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 70.6%; Score 429; DB 1; ilarity 69.5%; Pred. No. 3.6e-36; Conservative 15; Mismatches 19
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13246 MW; BC34FC8F31CD41B3 CRC64;
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Perfect score:
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608
1 EVQLLESGGGLVQPGGSLRL.....AKPFPYFDYWGQGTLVTVSS 116
 830525 seqs, 258052604 residues
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|   | 336.5              | 337    | 337.5  | 339                  | 340    | 340.5              | 342.5  | 343    | 343.5  | 345    |                 | 353.5  | 369    | 370    | 386    | 392.5  | 398.5  | 398.5  | 400                  | 403    | 411    | 417.5  | 418    | 420    | 427.5  | 432.5              | 438.5  | 443.5  | 452      |
|   |                    |        |        |                      |        |                    |        |        | 56.5   |        |                 | 58.1   | 60.7   | 60.9   | 63.5   | 64.6   | 65.5   | 65.5   | 65.8                 | 66.3   | 67.6   | 68.7   | 68.8   | 69.1   | 70.3   | 71.1               | 72.1   | 72.9   | 74.3     |
|   | 484                | 145    | 117    | 61:3                 | 116    | 146                | 119    | 241    | 117    | 463    | 125             | 473    | 124    | 124    | 124    | 104    | 521    | 112    | 298                  | 484    | 437    | 480    | 95     | 469    | 486    | 493                | 131    | 479    | 473      |
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# ALIGNMENTS

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| 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK-PFPYFDYWGQGTL 111<br> | 1 EVQLLESGGGLVQPGGSLRLSCAASGFTESSFSMSWVROAPGKGLEWVSSISGSSGTTYY 60<br> | Query Match 86.4%; Score 525.5; DB 4; Length 597; Best Local Similarity 83.2%; Pred. No8.2e-46; Matches 104; Conservative 8; Mismatches 4; Indels 9; Gaps 2; | Hypothetical protein.<br>SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64; | PROSITE; PS00290; IG_MHC; 3. | v; 1. | Pfam; PF00047; 1g; 5. | IPR003006; | InterPro; IPR007110; Iq-11ke. | EMBL: BC015760: AAH15760 1. |     | TISSUE=B-cell; |    |    | NCBI_TaxID=9606; | Mammalia: Eutheria: Primates: Catarrhin: Wominiana; J | Fikaryota: Wotagoa: Characte | Hypothetical protein. | 01-MAR-2003 (TrEMBLrel. 23, | 01-DEC-2001 (TrEMBLrel. 19, |    |      | O96BB9 BEETTMINDY. | RESULT 1 |  |

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EMBL; BC024289; AAH24289.1; -.
Interpro; IPR007110; Ig-like.
Interpro; IPR003006; Ig_MHC.
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01-MAY-2000 (TrEMBLrel. 13, Created)
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01-MAR-2000 (TrEMBLrel. 23, Last annotation update)
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 Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Cl
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 NCBI_TaxID=9606;
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
 Q9UL91
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 Wu X., Liu B., Young D.C.;
 SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
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 (Fragment).
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Hypothetical protein.
 Homo sapiens (Human).
Eukaryota; Metazoa; Ch
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NCBI_TaxID=9606;
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Myosin-reactive immunoglobulin heavy chain variable
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Myosin-reactive immunoglobulin heavy chain v
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 SEQUENCE FROM N.A.

KIKUChi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

"An antibody fragment2A3 specific for native lysozyme :Isolaion human synthetic phage display library and characterization.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB049915; BAB16829.1; -.

HSSP; P01772; 2FB4.
 Q9HCC1;
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 01-MAR-2001 (TIEMBLIEL 16, 01-MAR-2001 (TIEMBLIEL 16, 01-MAR-2003 (TIEMBLIEL 23, Single chain Fy (Fragment).
 NCBI_TaxID-9606
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 SEQUENCE FROM N.A.

MEDLINE=96071149; PubMed=7475288;

Cao J., Vescio R.A., Rettig M.B., Hon
Lichtenstein A.K., Berenson J.R.;

"A CD10-positive subset of malignant."
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 EMBL;
 MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L. Young D.C.; "Myosin-reactive autoantibodies in fetus.";
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SEQUENCE
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Mammalia; Eutheria; Primates;
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EMBL; S80860; AAD14339.1; -.
HSSP; P01772; 2FB4.
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erPro; IPR003596; Ig_v.

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P01772; 21
 Immunol.
 60
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 147
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 PRT;
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 B4D1A5944B2D5CCA CRC64;
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 'n
 Hong
 rheumatic carditis and
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 С.н.,
 immunoglobulin gene primers.";
 N.N., Berney
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 Length 147;
 Length 118;
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RESULT 11
Q9UL84
ID Q9UL8
AC Q9UL9
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Mammalia; Eutheria;
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 01-MAR-2002
01-MAR-2002
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 Wu X., Liu B., Young D.C.;
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 sequence update) annotation update)
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 122
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 Hominidae;
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 Euteleostomi;
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 Gaps
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SEQUENCE
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01-MAR-2003
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MEDLINE-98277139; PubMed-9614934;
Fin B., Van der Merwe P.L.,
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HSSP; P01772; 2E
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 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Atkin J.D., Tape A., Jenning
"Definition of the Idiotope
in Manumalian Cells.";
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annotation
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 Length 494;
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 Euteleostomi;
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 US-09-075-338C-20
US-09-300-425B-20
 SUMMARIES
 5580241
 Description
Sequence 20,
Sequence 20,
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|---|-----------------|--------------|--------------|----------------|---------------|------------------|---------------|-----------------|-------------------|--------------------|--------------------|-------------------|----------------|-----------------|--------------|---------------|---------------|-----------------|---------------|------------------|----------------|---------------|----------|-------------------|----------------|-----------------|---------------|----------------|--------------|--------------|------------------------------------|-------------|-------------------|------------------|------------------|------------------|-----------------|------------------|------------------|-------------|-------------------|-----------------|--|
|   | 71.             | 71.          | 71.          | 71.            | 11.           | 12               | 1.            | ? <u>`</u>      | 71.               | 17.                | ر<br>ء د           | J / 4             | 74.            | 1.4             | 7.4          | 74.           | 74.           | 74.             | 75.           | 75.              | 75             | 75            | 75       | 75                | 78.            | 78.             | 78.           | 7 78.          | 7 78.        | 7 78         | 100                                | 100         | 100.              | 100.             | 100.             | 100.             | 100             | 100              | 100              | 3 100       | 3 100             | 3 100           |  |
|   |                 |              |              |                |               |                  |               |                 |                   |                    |                    | 1 0               |                |                 |              |               |               |                 |               |                  |                | -             |          |                   | -              | _               | •             | •              | •            | • •          | _ •                                |             | ٠.                | ٠                | · ·              | -                |                 |                  | , u              | 238         | ω                 | **              |  |
|   | 15              | 13           | 12           | 8<br>U         | c             |                  |               |                 |                   |                    |                    |                   |                |                 |              |               |               |                 | 28            | <u>د</u>         | 28             |               | 30       | 30                | 24             | 24              | 24            | 24             | 24           | 2 6          | ν<br>γ<br>γ                        | 1 2         | 2 2               | 22               | 22               | 22               | 22              | 22               | 2                | 22          | 22                | 19              |  |
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| : | equence 93, App | ce 800. Ap   | Sequence 9.  | quence         | equence 50,   | equence 50, Appl | uence 9,      | equence 377, Ap | equence 117435,   | equence 50938,     | equence 64189,     | 64613,            | equence 12325  | equenc          | equence 727, | 178822        | equenc        | equence 382. An | equence 64895 | equence 149. An  | Sequence 64869 | A             | 1215     | 140655            | oc, App        | יייין אַנְיייין | To, App       | 10 App         | 3 6          | 1026, A      | 1, Ap                              | 78827       | 78383,            | 78382,           | 78381,           | 78380.           | 78365           | 78364            | 78362,           | 7836        | quence 78345,     | equence 20, Apr |  |

# ALIGNMENTS

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US-09-075-338C-20

Sequence 20, Application US/09075338C

SEQUENCE 1 INFORMATION:
APPLICANT: NERI, Dario
APPLICANT: TARLI, Lorenzo
APPLICANT: TARLI, Lorenzo
APPLICANT: BIRCHLER, Manfred
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY
FILE REFERENCE: SCH-1733
CURRENT FILING DATE: 198-05-11
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antibody linker
US-09-075-338C-20
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Sequence 20, Application US/09300425B GENERAL INFORMATION:

NERI, Dario

APPLICANT:

TARLI, Lorenzo VITI, Francesca

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:

PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998 (
NUMBER OF SEQ ID NOS: 34

1998-05-11

09/075,338

PatentIn Ver. 2.1

APPLICANT: BIRCHLER, MANIFED TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF TITLE OF INVENTION: ANGIOGENESIS FILE REFERENCE: SCH-1733P1
CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28

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, OTHER INFORMATION: Description of Artificial Sequence: antibody linker \ensuremath{\mathtt{US}}\xspace-09-300-425B-20
 US-09-512-082-20
 US-09-512-082-20
 Sequence 20, Applica GENERAL INFORMATION:
 Matches
 NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn V
SEQ ID NO 20
 APPLICANT: NERI, DATIO
APPLICANT: TARLI, LOTENZO
APPLICANT: VITI, Francesca
APPLICANT: VITI, Francesca
APPLICANT: BIRCHLER, MANIFED
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
TITLE OF INVENTION: ANGIOGENESIS
TITLE OF INVENTION: ANGIOGENESIS
Matches
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CURRENT APPLICATION NUMBER: US/09/512,082
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 09/300,425
 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
 PRIOR FILING DATE:
 ORGANISM: Artificial Sequence
 FEATURE:
 TYPE: PRT
 OTHER INFORMATION: Description of Artificial Sequence: antibody linker
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 PatentIn Ver. 2.1
 Application US/09512082
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 1999-04-28
 1998-05-11
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100.0%; Pred. No. 0.04;
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LUCANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791.537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEO ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEO ID NO 78361
LENGTH: 238
TYPE: PRT
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 US-09-791-537-78345
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 ; ORGANISM: Homo sapiens US-09-791-537-78361
 US-09-791-537-78362
 CURRENT FILING DATE: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 78345
 APPLICANT: Bionomix, Inc.
 Matches
 Query Match
 Sequence 78362, Application US/09791537 GENERAL INFORMATION:
 Matches
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Best Local Similarity
 APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
APPLICANT: Danzer, Joseph TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE: 261/210
 APPLICANT:
 APPLICANT: Bionomix, Inc. APPLICANT: Debe, Derek
 LENGTH: 238
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Local Similarity 100.0%;
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 NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 78365
LENGTH: 238
TYPE: PRT
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 ; ORGANISM: Homo sapiens US-09-791-537-78362
 Query Match
Best Local Similarity
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CURRENT FILING DATE: 2001-02-22
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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 CURRENT APPLICATION NUMBER: US/09/791,537 CURRENT FILING DATE: 2001-02-22
 APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILB REFERENCE: 261/210
 GENERAL INFORMATION
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Best Local Similarity 100.0%;
Matches 14; Conservative 0
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APPLICANT: Debe, Derek
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
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Pred. No.
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 RESULT 11
US-09-791-537-78382
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 RESULT 10
US-09-791-537-78381
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 GENERAL INFORMATION
CURRENT APPLICATION NUMBER: US/09/791,537
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 SOFTWARE: PatentIn version 3.0 SEQ ID NO 78380 LENGTH: 238 TYPE: PRT
 APPLICANT: Bionomix, Inc. APPLICANT: Debe, Derek
 APPLICANT: Bionomix, Inc.
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APPLICANT: Denzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
 GENERAL INFORMATION
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
 APPLICANT: Danzer, Joseph
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TITLE OF INVENTION: METHODS OF USE THEREOF
 APPLICANT: Bionomix, Inc.
 117 GDGSSGGSGGASTG 130
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 Application US/09791537
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 Application US/09791537
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SOFTWARE: Patentin version 3.0
SEQ ID NO 78383
LENGTH: 238
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 RESULT 12
US-09-791-537-78383
 RESULT 13
US-09-791-537-78827
Sequence 78827, Application US/09791537
GENERAL INFORMATION:
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US-09-791-537-78383
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 SOFTWARE: PatentIn version 3.0
SEQ ID NO 78382
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Best Local Similarity 100.
Matches 14; Conservative
 Sequence 78383, Appl: GENERAL INFORMATION:
 APPLICANT: Debe, Derek
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
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TILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
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CURRENT FILING DATE: 2001-02-22
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
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US-09-075-338-1
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US-10-276-781-1626
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 ; ORGANISM: Homo sapiens US-10-276-781-1626
Search completed: August 20, 2003, 13:13:38 Job time : 144.289 secs
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SOFTWARE: FastSEQ for
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 TITLE OF INVENTION: Binding Molecule FILE REFERENCE: Sequence CURRENT APPLICATION NUMBER: US/09/075,338 CURRENT FILING DATE: 1998-05-11 NUMBER OF SEQ ID NOS: 1
 APPLICANT: Nerli
APPLICANT: tarli
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 APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al.
APPLICANT: Tang et al.
ITIE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-018 (785 contig)
CURRENT APPLICATION NUMBER: US/10/276,781
CURRENT FILING DATE: 2002-11-18
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PRIOR FILING DATE: 2000-01-25
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| hypothetical glyci | hypothetical gluct | homeotic protein s | homeotic protein s | merozoite surface | merozoite surface | keratin, type I, c | hypothetical glyci | _      | zinc finger bindin | <u> </u> | wingless receptor |        | ica    |        | F5D14.12 protein - |

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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C; Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; C.; Harris, D.; Hamlin, Holroyd, Gordon

A;Athors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Experimental source: strain

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C; Genetics:

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Š Query Match Best Local Matches Local 313 GNGGNGGNGGASTG 1 GDGSSGGSGGASTG 10; Similarity Conservative 79.5%; 14 ű, Score 58; Pred. No. Mismatches 4.9; 2 Length 801; Indels 0 Gaps

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RESULT 2 F70971

В

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hypothetical glycine-rich protein Rv3367 - Mycobacterium tuberculosis (strain H37RV) c;Species: Mycobacterium tuberculosis (;Species: Mycobacterium tuberculosis (;Species: Mycobacterium tuberculosis (;Accession: F70971 c;Accession: F70971 f;Accession: F70971 f;Acces Holroyd,

Z3BPM3 Z3BPF1 Z3BPF1 S48172 C70720 B70807 D70807

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related to hypothetical

RNA-bin

heat-shock

geno

A;Status: preliminary; nucleic acid sequence not shown; translation not

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C;Genetics:
 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: E70806
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ht. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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Pred. No. 8.7;
 Score 55; DB Pred. No. 19;
 Score 55; DB Pred. No. 15;
 Mismatches
 Mismatches
 not shown; translation not shown
 2;
 2
 1;
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 2;
 Length 588;
 Length 1022;
 Length 1381;
 Indels
 Indels
 Indels
 0
 0,
 0;
 the complete
 Gaps
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 0
 Holroyd,
 0;
 0
 H37RV)
 Gordon,
 genome
```

RESULT 7 H70663

hypothetical

glycine-rich protein Rv1840c -

Mycobacterium

tuberculosis

(strain

H37RV)

```
F;152-159/Region: 8
F;164-175/Region: 1
F;164-171/Region: 8
F;176-183/Region: 8
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squar Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell A;Title: Deciphering the biology of Mycobacterium tuberculosis from the A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: A70869
 hypothetical glycine-rich protein Rv2490c - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: A70869
 A; Gene: Rv2490c
C; Superfamily:
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamilin, N.; H
 R;Shvets, Y.P.; Chumakov, I.M.; Kisselev, L.L. Mol. Biol. 24, 663-677, 1990
A;Title: Sequencing the fragment from a transcriptionally A;Reference number: PN0109
A;Accession: PN0109
 keratin-like protein - rat (fragment) C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Sep-1993 #sequence_revision 30 C;Accession: PN0109
 В
 Ω
 A;Cross-references: GB:AL021246; GB:AL123456; NID:93261507; A;Experimental source: strain H37Rv
 A; Molecule type: DNA
A; Residues: 1-1660 <COL>
 A; Status: preliminary; nucleic acid sequence not shown; translation
 F;93-100/Region: 8-residue repeat
F;105-112/Region: 8-residue repeat
F;118-125/Region: 8-residue repeat
F;152-163/Region: 12-residue repeat
 A; Gene: K51
C; Superfamily: loricrin
C; Keywords: duplication
 A; Molecule type: mRNA
A; Residues: 1-183 <SH
C; Genetics:
 RESULT
PN0109
밁
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 F;73-88/Region: 16-residue repeat
F;77-84/Region: 8-residue repeat
 F;34-41/Region:
 F;89-104/Region: 16-residue repeat
 F;21-28/Region:
 Query Match
Best Local
 Genetics:
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 Query Match
 Matches
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 Rv2490c
 1377
 123
 Similarity
9; Conserva
 1 GDGSSGGSGGASTG 14
 10;
 Similarity
 GDGSSGGSGGASTG
 GDGGAGGAGGTQTG
 GGGSSGGGGGGSSG 136
 collagen alpha 1(IV)
 8-residue repeat
16-residue repeat
 8-residue repeat
 DNA
 Conservative
 Conservative
 12-residue repeat
8-residue repeat
8-residue repeat
 8-residue repeat
12-residue repeat
8-residue repeat
 75.3%;
 J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares,
 74.0%;
 1390
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 Score 55;
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 Score 54; DB Pred. No. 3.9; 1; Mismatches
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 30-Sep-1993
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23;
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3.9;
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 #text_change 16-Feb-1997
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 Length 1660;
 Length
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 183;
 PIDN:CAA16067.1; PID:g279
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 complete
 B.G.
 .; Gordon
Holroyd,
 0
 0;
 H37RV)
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RESULT 8
A70812
hypothetical glycine-rich protein Rv0833 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 07-Mar-2003
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 07-Mar-2003
R;Cole, S:T; Brosch, R: Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gorde, Connor, R.; Davies, R.; Perlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroye
Rejandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete gel
A;Accession: A70812
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-749 <COL>
A;Cross-references: GB:AL022004; GB:AL123456; NID:g3261550; PIDN:CAA17639.1; PID:g2
C;Genetics:
A;Genetics:
A;Genee: Rv0833
C;Superfamily: elastin related uncharacterized glycine-rich protein, PE motif conta
 hypothetical glycine-rich protein Rv0746 - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis G;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 07-Mar-2003 C;Accession: E70824 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamilin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 C; Species: Mycobacte;
C; Date: 17-Jul-1998;
C; Accession: H70663
R; Cole, S.T.; Brosch
 A;Authors: Sqares, R.; Sulston, CA;Title: Deciphering the biology
 Rajandream, M.A.; Roge
Nature 393, 537-544, 1
A;Authors: Sqares, R.;
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 A:Gene: Rv1840c
C:Superfamily: uncharacterized glycine-rich
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 A;Cross-references: GB:283859; GB:AL123456;
A;Experimental source: strain H37RV
C;Genetics:
 A;Authors: Sqares, R., Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70663
 A; Molecule type: DNA
A; Residues: 1-515 <COL>
 A; Status: preliminary; nucleic acid sequence not shown;
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
 Query Match
Best Local
 Species: Mycobacterium tuberculosis Date: 17-Jul-1998 #sequence_revision
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9; Conserv
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9; Conserv
 GDGSSGGSGGASTG
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44, 1998
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 Score 54;
Pred. No.
 Pred. No. 15;
3; Mismatches
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 Score 54;
Pred. No.
 Mycobacterium
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 Length 515
 PE motif containing
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 translation not shown
 PIDN:CAB06114.1; PID:g1781207
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 PID:g29168
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 H37RV)
 H37RV)
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 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999 (C:Accession: S77300 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Io, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamad DNA Res. 3, 109-136, 1996 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analysis of the genome of the unicellular cyanobacterium (A:Title: Sequence analy
 A; Reference number: A; Accession: S77300
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 Query Match
Best Local
 Cross-references:
 Molecule type: DNA
Residues: 1-3016 <KAN>
 Status: nucleic acid sequence
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Local Similarity
 the nucleotide sequence was
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EMBL: D90907;

GB:AB001339; was submitted

NID:g1652618; PIDN:BAA17634.1; to the EMBL Data Library, June

PID:d101 1996

74.08; 71.48;

Score 54; Pred. No.

54;

2

Length 3016;

S74322;

MUID:97061201;

PMID: 890523 translation

not

shown;

not shown

of the genome of the unicellular cyanobacterium Synechocys

Yamada,

, Miyajima, w ; yas

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hypothetical protein s1r1403 - C:Species: Synechocystis sp. A:Variety: PCC 6803
 N; Alternate | C; Species: M:
 A;Molecule type: DNA
A;Residues: 1-1325 <HIM>
A;Cross-references: EMBL:AE000038; GB:U00089;
A;Note: the nucleotide sequence was submitted
 A; Genetic code:
C; Superfamily: M
 R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; I
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the
A;Reference number: $73327; MUID:97105885; PMID:8948633
A;Accession: $73723
 C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C;Accession: S73723
 A; Molecule type: DNA
A; Resiques: 1-783 <COL>
A; Resiques: 1-783 <COL>
A; Cross-references: GB:ALO21958; GB:AL123456; NID:g3261536; PIDN:CAA17513.1;
 A;Status: preliminary; nucleic acid sequence not
 A; Experimental source:
C; Genetics:
A; Gene: Rv0746
C; Superfamily: elastin
 probable lipoprotein H08_orf1325
N;Alternate names: MG309 homolog
 A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: E70824 A;Status: preliminary; nucleic acid sequence not shown;
 Matches
 Query Match
 Genetics:
 Matches
 Query Match
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 Local
 437
 553 GDGGAGGIGGAST 565
 ب
 1 GDGSSGGSGGAST 13
 10;
 Similarity
 GDGSSGGSGGASTG
 Similarity
 GGGGGGGGTSTG
 Mycoplasma hypothetical protein
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 related uncharacterized
 74.08;
71.48;
 74.0%;
76.9%;
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H08_orf1325
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 Score 54;
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 MG309
 1; Length 1325;
 glycine-rich
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 shown; translation not shown
 #text_change 10-Dec-1999
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ata Library, Novem
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mber 1996
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 PID: 9291
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RESULT 12
A47318
RNA-binding
 c;species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A47318
 C; Genetics:
A; Gene: Merc
C; Superfamily: u
F; 22-82/Domain:
 R;Michaud, E.J.; Bultman, S.J.; Stubbs, L.J.; Woychik, R.P. Genes Dev. 7, 1203-1213, 1993
A;Title: The embryonic lethality of homozygous lethal yellow A;Reference number: A47318; MUID:93307655; PMID:8319910
A;Accession: A47318
 Q
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 A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:134703, NCBIP:134704)
C;Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ri
F;22-82/Domain: ribonucleoprotein repeat homology <RRM1>
 A;Molecule type: mRNA
A;Residues: 1-296 <RES>
A;Cross-references: GB:S72641; NID:g619301; PIDN:AAC60688.1;
 A;Title: Pleiotropic effects of the mouse lethal yellow A;Reference number: 153142; MUID:94326666; PMID:8050375 A;Accession: I53142 A;Status: preliminary; translated from GB/EMBL/DDBJ
 gene Merc protein - mouse
C;Species: Mus sp. (mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05'Nov-1999
C;Accession: I53142
C;Accession: I53142
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 γ
 A; Molecule type: nucleic acid
A; Residues: 1-296 <MIC>
 A; Status: preliminary
coat protein A precursor - phage fd

(;Species: phage fd

C;Date: 30-Sep-1980 #sequence_revision 18-Aug-1

C;Accession: A04266; B04266

C;Accession: A04266; B04266

R;Beck, E.; Sommer, R.; Auerswald, E.A.; Kurz,

Nucleic Acids Res. 5, 4495-4503, 1978

A;Title: Nucleotide sequence of bacteriophage f
 R;Duhl, D.M.; Stevens, M.E.; Vrieling, H.; Saxon, P.J.; Miller, M.W.; Epstein, Development 120, 1695-1708, 1994
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 Matches
 Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotei; 22-82/Domain: ribonucleoprotein repeat homology <RRM1>
 Query Match
Best Local Similarity
Matches 10; Conserv
 2489
 209 GDSSSGGGGGSSGG 222
 10;
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 Similarity
 GDGVSGGGGGAGAG 2502
 GDGSSGGSGGASTG
 GDGSSGGSGGASTG 14
 GDGSSGGSGGASTG 14
 GDSSSGGGGGSSGG 222
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 72.6%;
71.4%;
 72.6%;
71.4%;
 Score 53; I
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Mismatches
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 18-Aug-1982 #text_change 23-Jul-1999
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Search completed: August Job time: 11.7831 secs

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A;Cross-references: GB:V00602; GB:J02451; GB:)
A;Experimental source: strain 478, Heidelberg R;Goldsmith, M.E.; Konigsberg, W.H.
Biochemistry 16, 2686-2694, 1977
 A;Residues: 1-24,7p',26,'p' <GOL>
C;Comment: Coat protein A is necessary for adsorption of the end of the phage particle.
C;Comment: Bacteriophages fd, M13, and fl are male-specific f
 A;Title: Adsorption protein of the bacteriophage fd: isolation, A;Reference number: A90402; MUID:77242231; PMID:329863 A;Accession: B04266
 A; Reference number:
A; Accession: A04266
A; Molecule type: DNJ
 coat protein A precursor - phage M13
C;Species: phage M13
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
C;Accession: C04266; A04266
C;Accession: C04266; A04266
R;van Wezenbeek, P.M.G.F.; Hulsebos, T.J.M.; Schoenmakers, J.G.
 C;Superfamily: class I filamentous phage coat protein C;Keywords: coat protein F;19-424/Product: coat protein A #status predicted <CF
 A; Residues: 1-424 <BEC>
 A;Cross-references: GB:V00604; GB:J02461; C;Comment: Coat protein A is necessary for end of the phage particle.
C;Comment: Bacteriophages fd, M13, and f1
 Gene 11, 129-148, 1980
A; Title: Nucleotide sequence of the filamentous bacteriophage A; Reference number: A91470; MUID:81067903; PMID:6254849
A; Accession: C04266
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 C; Genetics:
 A; Molecule type: protein A; Residues: 1-24, 'P', 26,
 C; Keywords: coat F
F; 19-424/Product:
 A; Molecule type: DNA
A; Residues: 1-424 < VAN>
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 A;Gene:
 C; Genetics:
 Query Match
Best Local S
Matches 10
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 Superfamily: class I filamentous phage Keywords: coat protein
 Matches
 236 GGGSGGGSEG
236
 1 GDGSSGGSGGASTG 14
 1 GDGSSGGSGGASTG
 10;
 Similarity
 Similarity
 GGGSGGGSEG
 Conservative
 Conservative
 coat protein A #status predicted
 A93690; MUID:79136480; PMID:745987
 71.2%;
 71.2%;
 14
 249
 0,
 0;
 Score 52;
Pred. No.
 Score 52;
 Mismatches
 31-Dec-1991 #text_change 23-Jul-1999
 51; GB:M10377; NID:g14959; PIDN:CAA23862. for adsorption of the virion onto the F-
 ŏ
 predicted <CPA>
 coat protein A
 GB:M10731;
 are male-specific
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 Length 424;
 Length 424
 GB:M10767;
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 GB:M21666;
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 GB:M21667;
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Minimum DB :
 Title:
Perfect score:
Sequence:
 Database
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Total number of hits satisfying chosen parameters:
 OM protein -
 Scoring table:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 4 8
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 seq length: 0 seq length: 2000000000
 protein search, using sw model
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74.0
74.0
71.2
668.5
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 SwissProt_41:*
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Y140_MYCTU
Y309_MYCAU
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RALY_MOUSE
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MSA2_PLAFB
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EMBL; AE006968; AAK45011.1; -.
PIR: F70824; F70824; F70824.
TIGR; MT0772.5; -.
TubercuList; Rv0747; -.
InterPro; IPR000084; PE_region.
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# ALIGNMENTS

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| 3 5         | 2000 (Rel. 39,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
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| בן<br>ק     | To-CCT-2001 (Rel. 40, Last annotation update)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| GN          | RV0747 OR MT0772.5 OR MTV041.21.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| $_{\rm so}$ | Mycobacterium tuberculosis.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| 8           | Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| 8           | Corynebacterineae; Mycobacteriaceae; Mycobacterinom/cecares;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| 0×          | NCBI_TaxID=1773;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| RN          | [1]                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| RP          | SEQUENCE FROM N.A.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| RC          | STRAIN-H37Rv;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| RX          | MEDLINE=98295987; PubMed=9634230;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| RA          | R., Parkhill J., Garnier T., Churcher C                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| RA          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 8 8         | BadCock K. Basham D., Brown D., Chillingworth T., Connor R.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| RA:         | Hornshy T Tarols v vencki T., Gentles S., Hamlin N., Holroyd S.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| RA          | Oliver S., Osborne J., Oneil M. A. Batandroam A. Dorney L.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| RA          | Rutter S., Seeger K., Skelton S., Squares S., Squares S., Squares S.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| Z Z         | Sulston J.E., Taylor K., Whitehead S., Barrell B.G.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 7 X         | "Decliphering the biology of Mycobacterium tuberculosis from the                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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| 2           | [2]                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| RP          | SEQUENCE FROM N.A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| RC          | STRAIN-CDC 1551 / Oshkosh;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| RA          | Fleischmann R.D., Alland D., Eisen J.A., Carpenter I., White O                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| RA          | Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| RA          | Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| R 7         | Descher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
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| RL          | Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| 3 6         | -!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| 36          | SUBFAMILY.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
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RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Badres R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares R.,
Rutter S., Seeger K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
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Hypothetical PE-PGRS family protein Rv1840c.
RV1840C OR MT1888 OR MTCY1A11.04 OR MTCY359.33.
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STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

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Kolonay J.F., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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 Mycobacterium tuberculosis
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 use by modified
 laboratory strains.";
submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential-
-i- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
 SEQUENCE FROM N.A.
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Himmelreich R., Hilbert H., Plage
 Mycoplasma pneumoniae. Bacteria; Firmicutes;
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 -1- SIMILARITY: BELONGS TO THE MG307 / MG309 / MG338 FAMILY.
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 -!- SUBCELLULAR LOCATION:
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RA Kawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrinl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schrinl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RT "Functional annotation of a full-length mouse cDNA collection.",
RL Nature 409:687-680707011
 (Mouse).

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Mus musculus (Mouse).

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Ropkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 TISSUE=Mammary gland, MEDLINE=22388257; Pul
 SEQUENCE FROM N.A. (ISOFORM
 SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN-C57BL/6J; TISSUE-Embryonic |
MEDLINE-21085660; PubMed-11217851;
 *Pleiotropic effects of the mouse lethal yellow explained by deletion of a maternally expressed simultaneous production of agouti fusion RNAs.", Development 120:1695-1708(1994).
 [2]
SEQUENCE FROM N.A.
 RALY_MOUSE STANDARD; PRT; 312 AA. 064012; Q99K76; Q9CXH8; Q9CXK6; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) RNA-binding protein Raly (hnRNP associated with lethal (Maternally expressed hnRNP C-related protein).
 SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-94326666; PubMed-8050375;
Duhl D.M., Stevens M.E., Vrieling
 Michaud E.J., Buitman S.J., Stubbs L.J., Woychik R.P.;
"The embryonic lethality of homozygous lethal yellow mice (Ay/Ay)
associated with the disruption of a novel RNA-binding protein.";
Genes Dev. 7:1203-1213(1993).
 MEDLINE-93307655; PubMed-8319910;
 SEQUENCE FROM N.A. (ISOFORM
 409:685-690(2001).
 PubMed=12477932;
Feingold E.A., Grouse L.H.,
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 CONFLICT
 -I-TISSUE SPECIFICITY: Widely expressed. Expressed in brain, testis, lung, spleen and kidney. Weakly expressed in liver.
-I-DEVELOPMENTAL STAGE: Expressed in the unfertilized egg, in the blastocyst, as well as in the developing embryo and fetus.
-I-DISEASE: Defects in RALY are the cause of lethal yellow mutation (A(y)), a dominant allele that cause embryonic lethality when homozygous, and pleiotropic effects when heterozygous, including yellow pelage, obesity, non-insulin dependent diabetes and increased tumor susceptibility. A(y) is due to a 170 kb deletion RALY and links them to the ASIP/Agouti gene.
-I-SIMILARITY: Contains I RNA recognition mottif (RRM) domain.
 SEQUENCE
 EMBL;
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 VARSPLIC
 PROSITE; PS00030; RRM_RNP_1; 1.
Ribonucleoprotein; RNA-binding; Nuclear protein; Alternative
 PROSITE; PS50102; RRM, 1.
PROSITE; PS00030; RRM_RNP_1;
 EMBL;
 EMBL; AF148458; MGD; MGI:97850;
 InterPro; IPR000504; RNA_rec_mot
 Fahey J., Helton E., Kettéman M., Madan A., Rodrigues S., Sanches Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Grene E.D., Dlickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 +
 SEQUENCE OF 100-135 FROM N.A. (ISO MEDLINE-99431566; PubMed-10500250;
 Richards S., Worley K.C., F
Villalon D.K., Muzny D.M.,
 L; S72641; AAC60688.1; -L; L17076; -; NOT_ANNOTATED_C
L; L17076; -; NOT_ANNOTATED_C
L; BC014851; BAH04851.1; -L; BC016897; AAH16587.1; -
 SUBCELLULAR LOCATION: Nuclear (Probable).
 Event-Alternative splicing; Named isoforms-2;
 PF00076; rrm; 1.; SM00360; RRM; 1.
 . Similarity
10; Conser
 IsoId=Q64012-2;
 IsoId=Q64012-1;
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 72.68;
 ANNOTATED_CDS.
 Sequence=VSP_005805;
 Sequence=Displayed;
 D.M., Sodergren E.J., Lu x., Gibbs R.A., Ketteman M., Madan A., Rodrigues S., Sanch Young A.C., Shevchenko Y., Bouffard G.G., man J.W., Green E.D., Dickson M.C.,
 ₩;
 RNA-BINDING (RRW).
Missing (in isoform 1).
/FTId=VSP_005805.
G -> S (IN REF. 2 AND 3)
T -> I (IN REF. 1).
Score 53; DB Pred. No. 6.1; Mismatches
 BF68E0E8876BFC50 CRC64;
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 suggested by the structure of the membrane penetration domain minor coat protein gap from phage fd.";
Structure 5:265-275[1997).
 MEDLING- Sommer R., Auerswald H., Sehaller H., Sugimoto K., Sugisaki H., Schaller H., Sugimoto K., Sugisaki H., Nucleotide sequence of bacteriophage "Nucleotide sequence of bacteriophage acids Res. 5:4495-4503(1978).
 COAA_BPFD
 MEDLINE-77242231; PubMed-329863; Goldsmith M.E., Konigsberg W.H.; Goldsorption protein of the bacteriophage properties, and location in the virus.";
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MEDLINE=79136480;
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Viruses; ssDNA viruses; Inoviridae;
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 MEDLINE=97184691;
Holliger P., Riec
 STRUCTURE BY NMR OF 20-85
 Biochemistry
 SEQUENCE OF 19-27.
 NCBI_TaxID=10864;
 EMBL; V00602; CAA23851.1;
EMBL; J02451; AAA32309.1;
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 Phage recognition;
SIGNAL 1
 FUNCTION: COAT PROTEIN A IS NECESSARY FOR ADSORPTION OF THE VIRION ONTO THE F-PILUS OF THE HOST CELL.
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 A04266; Z3BPFD.
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1 A precursor (G3P).
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 16:2686-2694(1977).
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 PubMed=9032075;
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with its coreceptor, the C-terminal dom
Structure 7:711-722(1999).
 WEDLINE-81067903; PubMed-6254849;
van Wezenbeek P.M.G.F., Hulsebos T.J.M.,
"Nucleotide sequence of the filamentous
comparison with phage fd.";
Gene 11:129-148(1980).
 COAA_BPM13
P03662;
 SEQUENCE
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 SEQUENCE FROM N.A. SPECIES-Phage f1; MEDLINE-83059882;
 "Nucleotide sequence and bacteriophages f1 and fd. Gene 16:35-58(1981).
 Coat protein
 STRAND
 SEQUENCE FROM N.A. SPECIES=Phage f1; MEDLINE=82211801;
 SEQUENCE FROM N.A. SPECIES=Phage M13; MEDLINE=81067903;
 Bacteriophage
 Bacteriophage
 NCBI_TaxID=10870,
 Viruses;
 Lubkowski J., Hennecke F., Plueckthun A"The structural basis of phage display structure of the N-terminal domains of structure of the N-terminal domains of Nat. Struct. Biol. 5:140-147(1998).
 SPECIES=Phage M13;
 X-RAY CRYSTALLOGRAPHY (1.46 ANGSTROMS)
 Beck E.,
 MEDLINE=98120978; PubMed=9461080;
 Hill D.F., Petersen G.B.;
"Nucleotide sequence of bacteriophage
 Virol.
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 CRYSTALLOGRAPHY (1.85
 Similarity 71.4
10; Conservative
 1 GDGSSGGSGGASTG
 ophage M13, and ophage f1. ; ssDNA viruses;
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 Zink B.;
 44:32-46(1982).
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n A precursor (G3P) (Minor
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Pfam; PF05357; Phage_Coat_A;
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 EMBL; V00604; CAA23862.1; -. EMBL; V00606; CAA23872.1; -. EMBL; J02448; AAA32215.1; -. EMBL; J02466; Z3BPM3.
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SUBUNIT: THERE ARE ABOUT FIVE COPIES OF THIS PROTEIN PER MATURE PHAGE.
DOMAIN: Consists of three domains (N1, N2, and CT). The N2 domains (N1, N2, and CT).
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 Coat protein; Signal; 3D-structure.
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EMBL; Z78020; CAB01461.1;
EMBL; AE007045; AAK46139.:
PIR; C70720; C70720.
TIGR; MT1866; -
 SEQUENCE FROM N.A. STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D.,
 MEDLINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Hoiroyd S
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
 Peterson J., DeBoy R.,
Kolonay J.F., Nelson W.
Delcher A., Utterback I
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
149pothetical PE-PGRS family protein Rv1818c.
RV1818C OR MT1866 OR MTCY1A11.25C.
 Bacteria; Actinobacteria;
Corynebacterineae; Mycoba
NCBI_TaxID=1773;
 Mycobacterium tuberculosis
 SEQUENCE FROM N.A.
 236 GGGSGGGSGGSEG 249
 GDGSSGGSGGASTG
 AAK46139.1; ALT_INIT
 STANDARD;
 Mycobacteriaceae; Mycobacterium,
 and D., Eisen J.A., Carpenter L., White O.,
, Dodson R., Gwinn M.L., Haft D., Hickey E.,
W.C., Umayam L.A., Ermolaeva M.D., Salzberg
T., Weidman J., Khouri H., Gill J., Mikula
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A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Hornsby T., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

A Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

A Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

Tocomplete genome sequence.";

L Nature 393:537-544(1998).

C :- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
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 Corynebacterineae;
NCBI_TaxID=1773;
 SEQUENCE FROM N.A.
STRAIN-H37Rv;
 Bacteria; Actinobacteria;
 Mycobacterium tuberculosis.
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 SEQUENCE
 Hypothetical protein; SIGNAL 1 3
 InterPro; IPR000084; PE_region. Pfam; PF00934; PE; 1.
 EMBL; AL022022; CAA17745.1; -.
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MEDLIND-91218803; PubMed-2090943;
Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
"Sequence comparison of alielic forms of the Plasmodium famerozoite surface antigen MSA2.";

MOI. Biochem. Parasitol. 43:211-220(1990).

MOI. BIOCHEM. PARASITOL IN THE MEROZOITE ATTACHMENT

-1- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT
 MSA2
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DJB1_HUMAN
P25685;
01-MAY-1992
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15-SEP-2003
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DOMAIN
 Eukaryota; Alveolata;
NCBI_TaxID=57266;
 Plasmodium
 Merozoite surface
 -1- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
 GPI-anchor;
 InterPro; IPR001136; MSA_2. Pfam; PF00985; MSA_2; 1.
 EMBL; M60190; AAA29690.1;
 HUMAN
 SEQUENCE
 PROPEP
 SIGNAL
 Malaria;
 ERYTHROCYTE.
SUBCELLULAR LOCATION: Attached to the membrane
 1831
 PLAF8
 (Potential).
 _
 72
 Similarity
9; Conserv
 GDAGAGGNGGSATG
 GDGSSGGSGGASTG
 Membrane;
 GDGSSGGSGGASTG
 falciparum (isolate 7G8
Alveolata; Apicomplexa;
 250
276 AA;
 Merozoite
 Conservative
 STANDARD;
 202
112
22
36
153
225
225
28172
 STANDARD;
 . 34, Created)
. 34, Last sequence upo
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e antigen 2 precursor (
 Glycoprotein; Antigen;
 20
252
276
 68.5%;
64.3%;
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N-B5FA62A70400DEB2 CI
 Score 50; DB Pred. No. 12; 2; Mismatches
 2;
 MEROZOITE SURFAC
HYDROPHOBIC, REN
(BY SIMILARITY)
 PRT;
 POLYMORPHIC REGION.
POLY-THR.
 7G8).
exa; Haemosporida; Plasmodium
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 update)
(MSA-2)
 276 AA
 340
 DB
12;
 SURFACE ANTIGEN
 n J.A.;
the Plasmodium falciparum
 A
 REMOVED DURING
 Signal;
 1;
 (Allelic form 4).
 Length 276;
 CRC64;
 Repeat,
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34, Last sequence update)
42, Last annotation updat

update)

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RC TISSUE-Brain, and Lung;
RX MEDLINE-22388257; PubMed-12477932;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer G.F., Bhat N.K.,
RA Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Wackernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences",

PT. Droc. Natl Acad Sci. H.S. A. 49:16809-16903/20021
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 STRUCTURE BY NMR OF 1-76.
 TISSUE-Placenta; MEDLINE-97131529; PubMed-8975727; MEDLINE-97131529; PubMed-8975727; Hata M., Okumura K., Seto M., Ohtsuka K.; "Genomic cloning of a human heat shock protein 40 (Hsp40) gene (HSPF1) and its chromosomal localization to 19p13.2.";
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Biochem. Biophys. Res. Commun. 197:235-240(1993).
 "Cloning of a cDNA for heat-shock protein hsp40, a bacterial DnaJ.";
 Ohtsuka K.
 MEDLINE-94071949; PubMed-8250930
 "A human homologue of the Escherichia coll DnaJ heat-shock protein.";
Nucleic Acids Res. 19:6645-6645(1991).
 DnaJ homolog subfamily B member 1 (Heat shock 40 kDa protein 1) (Heat shock protein 40) (HSP40) (DnaJ protein homolog 1) (HDJ-1).
DNAJB1 OR HSPF1 OR DNAJ1 OR HDJ1.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 SEQUENCE FROM N.A., AND
 MEDLINE-92093635;
 Homo sapiens (Human)
Eukaryota; Metazoa;
 send an
non-profit institutions as long as its content is and this statement is not removed. Usage by and for requires a license agreement (See http://www.isb-sib.an email to license@isb-sib.ch).
 Sci. U.S.A. 99:16899-16903(2002)
 PubMed=1754405
 SEQUENCE OF 1-48.
 BETWEEN HSC70 AND HIP.
 STIMULATE ITS
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 human
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 homologue
 a collaboration - MBL outstation -
 Hsp40
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ID LORI_MOUSE
AC P18165;
DT 01-NOV-1990 (
DT 01-NOV-1990 (
DT 28-FEB-2003 (
DE LORICTIAN
GN LORI
GN LORI
GN LORI
GN MUS MUSCUlus
OC MARMBALIA; Eut
OX NCBI_TAXID=1C
RN [1]
RN [1]
RN SEQUENCE FROM
RX MEDLINE=90275
RA MEDLINE=1 T., HG
 밁
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 RESULT
 Query Match
Best Local
 Matches
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
 HELIX
TURN
HELIX
SEQUENCE
 MEDLINE-90275605; p
Mehrel T., Hohl D.,
 SEQUENCE FROM N.A.
 TURN
HELIX
TURN
 CONFLICT
CONFLICT
CONFLICT
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 CONFLICT
 HELIX
 TURN
 PROSITE; PROSITE;
 PRINTS; PR00625; DNAJPROTEIN SMART; SM00271; DnaJ; 1.
 HELIX
 CONFLICT
 CONFLICT
 Pfam; PF00226; DnaJ; 1
Pfam; PF01556; DnaJ_C;
 EMBL;
EMBL;
EMBL;
 DOMAIN
 Heat shock;
 InterPro; IPR002939; DnaJ_C.
InterPro; IPR001623; DnaJ_N.
InterPro; IPR003095; Hsp_Dna
 Genew;
 *IL; X62421; CAA44287.1; -.
IL; D49547; BAA08495.1; -.
BL; D5429; BAA12819.1; -.
IL; BC002352; AAH02352.1; -.
SL; BC019827; AAH19827.1; -.
SL; JN0912; JN0912.
 GO: 0003773; F: heat shock
 74
 604572;
 IHDJ;
 S20062; S20062.
 1 GDGSSGGSGGASTG
 Similarity 64.3
9; Conservative
 HGNC:5270; DNAJB1.
 GSGPSGGSGGGANG
 PS00636; DNAJ_1; 1.
PS50076; DNAJ_2; 1.
 30
33
33
34
55
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58
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67
 ; Chaperone; 70
1 70
11 11
13 28
 (Rel. 16, Created)
(Rel. 16, Last seq
(Rel. 41, Last ann
 AA;
 STANDARD;
 PubMed=2190691;
 150
1183
320
320
10
114
129
29
31
35
40
56
66
66
66
67
71
 Rothnagel J.A.,
 68
136
 68.5%;
64.3%;
 Last sequence update)
Last annotation update)
 Hsp_DnaJ
 87
 14
 3D-structure
 WW;
 REF. 1).

G -> L (IN REF. 1).

SGGGANGTSSEXTFHGDPHAMFAEFFGGRNPFDTFFGQRNG
EEGMDIDDPFSGFPM -> TAREPMYPLSATHSMETLMPCL
LSSSVAEIPLTPFLGSGTGRKAWTLMTHSLASLW (IN
REF. 1).

R -> C (IN REF. 1).

M -> T (IN REF. 1).

V -> A (IN REF. 1).
 Score 50;
Pred. No.
 . . .
 Craniata; Vertebrata;
Sciurognathi; Muridae;
 L -> Q (IN REF. 1
RGASDEEIKRAYRRQA
 PRT;
 protein activity;
 -DOMAIN
 17545098B0C196DF CRC64;
 Mismatches
 Q (IN REF. 1).
Longley M.A.,
 481
 DB
15;
 ξ
 4
 Length 340;
 Indels
 AALGRGDQAGLPPPG
 Euteleostom1;
<u>٥</u>:
 0
 Gaps
 (IN
 0
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T711_HT 7711_HT 7711_H
 T7L1_HUMAN SIRVER
T7L1_HUMAN SIRVER
Q9HCS4; Q9NP00;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update
1 15-SEP-2003 (Rel. 42, Last annotation update
 Query Match
Best Local
 Matches
 EMEL; W34398; AAA39444.1; EMEL; W09189; AAA82152.1; PIR; A35628; A35628. HSSP; P02876; 9WGA. MGD; MGI:96816; Lor.
 Cheng C., Lichti U., Bisher M.E.,
Yuspa S.H., Roop D.R.;
"Identification of a major keratin
loricrin.";
Cell 61:1103-1112(1990).
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 differentiation-specific expression.";
J. Biol. Chem. 270:10792-10799(1995).
-I- FUNCTION: MAJOR KERATINOCYTE CELL ENVELOPE PROTEIN.
-I- SUBUNIT: MONOMERS ARE CROSSLINKED BY DISULFIDE AND
 "The proximal promoter of the mouse functional AP-1 element and directs
 _HUMAN
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 Roop D.R.;
 Disepio D., Jones
 SEQUENCE FROM N.A.
 MEDLINE=95256248;
Castrop J., van Norren K., Clevers H.C.;
"A gene family of HMG-box transcription
1.";
 SEQUENCE
 Keratinization.
 TISSUE=Fetal lung;
MEDLINE=20535962; Pu
Sagara N., Katoh M.;
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 TCF7L1 OR TCF3
 SEQUENCE OF 331-419 FROM N.A. MEDLINE=92158676; PubMed=1741298;
 regulation."
 cancer cell line MKN28
 SEQUENCE FROM N.A.
 Homo sapiens
 "Mitomycin
 NCBI_TaxID=9606;
 GLUTAMYL) LYSINE ISODIPEPTIDE BONDS.
 187
 L
 Similarity
 GDGSSGGSGGASTG
 GGGSSGGCGGGSGG 200
 481 AA;
 C resistance induced by TCF-3 overexpression line MKN28 is associated with DT-diaphorase
 Conservative
 60:5959-5962(2000).
 (Human).
tazoa; Chordata;
heria; Primates;
 PubMed=7738016;
A., Longley M.A
 PubMed=11085512;
 37830 MW;
 68.5%;
71.4%;
 14
 keratinocyte cell envelope protein,
 0;
 Score 50;
Pred. No.
 м.а.,
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 97349A786FF239FE CRC64;
 Mismatches
 Steven
 Bundman
 loricrin gene contains
 keratinocyte-specific but not
 update)
 588
 update)
 transcription
 DВ
 A.C.,
 factors with homology to
 AA
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 Length 481;
 Rothnagel J.A.,
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RESULT 13
YD25_MYCTU
ID YD25_MYCTU
AC Q10637;
DT 01-OCT-1996 (
DT 01-OCT-1996 (
 Query Match
Best Local S
Matches
 EMBL; AB031046
EMBL; X62870;
HSSP; P27782;
 This SWI
between
 mammary gland epithelium.";
Am. J. Pathol. 154:29-35(1999).
 MEDIINE-99113953; PubMed-9916915;
Barker N., Huls G., Korinek V., Clevers H.;
"Restricted high level expression of Tcf-4 protein in intestinal
 TISSUE-SPECIFICITY
 Nucleic Acids Res. 20:611-611(1992).
 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 GO; GO:0005634; C:nucleus; NAS.
GO; GO:0003700; F:transcription factor activity; NAS.
GO; GO:0006325; P:establishment and/or maintenance of chromat.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
GO; GO:0030111; P:regulation of Wnt receptor signaling pathway; NI
InterPro; IPR000910; HMG_12_box.
Pfam; PF00505; HMG_box; 1.
 the European Bioinformatics Institute. They use by non-profit institutions as long a modified and this statement is not removed.
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 MIM;
 DOMAIN
DOMAIN
 PROSITE; PS50118; HMG_BOX_2; 1.
Transcription regulation; Activator; Repressor;
Nuclear protein; DNA-binding; Wnt signaling path
DOMAIN 1 74
CTNNB1 BINDING (BY
 Genew;
 DNA_BIND
 SEQUENCE
 DOMAIN
 complex (By similarity).

Complex (By similarity).

SUBCELLULAR LOCATION: Nuclear.

SUBCELLULAR LOCATION: Nuclear.

TISSUE SPECIFICITY: Detected in hair follicles and skin

RETATINGUES, and at lower levels in stomach epithelium.

Keratinocytes, and at lower levels in stomach epithelium.

DOMAIN: The putative Groucho interaction domain between the N-

DOMAIN: The putative Groucho interaction domain between the N-

DOMAIN: The putative Groucho interaction domain between the N-

DOMAIN: The putative Groucho interaction domain and the HMG-box is necessary for

terminal CTNNB1 binding domain and the HMG-box is necessary for
 FUNCTION: Participates in the Wnt signaling pathway. Binds to DN and acts as repressor in the absence of CTNNB1, and as activator in its presence. Necessary for the terminal differentiation of epidermal cells, the formation of keratohyalin granules and the development of the barrier function of the epidermis (By
 SIMILARITY: Belongs to the TCF/LEF family. SIMILARITY: Contains 1 HMG box domain.
 similarity). Down-regulates NQO1, leading to
 SUBUNIT:
 resistance
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 604652;
 (By similarity)
 AB031046; BAB18185.1; -.
 Pathol.
 11
 X62870; CAB91064.1;
P27782; 2LEF.
HGNC:11640; TCF7L1
 SM00398; HMG;
 ш
 9,
 Similarity
 GGGGGGGGSSAG
 GDGSSGGSGGASTG
 117
588
 Binds the armadillo repeat of CTNNB1 and
 Conservative
 A,
 STANDARD;
 PubMed=9916915;
., Korinek V., Clevers H.;
 TCF7L1.
 414
427
29
 326
62630
 68.5%;
 24
 14
 MW;
 Score 50;
Pred. No.
 NUCLEAR LOCALIZATION GLY-RICH.
 PRO-RICH
 HMG BOX.
 PRT;
 82FB0C9300482A02 CRC64;
 red. No. 26;
Mismatches
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 MEDLINE-98295987; pubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
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 SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg;

Belcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula
 This
 "Whole genome comparison of laboratory strains.";
Submitted (APR-2001) to the
-i- SIMILARITY: BELONGS TO 7
 16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PE-PGRS family protein Rv1325c precursor.
RV1325C OR MT1367 OR MTCY130.10C.
 SEQUENCE
 DOMAIN
 Hypothetical
SIGNAL
 Pfam; PF00934; PE;
 TIGR; MT1367; -.
TubercuList; Rv1325c;
 PIR; A70770; A70770.
 EMBL; AE007010; AAK45630.1;
 EMBL; 273902; CAA98089.1; -
 Bishai W.;
 SEQUENCE FROM N.A.
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 Mycobacterium tuberculosis
 nterPro;
 SUBFAMILY.
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 Similarity
8; Conserv
 PD001223;
GNGGTGGTGGTGTG
 GDGSSGGSGGASTG 14
 IPR000084; PE_region.
 Conservative
 protein;
 PE_region;
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132
135
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 49575
 68.5%;
57.1%;
 Repeat;
 the EMBL/GenBank/DDBJ databases.
TO THE MYCOBACTERIAL PE FAMILY. PGRS
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 GLY-RICH.
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G -> D (I
G -> D (I
L -> F (I
 Score 50;
Pred. No.
 Pred. No. 26;
3; Mismatches
 RV1325C
 HYPOTHETICAL PE-PGRS FAMILY PROTEIN
 POTENTIAL.
 Signal; Complete proteome
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 RESULT 15
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 Query Match
Best Local :
 Genes Dev. 4:1516-1527(1990).

-i- FUNCTION: INVOLVED IN THE DEVELOPMENT OF THE DROSOPHILA SYSTEM AND OCELLAR VISUAL STRUCTURES.

-i- SUBCELLULAR LOCATION: Nuclear (Probable).

-i- DEVELOPMENTAL STAGE: EXPRESSED IN THE ANTERIOR REGION OF EMBRYO BEFORE CELLULARIZATION AND BECOMES LOCALIZED TO TEMBRYO BEFORE CELLULARIZATION AND BECOMES LOCALIZED TO TEMBRYO BEFORE CELLULARIZATION AND BETOMES LOCALIZED TO TEMBRYO BEFORE STADLED REGION FOLLOWING GASTRULATION.

-i- DOMAIN: CONTAINS MULTIPLE REPEATS CONSISTING OF SINGLE AGENCY AND AND PAIRS OF AMINO ACIDS OF TAXABLE AND ASIN AND PAIRS OF AMINO ACIDS
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 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 Finkelstein R., Smouse D., Capaci T.M., Spradling A.C., Perrimon N., "The orthodenticle gene encodes a novel homeo domain protein involve in the development of the Drosophila nervous system and ocellar visual structures.";
 This
 DROME
 SEQUENCE
 ProDom; PD000010; Homeobox; 1. SMART; SM00389; HOX; 1.
 FlyBase; FBgn0004102; oc. InterPro; IPR001356; Homeobox. InterPro; IPR007104; Paired_homeo. Pfam; PF00046; homeobox; 1.
 EMBL; X58983; CAA41732.1;
PIR; A35912; A35912.
HSSP; P06601; IFJL.
 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
 Transcription
DNA_BIND 7
 PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
 between
 MEDLINE=91071580; PubMed=1979296;
 SEQUENCE FROM N.A.
 P22810;
 HMOC_DROME
 DOMAIN
 FRANSFAC; T02078;
 SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX FAMILY.
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 352
 Similarity
9; Conserv
 GDGSSGGSGGASTG
 protein orthodenticle
 GGGGGGGGGASSG
 DNA-binding; Developmental protein; Nuclear protein;
 248
671 AA;
 Conservative
 n regulation;
73 132
229 266
229 247
229 247
248 266
 STANDARD; 09VVX2;
 STANDARD;
 69666 MW;
 64.3%;
 14
 Repeat
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Pred. No.
 HOMEOBOX.
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RA Beeson K.Y. Benos P.V. Berman B.P. Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Colsin K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Doubin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.
RA Fosler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M., H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.
RA Mount S.M., Woy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rahert K., Remington K., Sannders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Waissenbach J.,
RA Wang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.
RA Zheng X.H., Zhong W., Rubin G.M., Venter J., Sith H.O.
RA Zheng X.H., Zhong W., Rubin G.M., Venter J.,
RC 1- FUNCTION: Receptors for Mnt proteins. Most of frizzled receptors
 28-FEB-2003
28-FEB-2003
15-SEP-2003
Frizzled pro
 Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Walling J.F., Agbayan B., An H.-J., Andrews Pfannkoch C., Baldwin D., Baldwin D
 SEQUENCE FROM N.A., & MEDLINE-96353971; Pul Bhanot P., Brink M.,
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Neoptera; Endopterygota; Diptera; Brachycera; Muscoephydroidea; Drosophilidae; Drosophila.
 Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Hexa
 MEDLINE=20196006; PubMed=10731132;
 SEQUENCE FROM N.A.
 Wingless
 Andrew D., Nathans J., Nusse R.;
"A new member of the frizzled family from Drosophila functions as
 FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to be required to the canonical pathway, as PKC seems to be required to wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to be required to the canonical pathway as PKC seems to be required to wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to be required to wnt-mediated inactivation of GSK-3 kinase.
 to involve interactions with G-proteins. Required the cytoskeletons of epidermal cells to produce a of cuticular hairs and bristles.
 OR.
 ۳.,
 ed protein 2 precursor (Frizzled-2) (dFz2). CG9739/CG14083.
 382:225-230(1996).
 receptor.
 (Rel.
 ., AND BINDING TO WINGLESS THROUGH FZ DOMAIN.
PubMed-8717036;
J., Samos C.H., Hsieh J.C., Wang Y., Macke J.P.,
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 InterPro; IPR000539; Frizzled.
InterPro; IPR000024; Fz_domain
InterPro; IPR0000832; GPCR_secro
Pfam; PF01534; Frizzled; 1.
Pfam; PF01392; Fz; 1.
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 PRINTS; PRO0489; FRIZZI SMART; SM00063; FRI; 1.
 Flybase; FBgn0016797; fz2.

GO; GO:0015021; C:integral to membrane; NAS.

GO; GO:0017147; F:wnt-protein binding activity; IDA.

GO; GO:0007163; P:establishment and/or maintenance of cell

GO; GO:0016055; P:wnt receptor signaling pathway; IDA.
 EMBL; AE003518; AAF49185.2; -. PIR; S71786; S71786.
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 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
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 PROSITE; PS50038; FZ; 1.
PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
 the European Bioinformatics Institute. Th
 TRANSMEM
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 -!- SIMILARITY: Contains 1 frizzled (FZ)
 SIMILARITY: BELONGS
 DOMAIN: The fz
 between 15 and 70 per cent of egg length, including the invaginating cells of the ventral furrow. Stripe pattern is emerging by early stage 8. From stage 9 and continuing throughout embryogenesis, expression is seen in the developing CNS. At stage 10, expressed in 15 stripes in the presumptive head and trunk regions, in the posterior midgut primordium, in a subset of cells of anterior midgut invagination and in the procephalic lobe. At stage 12, expression declines in epidermis and increases in the midgut and visceral mesoderm. At stage 17, only expressed in the CNS, hindgut and dorsal vessel.
 DOMAIN:
 the Wnt/beta-catenin signaling pathway (By similarity). DOMAIN: The fz domain is involved in binding with Wnt ligands.
 DEVELOPMENTAL STAGE: Expression starts at stage 6 in
 RECEPTORS
 U65589; AAC47273.1;
 an email to license@isb-sib.ch).
 family; Receptor;
 316
337
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508
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78
 Lys-Thr-X-X-X-Trp motif is involved in the activation
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 EXTRACELLULAR (POTENTIAL)
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6C510F13CBAFB096 CRC64;
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 (See http://www.isb-sib.ch/announce/
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|   |   |  | Search completed: August 20, 2003, 12:34:50<br>Job time : 7.42436 secs | Qy 3 GSSGGSGGASTG 14<br>       :: <br>Db 190 GSSGGSGGSGS 201 | Best Local Similarity 75.0%; Pred. No. 30; Matches 9; Conservative 2; Mismatches |
|---|---|--|------------------------------------------------------------------------|--------------------------------------------------------------|----------------------------------------------------------------------------------|
|   |   |  |                                                                        |                                                              | 1;                                                                               |
|   |   |  |                                                                        |                                                              | Indels                                                                           |
|   |   |  |                                                                        |                                                              | 0;                                                                               |
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Result
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 Title:
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Sequence:
 Database
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Minimum DB seq
Maximum DB seq
 Total number of hits satisfying chosen parameters:
 Scoring table:
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14
16
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 length: 0
length: 2000000000
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 US-09-512-082-20
 830525 seqs, 258052604 residues
 August 20,
 SPTREMBL_23:*
 GDGSSGGSGGASTG 14
 GenCore version Copyright (c) 1993 - 2003
 sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
 sp_bacteria: *
 sp_phage: *
 sp_mammal:*
 sp_invertebrate: *
 sp_human:∗
 sp_fungi:*
 sp_archea: *
 sp_organelle:*
 sp_rodent:*
 sp_vertebrate:*
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 Length
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Q9U181
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08vj19 mycobacteri
091k43 arabidopsis
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| 5    | 51   | 51                 | 51   | 51   | 51   | 51   | 51     | 51                 | 51                 | 51                | 51         | 51         | 51   | 51                 | 51         | 52                 | 52   | 52         | 52   | 52                | 52           | 52   | 52                | 52     | 52   | 52    | 53     | 53                 |
| 69.9 | 69.9 | 69.9               | 69.9 | 69.9 | 69.9 | 69.9 | 69.9   | 69.9               | 69.9               | 69.9              | 69.9       | 69.9       | 69.9 | 69.9               | 69.9       | 71.2               | 71.2 | 71.2       | 71.2 | 71.2              | 71.2         | 71.2 | 71.2              | 71.2   | 71.2 | 71.2  | 72.6   | 72.6               |
| 1715 | 1507 | 837                | 775  | 731  | 588  | 549  | 542    | 501                | 491                | 449               | 436        | 424        | 399  | 384                | 261        | 1489               | 1472 | 1217       | 1079 | 1016              | 622          | 585  | 509               | 429    | 203  | 203   | 1001   | 486                |
|      |      | 16                 |      |      |      |      |        |                    |                    |                   |            |            |      |                    |            |                    |      |            |      |                   |              |      |                   |        |      |       | 11     |                    |
|      |      |                    |      |      |      | _    | Q9SV40 |                    |                    | _                 | Ω          |            |      |                    |            | 053559             |      |            |      | 0                 |              |      |                   | Q26977 |      | o     |        |                    |
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# ALIGNMENTS

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01-OCT-2000 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
P0009G03.13 protein.
P0009G03.13.
 STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0009503.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002522; BAB03613.1; -.
Gramene; O9LGJ3; -.
InterPro; ITR000834; Zn_carbOpept.
PROSITE: P800133; CARBOXYPEPT_ZN_2; 1.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
 SEQUENCE FROM N.A.
 Oryza sativa (Rice).
 Q9LGJ3
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 10;
 Similarity 71., 10; Conservative
 ; IPRO00834; Zn_carbopept.
PS00133; CARBOXYPEPT_ZN_2; 1.
PS07 AA; 58755 MW; F9069BABA60A271D CRC64;
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 GDSSGGGGGGGSTG
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15, Last sequence update)
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A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

A Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

A Rutter S., Seeger K., Skelton S., Squares S., Squares S.,

A Rutter S., Seeger K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

"Complete genome sequence.";

Nature 393:537-544(1998).

"REMEL; AL009198; CAA15752.1; **.
 Query Ma
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 O50396;

01-JUN-1998 (TrEMBLrel. 0

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01-MAR-2003 (TrEMBLrel. 2

PGRS-family protein.

RV3367 OR MTV004 25.
 SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Ei.

Peterson J., DeBoy R., Dodson R

Kolonay J.F., Nelson W.C., Umay,

Delcher A., Utterback T., Weidm
 Q8VJ19 PRELIMINARY;
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PE_PGRS family protein.
MT3476.
 InterPro; IPR002952; IInterPro; IPR000084; IInterPro; IPR002173; IPF002173; IPF6am; PF00934; PE; 1.
 Corynebacterineae; Mycobacteriaceae; Mycobac
NCBI_TaxID-1773;
 Complete SEQUENCE
 Mycobacterium tuberculosis. Bacteria; Actinobacteria; A
 STRAIN-H37Rv;
 SEQUENCE FROM N.A.
 Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
 PRINTS; PR01228; EGGSHELL.
ProDom; PD001223; PE_region; 1.
PROSITE; PS00583; PFKB_KINASES_1; 1.
 TubercuList; Rv3367;
 laboratory strains.";
submitted (APR-2001) to the
EMBL; AE007154; AAK47814.1;
 Bishai W.;
 InterPro;
 Whole genome comparison of Mycobacterium tuberculosis clinical and
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DNA RES. 7:217-221(2000).
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EMBL; AP000377; BAB01851.1;
HSSP, P11362; IFGK.
 InterPro; IPR000084; PE_re
InterPro; IPR002173; PfkB.
Pfam; PF00934; PE; 1.
 PRINTS; PR01228; EGGSHELL.

PRODOM; PD001223; PE_region; 1.

PROSTTE; PS00588; PFKB_KINASES_1; 1.

SEQUENCE 628 AA; 53828 MW; 9F62B1E7CC2C567E CRC64;
 01-OCT-2000 (TIEMBLIE1. 15, Created)
01-OCT-2000 (TIEMBLIE1. 15, Last sequence update)
01-MAR-2003 (TIEMBLIE1. 23, Last annotation update)
similarity to receptor protein kinase.
 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core es
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 Q9LK43;
 Q9LK43
 Kaneko T., Kato T., (Submitted (JUL-1999)
 SEQUENCE FROM N.A. STRAIN-Columbia;
 eurosids II; Brassicales; Brassicaceae; NCBI_TaxID=3702;
 pfam; pF00560; LRR; 9;
pfam; pF00050; pkinase; 1.
probom; pp000001; prot_kinase; 1.
prOSITE; pS50502; LRR_PS; 4.
pROSITE; pS00107; pROTEIN_KINASE_ATP; 1.
pROSITE; pS00108; pROTEIN_KINASE_ST; 1.
pROSITE; pS00108; pROTEIN_KINASE_ST; 1.
 InterPro; IPR001611; LRR.
InterPro; IPR007090; LRR.
InterPro; IPR000719; Prot
InterPro; IPR002290; Ser_
 MEDLINE-20363099; PubMed-10907853;
 SEQUENCE FROM N.A.
 Nakamura Y.;
 "Structural analysis
 ATP-binding; Kinase;
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RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,

RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

RA Rutter S., Seeger K., Skelton S., Squares R.,

RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

RA Tuberphering the biology of Mycobacterium tuberculosis from the

RA RALO2202; CAA17744.1; -.

RA LAU2202; CAA17744.1; -.

RT Tuberculist; Rv3507; --

REMBL; ALO2202; CAB17744.1; -.

R Tuberculist; Rv3507; --

R Tuberculist; Rv3507; --

R Tuberculist; Rv3507; --

RA InterPro; IPR0002173; pfkB.

REMBL; ALO2202; Eggshell.

R InterPro; IPR002173; pfkB.

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 PRINTS; PR01228; EGGSHELL.
PROSITE; PS00583; PFKB_KINASES_1;
 01-JUN-1998 (TrEMBLrel.
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01-MAR-2003 (TrEMBLrel.
 053552
 EMBL; AF
 Mycobacterium tuberculosis. Bacteria; Actinobacteria; A
 PGRS-family protein.
RV3507 OR MTV023.14.
 Iranfar N., Loomis W.F.;
Submitted (JUL-1998) to the
EMBL; AF076601; AAC31540.1;
 SEQUENCE FROM N.A.
 Corynebacterineae;
NCBI_TaxID=1773;
 Dictyostelium discoideum (Slime mold)
Eukaryota; Mycetozoa; Dictyosteliida;
 Developmental DG1105.
 SEQUENCE
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 NCBI_TaxID-44689;
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 1 GDGSSGGSGGASTG 14
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A; 112463 MW;
 Mycobacteriaceae;
 75.3%;
64.3%;
 110624 MW;
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 Actinobacteridae; Actinomycetales; cteriaceae; Mycobacterium.
 Score 55; DB Pred. No. 55; 3; Mismatches
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RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davies R., Devlin K., Feltwell T., Gentles S., Hamiln N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Rutter S., Seeger K., Skelton S., Squares R.,

Complete S., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:537-544(1998).
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InterPro; IPR002173; I
Pfam; PF00934; PE; 1.
PROSITE; PS00583; PFKI
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01-MAR-2003 (TrEMBLrel. 23, Last anno
PGRS-family (PE_PGRS family protein).
RV2490C OR MT2564 OR MTV008.46C.
 SEQUENCE FROM N.A.
 Corynebacterineae;
 Bacteria; Actinobacteria;
 Mycobacterium tuberculosis.
 SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzbe
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Miku
 "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.".

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL: AE007163; AAK47970.1; -.
 Mycobacterium tuberculosis.
Bacteria; Actinobacte
Corynebacterineae; Mycobacteriaceae;
RCBI_TaxID=1773;
 SEQUENCE
 TIGR; MT3612;
 MT3612
 PE_PGRS family protein
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9; Conserv
 GDGGAGGAGGAANG
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 1384 AA;
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A; 110839 MW;
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STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.

Kolonay J.F., Nelson W.C., Weldman J., Khouri H., Gill J., Mikula
 laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ
EMBL; AL021246; CAA16067.1; ALT_INIT.
EMBL; AE007093; AAK46868.1; -.
 O92K72 PRELIMINARY; PRT; 5:
092K72: 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequen
01-MAR-2002 (TrEMBLrel. 20, Last annota
Hypothetical lipoprotein transmembrane.
R01981 OR SMC04335.
 proDom; pD001223; PE_region; 1.
prOSITE; pS00583; pFKB_KINASES_1; 1.
prOSITE; pS01287; RTC; 1.
 TIGR; MT2564; -. TubercuList; Rv2490c; -.
 Bishai W.;
 Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S. Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont sinorhizobium meliloti strain 1021."; Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 InterPro; IPR000084; PE_region.
InterPro; IPR002173; PfkB.
InterPro; IPR000228; RNA3'_term_cycl
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 Whole genome comparison of
 SEQUENCE FROM N.A. STRAIN=1021;
 Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria;
Rhizobiaceae; Sinorhizobium.
 Pfam; PF00934; PE;
 MEDLINE=21396507; PubMed=11481430;
 NCBI_TaxID=382;
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 GDGGAGGAGGTQTG 1395
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 GSGSMGGSGGGSSG
 GDGSSGGSGGASTG 14
 1665 AA;
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 5230 MW;
 75.3%;
64.3%;
 133700 MW;
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 Mycobacterium tuberculosis clinical and
 Last sequence up
 Score 55; DB
Pred. No. 67;
2; Mismatches
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 85B5DE2FEB118302 CRC64;
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 Eukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae; Glycine
 Extensin-like protein. Glycine max (Soybean).
 pfam; pF00234; tryp_alpha_amyl;
smART; SM00499; AAI; 1.
SEQUENCE 179 AA; 17117 MW; 7
 "A Glycine max root specific pusubmitted (JUN-2002) to the EMI
EMBL; AF520576; AAN75351.1; -.
InterPro; IPR003612; AAI.
 Nielsen P.S., Clark A.J., Oliver R.B., Huber M., Spanu "HCf-6, a novel class II hydrophobin from Cladosporium Microbiol. Res. 156:1-5/2001).
EMBL; AJZ51294; CAC27407.1; -.
InterPro; IPR002952; Eggshell.
PRINTS; PR01228; EGGSHELL.
CHAIN 17 184 HYDROPHOBIN.
 STRAIN-cv. maple ar Farah S., Singh J.;
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 STRAIN=Race 4;
MEDLINE=21265535; PubMed=11372645;
MEDLINE=21265535; PubMed=11372645;
 Cladosporium fulvum (Fulvia fulva).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Dothideomycetes et Chaetothyriomycetes incertae sedis;
Mycosphaerellaceae; mitosporic Mycosphaerellaceae; Cla
 Q9C2X0
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 NCBI_TaxID=3847;
 Hydrophobin.
HCF-6.
053844;
01-JUN-1998
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 NCBI_TaxID=5499;
 82
 99
 1 GDGSSGGSGGAST 13
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82 GSGGSGGSGGSST 94
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 Similarity 9; Conserv
 GNGGNGGSGGGNTG
 GDGSSGGSGGASTG 14
 184 AA;
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Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,

Badcock K., Basham D., Brown D., Chillingworth T.,

Davles R., Deviln K., Feltwell T., Gentles S., Haml
 O53809 PRELIMINARY; PRT; 783 AA.
O53809; O1-JUN-1998 (TIEMBLrel. 06, Created)
O1-JUN-1998 (TIEMBLrel. 06, Last sequence update)
O1-MAR-2003 (TIEMBLrel. 23, Last annotation update)
PGRS-family protein (PE_PGRS family protein).
RV0746 OR MT0772.1 OR MT0741.20.
 Mycobacterium tuberculosis.

Bacteria; Actinobacteria, Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

NCBI_TaxID-1773;
 SEQUENCE FROM N.A.
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STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzber Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mik
 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Ogborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
 laboratory strains.";
Submitted (APR-2001) to the
EMBL; AL022004; CAA17639.1;
EMBL; AE006974; AAK45096.1;
 TubercuL1st; Rv0833; -.
 "Whole genome comparison
 MEDLINE-98295987;
Cole S.T., Brosch
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 te genome sequence.
393:537-544(1998).
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Synechocystis sp. strain PCC6803. II. Sentire genome and assignment of potenti DNA Res. 3:109-136(1996).

EMBL; D90907; BAA17634.1; ...
Interpro; IPR003644; Calx_beta.
Interpro; IPR002860; GH_BNR.
Interpro; IPR001343; Hemlysn_Ca_bind.
Interpro; IPR000413; Integrin_alpha.
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 P73590;
01-FEB-1997 (
01-FEB-1997 (
01-OCT-2002 (
Hypothetical
SLR1403.
 Whole genome comparison of M laboratory strains "; Submitted (APR-2001) to the ELEMBL; AL021958; CAAL7513.1; EMBL; AE006968; AAK45009.1; TIGR; MT0772.1; """
 Miyajima N., Hirosawa M., Sugiura M., Sasamizı
Hosouchi T., Matsuno A., Muraki A., Nakazaki N.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yan
 Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales;
NCBI_TaxID=1148;
 SEQUENCE FROM N.A. MEDLINE-97061201; PubMed-8905231;
 COMPLICT
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 Tabata S.;
"Sequence analysis
 P73590
 PRINTS;
 Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Moliver S., Osborne J., Quail M.A., Rajandream M.A., Rog Rutter S., Seeger K., Skelton S., Squares S., Squares R. Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis complete genome sequence."; Nature 393:537-544(1998).
 ProDom;
 Pfam; PF00934;
 InterPro; IPR000084; InterPro; IPR000817;
 Peterson J., DeBoy R., Dodson R., Gwinn M., i
Kolonay J.F., Nelson W.C., Umayam L.A., Ermol
Delcher A., Utterback T., Weldman J., Khouri
 STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D.,
 Bishai W.;
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Search completed: August 20, 2003, 12:40:15 Job time : 30.593 secs
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Best Local Similarity 71.4
Matches 10; Conservative
 Query Match 72.6%; Score 53; DB 5; Length 362; Best Local Similarity 71.4%; Pred. No. 25; Matches 10; Conservative 1; Mismatches 3; Indels
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PRINTS; pR001185; INTEGRINA.
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SMART; SM00237; Calx_beta; 1.
SMART; SM00237; Calx_beta; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete B34D83B005D0717A CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 37.3 kDa protein.
 "A physical map of the Leishmania major Friedlin genome."; Genome Res. 8:135-145(1998).

EMBL; AL133468; CAB63136.1; -
Hypothetical protein.
SEQUENCE 362 AA; 37271 MW; 4FB3EC8976A956C2 CRC64;
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STRAIN-Friedlin;
MEDLINE-98146435; PubMed-9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
 Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
 Q9U181
 SEQUENCE FROM N.A.
STRAIN=Friedlin;
Wedler H., Hilbert H., Duesterhoeft A., Ivens A.C., Murphy L.,
Wedler H., Rajandream M.A., Barrell B.G.;
Quall M., Rajandream M.A., Barrell B.G.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 2489 GDGVSGGGGGAGAG 2502
 301 GAGSSGGGGGAAVG 314
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 Kinetoplastida; Trypanosomatidae; Leishmania.
 Score 54; DB 16; Length 3016; Pred. No. 1.7e+02; 0; Mismatches 4; Indels
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